SUMMARIES

Result No. S	,	ttgatctaa 2139 9 1	10 1 11 1 12 1 12 1 13 1 14 0 15 15	20 21 21 21 22 22 22 22 22 22 22 22 22 22	23 24 1 5 25 . 26		****	*****	A1997. DAT:* DE POFPH A1999. DAT:* XX A1999. DAT:* XX A2000. DAT:* KW DIPP-7 KW DPP-7 KW DPP-7
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 12:14:56 ; Search time 113 Seconds (Without alignment)	Title:  WS-10-008-355-1  Perfect score: 3820  Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa	Scoring table: BLOSUM62  Xgapop 10.0 , Xgapext 0.5  Ygapop 10.0 , Ygapext 0.5  Fgapop 6.0 , Fgapext 7.0  Delop 6.0 , Delext 7.0	of length: 0	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -WODEL-frame+_n2p.model -DEV=xlp -Q-CGn2_L1V3PPQ_SEPO1/VOISIO08355/runat_16052003_110337_9308/app_guery.fasta_1.2311 -Q-CG02_L1V3PPQ_SEPO1/VOISIO08355/runat_16052003_110337_9308/app_guery.fasta_1.2311 -DB-A_Geneseq_101002 -QEMT=fasta_1 -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -GNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORET=0.Cd -THR_MN=0 -ALIGN=15 -MODE-LCCAL -OUTFMT=pto -NORM-ext -HEADS1ZE=500 -MINLEN=0 -MAZEN=20000000000 -USER=USI0008355_CCGN_1_1_153_@runat_16052003_110337_9308 -NOPU-6 -ICPU=3 -NO_MMAP -LAREADSGUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120 -WARN_THEOUT=30 -THREADS=1 -XGAPEXT=7 -YGAPOPP=10 -YGAPEXT=0.5 -PELOP=6 -DELEXT=7	Geneseq_101002:*  '/SIDS2/gcgdata/geneseq,	9: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1988.DAT:* 10: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1988.DAT:* 11: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1999.DAT:* 12: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1991.DAT:* 13: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1991.DAT:* 14: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1991.DAT:* 15: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1993.DAT:* 16: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1994.DAT:* 17: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1995.DAT:* 18: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1995.DAT:* 18: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1995.DAT:*	

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ALIGNMENTS

pptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage;
-7 inhibitor identification; periodontal disease; gingivitis;
todontitis. ohyromonas gingivalis dipeptidylpeptidase-7 (DPP-7). .5205 standard; Protein; 712 AA. SEP-2002 (first entry) Porphyromonas gingivalis. 15205; 

WO200238742-A2.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

16-MAY-2002.

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Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amiddlytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or pariodontitis). The present amino acid sequence represents the porphyromonas gingivalis (DPP-7) enzyme of the
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                                                                                                                                                                                                            Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis -
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N-PSDB; AAL43635.
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              08-NOV-2001;
                                                                                                                        Travis J,
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120 180 240 300 100 360 120 420 140 480 40 9 9 20 8.0 TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT CAGGGCCTGATCTTTACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAA GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGC US-10-008-355-1 (1-2139) x AAO15205 (1-712) 21 41 181 121 61 241 301 101 121 361 421 81 q g ρņ ò ò g ô g ò g ò g ò õ

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                      1621 TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA
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              1561 CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylepetidase-7 (DPP-7) ensyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the
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The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23619 and AAB5981), tut! (AAF23630 and AAB59832), tutF (AAF23631 and AAB59834) and tutG (AAF23632 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. Toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of toluene and its analogs contained in liquid or solid waste source. The present sequence is a protein sequence for toluene degrading enzyme, TutD.
                             Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 ATGCCGTGGTTATCT-----TCGGTGGCGGATGTACCG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGAGAACCAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACGTTCGTATGGTATTTGCTCCTCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGG
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Matches:
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ThrargalaalaThrProArgargLysThrProCys----
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                                                                                          Disclosure; Fig 5; 122pp; English
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174.00
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N-PSDB; AAF23625, AAF23627
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8 8	22		7
2 g		rgArgArgCysAlaGlyPheSerSerAlaSerAlaThrAspSerAlaIleArgArgSe	33
Qy	707 A	CAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCG	16
q	340 S	rgSerArgAr	35
yo da	767 C	7 CCGTATCCATGCAAGCGTACAAGGCTGACGACTATGCCATGACGA 111 :::	811
3 3		10111111101	5 0
do do	380 T	/sLysP	399
Qy	851 G	TATCGAAAACGAG	910
Op	400 S	erCysTrpLysSerArgSerMetThralaThr	410
Qy	·	TC	96
QQ	411 -	ThrGlyArgThrProThrCysAsnSerAlaArgArgProValIleSerArg	427
Qy	962 A 428 A	AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACC	1021
δλ	1022 G	GGTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCG	1081
qq	439 A		457
λo i	82	ACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGGAAA	1 5
qq		serserAlaserCysArgCy	473
Oy	0	CTTATAAGGAAGGAG	11
qq	474 T	ThrAlaAlaTrpAsnSerGlyTrpThrProAlaProCysProSerSerProMetAlaGly	493
λ d	1169 A 1 494 T	ACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTT	1225
0	26	TGCACAGTTTGCCAACGCATTGGCTACAATCCTGATGCTCATGCCGGTATCCTCA	7
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Qy	1283 A	ATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCGCTCG	1342
qq	516 A	:: ArgargasnThrProSerSerasnSeralaLysargArgArgThrGlyLysValSerArg	535
ΟŊ	1343 C	CATGCTCGATATTGTACGCCGGCGTATCCCTGCCG	1378
q	536 L	LysCysAlaSerThrSerSerGlyArgArgSerGlyAlaThrThrMetIleThrProThr	555
Οy	1379 A	CAAGCTCCCCGATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGA	1435
QQ	556 V	ValSerProAlaSerThrArgLysSerSerAlaAlaLysCys	570
οy	S	AGAAGTAIGCAGACTICGTAITCGACAAGAGTGTGGTTCCTTAIAGCGACAAGTTCC	14
QQ	571 A	AlaArgSerProThrThrLeuValValArgSerCysArgLeuValArgLeuSerAla	589
οy	93 A	TGCCATGCTC	
QQ	- 065	1	
٥y	1544 A	AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG	1603

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1619   1614 ATGCGATGGCCANTGCCCANTGCACTGAAGGCCAAGCCCTTTTCTTTCCTTTGCCGGTTTCC   1619   1619 ATGCGATGGCCANTGCCANTGCANTGCANTGCANTGCTTTTCCTTTCC			tutF (AAF23631
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GTGAGATGTAGA  A AGALGTHANGARGAIATHACGASTHACGASTHACGATGGTAGGCTAGGCTCCATC  1		CC tolu	toluene degradi compounds and i
A RAGARGATARAGARATARICYSTHING  CATGGTATGAGCTACGGCTCCATC  III :: :: :: :: :: :: :: :: :: :: :: ::	80		analogs contain is a protein se
CCATGCGTATGAGCTACGGCTCCATC			Sequence 1615
1CysAlaproSerrMethin  NACTATC		Alignment Scores	t Scores:
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1 IlelleSerIleMetPheSerSerHe 1 GCAAGGGCTATTGGAGAAGCAGAT 1   1   1   1   1   1   1   1   1   1	33	Best Loca Query Mat	Fercent Similarity: Best Local Similarit Ouery Match:
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AlaAsnProArgSerThrMe 2TACAGGAAAATACCTC 3 G1ySerThrPheArgProMetG1yAr 3 CCGAGAACGCTCATATCGCT 3	31	US-10-008-355-1	8-355-1 (1
2TACAGGAGAATATCCTC 3 GlySerThrPheArgProMetGlyAr 5 CCGAGAACGGTCAGCTCCATATCGCT 5 AlaHisProlleSerSerSerThrSer 7 GTAACTCGGTAGCCCCGTAT 1957 111		Qy 65	_
GlySerThrPheAlgProMetGlyAr 3 CCGAGAACGCTCACATATCGCT 3 ::       :::  9 AlaHisProlleSerSerSerThrSer 7 GTAACTCCGGTAGCCCCGTAT 1957 9 SerArgProbroLeuProTyr 755 9826; APR-2001 (first entry) 1-	32	Dp 109	9 ProLysProA
CCGAGAACGCTCACTATCGCT :::       :::   AlaHisProlleSerSerSerThrSe   CTAACTCCGGTAGCCCGTAT 1957		Qy 125	5 recereager
9 AlaHisProlleGerSerSerTinis 7 GTAACTCGGTAGCCCGGTAT 1957 1	36	Db 729	9 SerProArgs
GTAACTCCGGTAGCCCGTAT 1957  SETATGPTOPOLOUPTOTY 755  9826 standard; Protein; 161  9826;  PR-2001 (first entry)  Lein #3 encoded by TutD/E ge  lene degradation; enzyme; wa  lene degradation; enzyme; wa  lene degradation.  Lene and tophilia.  Decra aromatica.  Londonoans maltophilia.  Decra aromatica.  DO072650-A2.  DO072650-A2.  DEC-2000.  AAY-2000; 2000WO-US14298.  JUN-1999; 99US-0323872.  DH-) UNIV OHIO.  Lhigano PW;  12001-041080/05.  SDB; AAF23627.  Dosition comprising toluene  parment of organic compounds,		Qy 155	
SerArgProbroLeuPiolyr 755 9826 standard; Protein; 161 99826; APR-2001 (first entry) Lein #3 encoded by TutD/E ge Lene degradation; enzyme; wa Lera arcmatica. Lhomonas maltophilia. Abacter metallireducens. Arcus tolulyticus. DEC-2000. AAY-2000; 2000WO-US14298. TUN-1999; 99US-0323872. DH-) UNIV OHIO. Chigano PW; 1 2001-041080/05. SDB; AAR-23627. POSSILion comprising toluene Atment of organic compounds,		Db 749	9 AlaGlyArgA
19826 standard; Protein; 161 19826; APR-2001 (first entry) Lein #3 encoded by TutD/E getene degradation; enzyme; watera aromatica. Lhomonas maltophilia. Dacter metallireducens. Dactor metallireducens. Dactor metallireducens. Dactor of Ovor 100 ov		0у 191	ATGC
19826; 19826; 19826; 19826; 198-2001 (first entry) 1-ein #3 encoded by TutD/E ge 1-era aromatica. 1-homonas maltophilia. 1-homonas maltop		Db 769	9 ArgProSerC
AAB59826; 04-APR-2001 (first entry) Protein #3 encoded by TutD/E ge Toluene degradation; enzyme; wa Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. W0200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000W0-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.		Qy 224	4 GTATCACAGI
04-APR-2001 (first entry) Protein #3 encoded by TutD/E ge Toluene degradation; enzyme; wa Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. AZOATCUS tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UVOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAR23627. Composition comprising toluene treatment of organic compounds, analogs.		Db 789	Ala
Protein #3 encoded by TutD/E ge Toluene degradation; enzyme; wa Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.		Qy 284	₽.
Toluene degradation; enzyme; wa Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAR23627. Composition comprising toluene treatment of organic compounds, analogs.		908 da	9 ThrArgAlaA
Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus. WO20072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO. Coschigano PW: WPI: 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.		Qy 344	4 TGGGTGAGGA
Geobacter metallireducens. Azoarcus tolulyticus. WO200072650-A2. 07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.		Db 821	1
WO200072650-A2.  07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UVOH-) UNIV OHIO. Coschigano PW: WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.		Qy 404	4 TAACGGACAA
07-DEC-2000. 24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.	,	Db 827	ProPro
24-MAY-2000; 2000WO-US14298. 01-JUN-1999; 99US-0323872. (UYOH-) UNIV OHIO.  Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.	•		
01-JUN-1999; 99US-0323872. (UVOH-) UNIV OHIO. Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.			
(UYOH-) UNIV OHIO.  Coschigano PW;  WPI: 2001-041080/05.  N-PSDB; AAF23627.  Composition comprising toluene treatment of organic compounds, analogs.			4 GCATCGTAGA
Coschigano PW; WPI; 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.			7 Arg
WPI: 2001-041080/05. N-PSDB; AAF23627. Composition comprising toluene treatment of organic compounds, analogs.			
Composition comprising toluene treatment of organic compounds, analogs		. DD 885	5 ArgThr 4 ACAACTGGAT
treatment of organic compounds, analogs -			
	its	Cy . 677	1
As Disclosure; Fig 12; 122pp; English.		Db 918	8 ArgArgArgC

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nvention relates to toluene degrading enzyme genes and (see AAR25629 and AAB59831), tuti (AAR23630 and AAB59832), 1 and AAB59833) and tutG (AAR23632 and AAB59834). The ding enzymes are homologues of pyruvate formate lyase. The ding enzymes are useful for biological treatment of organic in particular for the degradation of toluene and its ined in liquid or solid waste source. The present sequence sequence encoded by toluene degrading enzyme gene, TutD/E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |SerThrThrGlyArgArgTrpSerSerProAlaArgArgSerAlaGlyArg 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ATTCGCTCTACAGTTTCGACAAGCCGTCCATTG-----CCA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAAAGCACGGTGGATCACCACTATCTGCGCGATGGTTTCGTTTCTCGCACGA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGTAGAAGGACACCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GTCACACGGCGACT--- 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TCAGCGTATTCCGCGTGTATGCCGGTGCCG 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgProThrCysArgProSerProGlyThrAlaArgArgValSerThrThr 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SerAlaArgProSerProProSerSerSerAlaIleProArgArgThrAla 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||::
|AlaGlyCysAlaArgSerSerArgLysThrSerArgProIleArgSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATCT------TCGGTGGCGGATGTACCG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaThrProArgArgLysThrProCys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3AGGTATGCCAAGAACTGGCCAAAAAAAAAAATGCAGAGAGGAGAACCAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyArgThrIleCysSerSerSerProSerAlaAlaProThrProArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGGCTTTACGCTCCCGTTGG-------
                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·2139) x AAB59826 (1-1615)
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174.00
34.00%
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4.55%
                                                                                                                                                                                                                .5 AA;
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Page

		OY 1604 ATGGGATGCCCAATGCCATTGAGAAGGCCAAGCGTTTTCTTTGCCGGTTTGC 1663
PS Disclosure; Fig 12; XX The present inventi CC proteins tuth (see	m 10	OY 1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCTGCTGCTAGTTCAGGCCG 1603
		1493 ATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543
DR WPI; 2001-041080/05 DR N-PSDB; AAF23627. XX DR Composition comprise	2 2	1436AGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGCTTGTAGCGACAAGTTCC 1492 
PA (UYOH-) UNIV OHIO. XX PI Coschigano PW; XX	0 8	13/9 ACANGTUCCCGATATATTCAAGAATGTAATTCAAAGAATTCAAAGGCGACACGA 1435 
PF 24-MAY-2000; 2000WO XX	æ.	1343 CCATGCTCGATATTGTACGCCGGC
PN WOZUU072550-A2.  XX PD 07-DEC-2000.  XX		1283 AATGGCTTGAGGACAAGTACAAAGACTACCTCCCTCGCTCG
	21 m	1226 TIGCACAGTTIGCCAACGCATIGGCTACAAATCCTGAIGCTCAIGCGGGTATCCTCA 1282
XX KW Toluene degradation XX XX OS Thangra aromatica	10 10	1169 ACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTT 1225 11
Protein #4 en		1072 ThralaalaTrpasnSerGlyTrpThrProalaProCysProSerSerProMetAlaGly 1091
AC AAB5982/; XX DT 04-APR-2001 (first		1142 AGGCTTATAAGGAAGGAG CCAAGGCCA
ID AAB59827 standard; XX		This is the property of the pr
RESULT 5		ATROCATOR TREGOLOGICAL GOOD THE COLUMN TO A TREGOLOGICAL TO A TREGOLOGICA TO A TREGOLOGICA TO A TREGOLOGICA TO A TREGO
		1022 GCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTGCCGAGAAAGAGCATTCGCAG 1081
Ov 1937 GTAACTCCGGTAGC	•	1026 ArgSerProSerArgMetPheGlyArgLeuSer 1036
1883	,	962 AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACC 1021
1307	10	:::
Qy 1832TACAG		odicysitybysodintyodimeniiina acceedana
		851 GGGGTGTGGAAGATCGTATCGAAAACGAGAATCCTCGTATCGAAGTTCGCGGTATCA 910
		978 ThrvalalaalaargargLysLysProValargLysValalaalaGlnSerSerArgPro 997
UY 1/09 ACIAIC		812 TCGGTTTCC
QY 1709 CCATGCGTATGAGC		938 Serinrinrargserataargserargasninrrroserseralaserinralainr 95/
   Db   1236 ArgArgThrArgAr		ACAACCGGCCGGCCGATTACATCGCTG :::

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lon relates to toluene degrading enzyme genes and AAE23629 and AAE59831), tutI (AAE23630 and AAE59832), AAE59833) and tutG (AAE23632 and AAE59834). The enzymes are homologues of pyruvate formate lyase. The enzymes are useful for biological treatment of organic articular for the degradation of toluene and its in liquid or solid waste source. The present sequence noe encoded by toluene degrading enzyme gene, TutD/E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sing toluene degrading enzyme useful for biological c compounds, especially for degrading toluene or its
                                                                                                                                                                                                                                                                                                                                                   TACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACA 1768
                                                                                              ------ATACGACAG 1783
                                                                                                                                                                                         :::|||
tPheSerSerMetSerSerAlaArgMetLysCysAlaLeuArgSer 1288
                                                                                                                                                                                                                                                                                     ||||||| ::::: ::: ::: | |||
-ArgSerThrMetIleLeuSerCysAlaPheProAlaThrAlaLeu 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCG------ 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCATATCGCTTTCCTATCGAACAACGACATCACGG-----GCG 1936
||||||||
galaThrCysThrSerAlaCysArgCysArgSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; enzyme; waste degradation; TutE; TutD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 1592 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by TutD/E gene.
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|uProTyr 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGTAT 1957
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educens.
us.
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XX SQ Sequence 1592 AA;	г
Alignment Scores:  Pred. No.:  154.50  Matches:  Percent Similarity:  Best Local Similarity:  21.128  Mismatches:  172  Mismatches:  172  Mismatches:  172  Mismatches:  22.  Gabs:  3.908  Mismatches:  36.  Gabs:  3805  Mismatches:  Mismatches:  3805  Mismatches:  Mismatches:  3805  Mismatches:  Mismatches	Oy 1276TACCGCCATGAGCAT
US-10-008-355-1 (1-2139) x AAB59827 (1-1592)	1025
QY 2080 AGAGAACGTAGCGGATGTCCACGCTGATTGTGCGCTGCAGATCGGGTTCGAACTCGATGT 2021	Qy 1219
OY 2020 CACCACTCATAGCTTCCCAGTTGCCATCGAAAGCAAGACGATCAGACGGCCGTTCTTAT 1961  Db 780 ProGlyProArgSerAlaProSer1leArgArgGlySerArgAsgArgSerArgAsgr 799	Qy 1204 CGAAGACONTRACT TO THE SET ALL TO THE SET ALACYSC DD 1065 ArgArgArgGlyThrArgAlaAlaTrpHisSerAlaCysC
CGAATACGGGGGTAACGGGGGCGTGATGT	Qy 1177 TCTCACGGTTGGCCTTGGCTCCTTAT by 1177 TCTCACGGTTGGCTTGGCTTAT. by 1085 SerSerGlyArgProTrpSerValProlleArgProSer8
TGTTCGATAGGA	Qy 1147AAGCCTTTTC  :::        Db 1105 GlyLeuThrSerProSerSerProLeuAsnArgProPhek
GACCATAGTTTTGGTGCGGAAGAGGTCGAGGA 18	Qy 1117 CATAGACAGCACTCTTGCCGTTCTTACGGAI    ::   ::
1843 TATTCTCTGTACGGCAAACTCATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCT  1865 ArgClubranhycolarianny	Qy 1066 CCTCGGCAC
1786 TGC	Qy 1027 GACCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGG                 Db 1163ArgGly
7	Qy 967 CATATTGATACGGGTAGCCTGATCTGCGCTCA
1720 TCATACGCATGGTGAAGTTGCCATCGCCTCGCCA	Qy 919 TGCCTTGCTTGATACCGCGAACTTCGATACGAGGATTGTT
1684 CACGTCCGGGGTACATCTCACGCAAAC   1614   1	Qy 859 CCACACCCCAAGAAGTGAGGTAGCGATCCGTACTGCC
1624 CATAGGCATTGGCCATCGCCTGAATAGCGCGAGCAGCAGCTATTACGCTCTTGG	Qy 820GGAAACCGATGGTCATGGCATAGTC
1564 AAAGCICTACIGCCGGATCTTICTCGATAGCCTTGGCAAACTTTTCCTTGTCCATGGACT	Qy 784
TATAAGGAACCACACTTGTCGAATACGAAGT  TATAAGGAACACACACTTGTCGAATACGAAGT  TITTELL	Qy 760AGTAAAGGGGCTTATAGGGTTTAT ::::: ::       :: Db 1242 SerSerLysAlaArgAspSerTyrArgAspHisGluThr
1447 CTGCATACTTCTTCGTGTCGCCTTTGAATTTCTTGTCGATTACATTCTTGAATATTCGC	Qy 730TGCTGTATTCGGCCGCCGGTTGTCGGCACC :::
1387 GGAGCTTGTCGCAGGCATACGCCGCGTACAATATCGAGCATGGCGGGCA	Qy 679 TGAAGTCGCCCGTGTGACGCGCCCACATCCAGTTGT :::            Db 1282 GluThrArgLeuCysGluSerArgHisAlaSerCysTrp?
Db 966 AspGlyCysSeralaPhePheGlyAsnProLeuHisArgSerLeuArgGlyProTrpAla 985	Qy 637 CGCCTCCGA 629

:|||| gThrAlaSerSerArgAlaAla 1044 CCTATCACGTCAAGACGAGCGA 1028 | ::: ||||||| ::: pProAlaSerGlnAspProGln 1162 | ||| ||| ||||::: |||| |rArgArgCysAlaValArgGly 1004 AACTGTGCAAAACGAA---- 1220 -----CCACCTCGGTACCAC 1205 -GCGTCTCGCTCAAATAAGTCA 1178 ||| || || :: sGlySerSerArgArgPro 1084 ||||| ySer-----ArgArgProPhe 1142 TTGTCGTCAAGCGATTTGAGGA 1277 OHISLYSProProLysGlyCys 1024 ||| ||| gSerCysProValArgSerPro 1064 ----- 1148 rSerIleCysGlyArgAlaVal 1104 TCGAGAGACAATACATCGC 1118 ATCCAGTCTGCGAATGCTCTTT 1067 ||| ||| ||| sProGlyTrpAlaPro---- 1177 |||| ------ArgAlaSerArg 1181 ||||| | SProPheArgCysSerProAla 1201 |||| rArgPheArgSerSerThrCys 1241 | eAlaArgArgSerAlaProAla 1124 | | | |||||| | rGlySerProCysGlyAlaSer ||||||| | rHisArgCysProHisPheAla 1261 |||| gAlaArgLysArgSerCysArg 1281 |||| | pArgGlyAspProValProAsn -----TGGCTTCCTTCCAGA 920 TTCTCGTTTTCGATACGATCTT 860 TCGTCAGCCTTGT----- 785 CCGGCATACACGCGGAATACGC 680 CCCG------ 821 GCGA----- 761 -----7GTCCT-----731 

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20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF235629 and AAB59813), tutf (AAF23630 and AAB59832), tutf (AAF23631 and AAB59833) and tutG (AAF23632 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. The toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of folluene and its analogs contained in liquid or solid waste source. The present sequence is a protein sequence for toluene degrading enzyme, TutD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2080 AGAGAACGTAGCGGATGTCCACGCTGATTGTGCGCTGCAGATCGGGTTCGAACTCGATGT 2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2020 ---CACCACTCCATAGCTTCCCAGTTGCCATCGA---AAGCAAGACCGATCAGACGGCCGT 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgSerArgSerArgGly-----SerProLeuCysGlyAlaThrAlaThrSer 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 ProGlyProArgSerAlaProSerIleArgArgGlySerArgAspArgSerArgAlaSer 204
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143
45
170
40
                                                                                                                                                                                     Toluene degradation; enzyme; waste degradation; TutD.
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Matches:
Conservative:
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                                                                    AAB59817 standard; Protein; 999 AA.
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153.50
28.27%
21.50%
3.88%
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                                                                                                                                                                                                                                                                                                                                           24-MAY-2000; 2000WO-US14298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF23625, AAF23627.
                                                                                                                              (first entry)
                                                                                                                                                                                                                            Xanthomonas maltophilia.
Geobacter metallireducens.
Azoarcus tolulyticus.
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             1302 ArgMetArg 1304
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                          TutD protein #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Coschigano PW;
                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1999;
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                                                                                                AAB59817;
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ر د	1924	serserglvCvsProHisProProVal 240
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Qy	1909 AAGCGATATGGAGCTGACCGTTC ::    241 ArgArgSerProValAsnSerSe	TCGCCATAGCGACCATAGTTTTGGTGCGGAAGAGGT 1850  ::: ::: ::: rLySArgAlaHisArgArgCySThrAlaArgArgGly 260
۰ م	1849 CCAGGATATTCTCCTGTACGGCAACTCAT	GCTCTTAGGATCCTGC
Dp	Db 261 ArgPheArgGlyProThrSerArgAspThrGlyArg	Arg 272
Οy	Qy 1792 CGCCCTTGC	1784
qq	273	ysargCysSerargargTrpGlyarg 292
Οy	Qy 1783CTGTCGTATGATAGTTGTACCAGGCACCGTCCTGCGGTTCAL	CTGCGGTTCATATCCCTTGATGGAGC 1727
Dp	293	TrpArg 305
ογ	1726 CGTAGCTCATACGCATGGTGAAGTTGGCAT	91
qq	306	SerSerAlaAlaSerProLysArgThrCys 324
οy	Qy 1687GAGCACGTCCGGGGTACATCTCACGCAAAC	CGGCAAAGAAAAGACGCTTGCT 1631
Op .	325 GlyArgArgValArgSerAs	rgSerArgCysProAla 341
Qγ	1630 CAATGCCATAGGCATTGGCC	ATCGCATCGCCTGAATAGCGCGAGCAGCAGCTATTACGC 1571
DÞ	Db 341	341
Qy	1570 TCTTGGAAAGCTCTACTGCCGGATCTTT	CTCGATAGCCTTGGCAAACTTTTCCTTGTCCA 1511
qq	Db 342	SerSerProlleArg 346
0y	1510 TGGACTTGAGCATGGCATGGAACTTGT	ATAAGGAACCACACTCTTGTCGAATA 1454
qq	Db 347 TrpThrGlyArgCysArgArg'	::::: TrpArgArgProLeuGlyCysSerPro 362
Qγ	1453 CGAAGTCTGCA	TTTCTTGTCGATTACATTCTTGAATA 1394
qq	363 ArgAlaThrCysThrAlaArgC	371
οy	1393	TACAATATCGAGCATGGCGG 1340
QQ	Db 372argaspGlyCysSerAlaPhePheGlyAsnProLeuHisArgSerLeuArg	roLeuHisArgSerLeuArgGlyPro 390
οy	1339GCAGCACCTTACGGTCGAGCGAGGGG	GTCTTTGTACTTGTCGTCAAGCGATT 1283
QQ	391	gSerArgSerThrThrArgArgCysAlaVal 409
ΟŸ	Qy 1282 TGAGGATACCGGCATGAGCAT	1262
đ.	410 ArgGlySerSerArgHis.	ThrargargProHisLysProProLys 429
Qγ	1261CAGGATTTGTAGCCAATGCGTTG	¥:
qq	430 GlyCysAlaTh	CysTrpProArgThrAlaSerSerArg 449
Οy	Qy 1219	STCG
QQ	Db 450 AlaAlaSerGlyAlaSerAlaLySArgThrArg	euArgArgSerCysProvalArg 469
οy	Qy 1210 TACCACGAAGA	GCGTCTCGCTCAAAT 1184
qq	470 SerProArgA	sSerAlaCysGlySerSerS
δo i	QY 1183 AAGTCATCTCACGGTTGGCCTTGGCTTCTTAT	AT
	100	

Asundi V, Wang J, Wang D;

Liu C, Zhou P, Drmanac RT;

Tang YT, Goodrich RW, Yamazaki V, Ujwal ML,

rang YT,

WPI; 2002-508509/54. N-PSDB; ABK94926.

30-NOV-2001; 2001WO-US47004.

WO200244340-A2.

06-JUN-2002

30-NOV-2000; 2000US-0028952

(HYSE-) HYSEQ INC.

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disease, ischaemia-reperficion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, ceperfusion injury in various tissues, immune deficiencies and disorders infections, autoimmune disorders e.g. multiple sclerosis and myasthenia including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia and coagulation disorders. Sequences ABG66666-ABG666758 represent human novel polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 CAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 TCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 AGTICGGAGGCGATACGGACAACTGGAIGTGGCCGCGTCACACGGGCGACTTCAGCGTAT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| ::: ||||::: ||||::: 572 ProSerThrAspMetIleThrSerHisThrAsnLeuThrArg---SerSerProLeu 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686 TCCGCGTGTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCÄAGGACAATAAACCCT 745
                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -
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Matches:
Conservative:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 604-607; 672pp; English,
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33.76%
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Best Local Similarity:
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cancer; wound healing; central nervous system disease; heematopolesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; mapeloid cell disorder; Imphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; allorgibrosis; liver fibrosis; autoimmune disorder; bacterial infection; fungaliprosis; thrombolysis; thrombosis; coagulation disorder; GTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTC 1588 1649 TCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTG------CTCTGCCGAGCGATG 1699 1055 GlnThrThrLeuThrThrTyrMetAspThrSerSerMetMetProGluSerGer 1074 ----- 1100 :::||||||::: | 1134 Thr1leLeuArgThrSerSerLysSerThrHisProSerProProThrThrArg----- 1151 1035 ProLeuThrValPheProPheThrThrGluMetValThrCysProThrSerIleSerIle 1054 -----TCAAGGGATATGAACCGCAGGACGTGCCTGGTACAACTATCATA 1777 1778 CGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGG 1837 . 1838 AGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACG---GTC 1894 1895 AGCTCCATATCGCTTTCCTATCGAACAACACCATCACGGGCGGTAACTCCGGTAGCCCCG 1954 1955 TATTCGATAAGAACGCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGA 2014 955 alGlySerAlaSerIleThrGlyPheProSerLeuSerSerSerAlaThrThrSerThrS 975 1589 GCGCTATTCAGGCCGATGCGATGCCCAATGCCATTGAGAAGGGCAAGCGTCTTT 975 erSerThrSerSerSerLeuThrThrAlaLeuThrGluIleThrPro-PheSerTyrIle 1700 CCAACTTCACCATGCGTA-------TGAGCTACGGCTCCA-----2015 GTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACG Human; inflammatory condition; shock; sepsis; immune response; 2015 TICTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125 ABG66756 standard; Protein; 1296 AA Human novel polypeptide #91. 1095 ThrSerThrArg-----(first entry) 30-AUG-2002 ABG66756; 1732 1732 1733 1555 RESULT 8 ABG66756 g ò pp ò qq ò Pp δy Db ò Op ò q ò qq δ q οy g δλ Db q ò

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The inventor restates to minimal moves purposed and adjusted are introduced to treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral carvous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclenosis. The sequences are involved in chemotactic or chemokinetic activity, requilation of haematopoiesis, treatment of myeloid or lymphoid call disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoporathritis, bone degeneratied disorders and periodontal disease. The sequences of the invention are also useful for gut corpection or regeneration and treatment of lung or liver fibrosis, creperfusion injury in various tissues, immune deficiencies and disorders controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coaqulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
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The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzhmier's or Huntingdon's disease) or acute traumatic injuries. Transgenic calls and organisms transfected with UNC-53 cDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the cDNA sequences can be used to intentify phomologues of the C. elegans unc-53 gene. The UNC-53 protein can be used to identify proteins which are active in the signal transduction pathway that can be used as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 TTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTG 387
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                                                                                                                                                                                                                                                                                                                             8A and 7A of Caenorhabditis elegans are new
                                                                                                                                                                                                                                        Caenorhabditis elegans UNC-53 protein 8A and 7A variants - useful promote neuronal regeneration, revascularisation or wound healing.
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Mismatches:
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                                                                                                 (STRI/) STRINGHAM E.
(VAND/) VANDEKERCKHOVE J.
                                                                                                                                                                                                                                                                                                                              protein variants
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Best Local Similarity:
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              31-MAY-1996;
                                                31-MAY-1995;
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446 rileValThrAlaileArg

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Page 13

68		AGGACAATAAACCCTAT 747         SeralaThrAsnProAs 159	CTGACGACTATGCCATG 807	LeuGlnThr 172	GGGGTGTGGAAGATCGT 867     ::: GlylleLysProLysTh 191		:::      AsnThrAsnSerPheAr 211	92	23	AGGAAGCCATGAGCGCA 942 :::    :::   euAsnArgProThrSerGl 251	GIGCIAACTATIGGAAG 1002	  ValAlaThrThrLy 270	GTCTTGACGTGATAGGT 1050	290	AGAACGGCAAGAGTGCT 1110 :::   GlyGlyGlyGlyMetLe 310	SAAGGAGGCCAAC 1170	AsnSerProGlnProTh 330	AAGGTGGTTGGTTTGCA 1230 :::     	GTATCCTCAAATCGCTT 1290	 ProValLysSerGlyLeuLy 354		iLeucysinrFroLy 3/3	<pre>NTATTCAAGAATGTAATC 1410         :::</pre>		As	3TCCATGGACAAGGA 1520	MetHisSerThrSerSe 426	GTAGAGCTTTCCAAGAG 1571 
		3 CGCGTGTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTAT 	AAGCCCGTTTACTTCGCTGCCGTATCCATG	nSerAsnPheProGlnMetSerThrs	ACCATCGGTTTCCCGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGT			GGTATCAAGCAAGGCATCTGGA	gProserserargserserGlyAsnAsnAsnValGlySerT	sSerLeuGluSerSerSerThrTyrSerSerIleSerAsnL			3 AATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGT :    :		<pre>1 CGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCT</pre>			CGTGAGATGACTTATTGAGGGAGGCTCTTCGGTGGTAGCCGAGGTGGTTCGTTTTGCA	CAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATG	::: rLysIleAlaAla	GACGACAAGTACAAAGACTACCTCCCCTCGACCGTAAGGTGCTGCCCGCCATGCTC   :::::::		1 GATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCT 1 ::	GACAAGAAATTCAAAGGCGACACGAAGAAGAG		GAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG	   III	1 AAAGTTTGCCAAGGCTATCCAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGG
628	136	688	748	159	808	868	191	904	117	926	943	251	1003	*	1051	1111	310	1171	1231	343	1291	900	1351	1411	389	1464	406	1521
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UNC-53 protein variants 8A and 7A of Caenorhabditis elegans are new.

The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or fur treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntingdon's disease) or acute traumatic injuries. Transgenic cells and or substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the conversion of the conversion of inducing cells or metastasis. Probes derived from the conversion of the signal transduction pathway that can be used as metioned above.
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                                                                                            C. elegans UNC-53 protein variant 7A.
AAW20057 standard; Protein; 1583 AA
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271 GGATACGGTGCTATC---CAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGGT 327
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LysArgLeuAlaLysIleThrSerAsnLeuAspGly---LeuGluThrCysLeuAspTyr
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                   GACGACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTC 1350
                                                                                                        GATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATC 1410
                                                                                                                                                                              1411 GACAAGAAATTCAAAGGCGACACGAAGAAG-----TATGCAGACTTCGTATTCGACAA 1463
                                                                                                                                                                                                                                                   1464 GAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAG.---TCCATGGACAAGGA 1520
                                                                                                                                                                                                                                                                                                                          1521 AAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCA------GTAGAGCTTTCCAAGAG 1571
                                                                                                                                                                                                                                                                                                                                             --- ProValLysSerGlyLeuLy
                                                                                                                                                                                                    406 nSerThrSerProThrSerSerSerThrGluGlySerLeuSerMetHisSerThrSerSe
                                                                     354 sProProThrSerLysLeuGlySerAlaThrSerMetSerLysLeuCysThrPro---Ly
                                                                                                                                          373 svalSerTyrArg------LysThrAspAlaProllelleSerGlnGlnAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 36734; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #6366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG06375 standard; Protein; 2570 AA
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  446 rIlevalThrAlaIleArg
 343 rLysileAlaAla--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73.
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequence of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. ::: ::: ||||::: ::: ||||:|:|
1890 SerLeuThrAsnTyrAlaThrSerLeuAsnThrProValSerTyrProProTrpThrPro 1909 1930 GluIleSerThrProLysThrSerPro---ProProThrSerGlnMetValGluPhe--- 1947 1967 TrpAsnIleProThrAlaGluGlySerGlnPheProIleSerThrThrIleAsnValPro 1986 956 GTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTA 1015 1016 TGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCAT 1075 TCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTC 1135 TCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGA 1195 838 727 784 491 CCAAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACA 550 1987 ThrSerAsnGluMetGluThrGluThrLeuHisLeuValProGlyProLeu---SerThr ---GCAAGGACAATAAACCCTATAAGCCCGTTTAACTTCGCTGCCGTATCCATGCAAGGCT 785 ACAAGGCTGACG-----ACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCT 899 TTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCG----CAGATCAGGCTACCC ---LeuVal 551 ACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTC 611 CCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGG ACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAG 2570 133 81 195 191 29 1877 SerAsnThrArgLysMetThrSerLeuLeuGluLysThr-----Length:
Matches:
Conservative:
Mismatches:
Indels: 1864 ProThrLysAsnValLysThrThrThrAsnCysPheSer-(1-2570)US-10-008-355-1 (1-2139) x ABG06375 0.000223 148.00 35.67% 22.17% 3.87% 2006 Pherhrala-----2570 AA; Best Local Similarity: Percent Similarity: Alignment Scores: Sequence Query Match: DB: 839 1948 2015 728 1076 2009 1136 1889 Pred. g QQ g 8 Q g Qγ g 9 q 9 ŏ ò g qq Ω qq δ ò ŏ ŏ ò δý

AGTICCATGCCATGCTCAAGT --- CCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543 2115 hrSerSerThrValGluValSerLysSerThrPheLeuThrSerAspMetIleSerAlaH 2135 1196 CGCICTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAA 1255 GTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAATTCAAAG 1426 GCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGCTTCCTTATAGCGACA 1486 ------LeuProAsnHisGlyLeuSer 1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCGCGCTATTCAGGCCG ------ACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGC TCGATAAGAACGCCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTG ProLeu-----IleSerThrGlyValThrTyrPro 2155 ThrileProThrProThrLeuGlyGlyIleThrThrGlyPheProThrSerLeuProMet --CCTGGTACAACTATCATACGACAGGCAAGGGCGTAT TGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCG----; TCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTAT SerLeu---LeuAsnIleMetThrThrThrSer----ThrValProGlyAlaSerPhe 2018 GTGACATCGAGT --- TCGAACCCGATCTGCAGC---GCACAATCAGCGTGGACATCCGCT GluAsnProSerLeuSerThrSerLeuArgAlaIleThrSerThrLeuAlaAspValLys 2135 isProPheThrAsnLeu-ThrThrLeuProSerAlaThrMetSerThrIleLeuThrArg TGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAAGTTCACCATGCGTATGA ATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGT------ACAAAG ACTACCTCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGC 2175 SerileAsnValThrAspAspileVal----TyrileSerThrHisPro--------GlualaSerSerArgThrThrIleThrAlaAsnProArgThrValSerHisProSer 2072 ACGITCITCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125 GCTACGGCTCCATCAAGG------GATATGAACCGCAGGACGGTG----HisThrPheGluLysMetThrThrSerValThrPro------SerPheSerArgLysThrMetSerProSerThrThrAsp-----ATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTC-2070 ThrThrLeuProSerIleLeu-2026 MetSerGlyIle----2278 2261 1796 1367 1487 2096 1721 2037 1307 1427 2079 1661 2222 g q g qq Db ò q ò g δ Db Óγ Db δ qq δŽ Q ò g δy qq ōλ d ò g ò g ò g ò g δ οŽ δ SerLysAspValMetAlaMetSerSerIlePro-----

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609 AsnGluGluAsnGluAspIleLeuGluAspIleValLeuThrLeuThrLeuPheGlu--- 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a Streptococcus ample. (I) is used to detectine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to accombinantly produce (I) and may be used in gene therapy. Antibodies to crombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                            Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antlinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grandi G,
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167
105
228
357
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Mismatches:
Indels:
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Matches:
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                                                                                                                                            Streptococcus polypeptide SEQ ID NO 4212.
                                   ABP27518 standard; Protein; 1368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3578; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001GB-0005640.
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31.74%
19.49%
3.84%
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Best Local Similarity:
Query Match:
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                                                                                                         02-JUL-2002
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Pettelin H;
                                                                     ABP27518;
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RESULT 12
                  ABP27518
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AATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTC 162

Gaps: (1-1368)

JS-10-008-355-1 (1-2139) x ABP27518

103

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964 TATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGC 1023
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163 TACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACC
                                                                                                                                            223 GGTATCACAGTGTCCGATCAGGGCCTG-----ATCTTTACCAACCACCACTGCGGATAC
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                                                                  -----AspArgGluMetIleGluGluArgLeuLysThrTyrAlaHis-----
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λ	1075		1104
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λ	1104		1104
ą	967	7 ArgLysAspPheGlnPheTyrLysValArgGluIleAsnAsnTyrHisHisAlaHisAsp	. 986
γ	1105		1143
q	987	AlaTyrLeuAsnAlaValValGlyThrAlaLeuIleLysLysTyrProLysLeuGluSer	1006
<u>۲</u>	1144	GCTTATAAGGAAGGAGCCAAGGCCAAC	1170
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Ď.	1027	7 GlnGlulleGlyLysAlaThrAlaLysTyrPhePheTyrSerAsnIleMetAsnPhePhe	1046
λ	1231		1287
ą	1047	7 LysThrGluIleThrLeuAlaAsnGlyGluIleArgLysArgProLeuIleGluThrAsn	1066
λ	1288		1329
q	1067	GlyGluThrGlyGluIleValTrpAspLysGlyArgAspPheAlaThrValArg	1084
λλ	1330		1368
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λ	1402	2 AATGTAATCGACAAGAAATTCGAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGAC	1461
ą	1120		1135
λ	1462		1497
q	1136	SerProThrValAlaTyrSerValLeuValValAlaLysValGluLysGlyLysSerLys	1155
λλ	1498		1530 .
q	1156		1175
λλ	1531		1554
ą	1176	LysAsnProlleAspPheLeuGluAlaLysGlyTy	1195
λ	1555		1614
q	1196	6 IleLysLeuProLysTyr	1201
λχ	1615	S AATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTT	1674 '
q	1202		1221
λ	1675	5 CCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGC	1722
g	1222	2 LysGlyAsnGluLeuAlaLeuProSerLysTyrValAsnPheLeuTyrLeuAlaSerHis	1241

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                       -----CGCTATGCC 1884
                  --GCCTGGTACAAC 1770
                                                            1771 TATCATACGACAGGCCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCC 1830
                                                                                                                                                                                     ---GAGAATATCCTCGACCTCTTCCGCACCAAAAC 1869
                                                                                                                                                      1278 LysArgValIleLeuAlaAspAlaAsnLeuAspLysValLeuSerAlaTyrAsnLysHis 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 36210; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                              1885 GAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGC 1935
                                                                                                                                                                                                                                                                                                                                  1338 SerThrLysGluValLeuAspAlaThrLeuIleHisGlnSerIleThrGly 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 36210.
 1723 TACGGCTCCATCAAGGGATATGAACCGCAGGACGGT--
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FTGTCTTCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACT 1182
                                                                                rcgarcggrargaaccgcggrcrcgcrcgrcrrgacgrgaraggrcgraagcgrgcc 1062
                                                                                                                                                                                         SAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGAT 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ThrGlyLysProThrThrThrProLysProSerThrArgThrThrProThrTh 721
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rLysValThrThrThrThrGlnIleThrThrThrThrProLeuArgSerSerThrGl 741
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rThrSerThrGlnProProThrThrThrThrThrProGlnProThrThrThrThrLe 761
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sThrThrThrGluLysThrSerThrValSerThrThr-----
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1732 TGGAGCCGTAGCTCATACGCATGGTGAAGTTGGCATCGCTCGGCAGAGCACGTCCGGGGT 1673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1846 GGATATTÒTCCCTGTACGGCAAACTCATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCT 1787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1786 TGCCTGTCG-----TATGATAGTTGTACCAGGCACCGTCCTGCGGTTCATATCCCTTGA 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1960 CGAATACGGGGCTACCGGAGTTACCGC-----CCGTGATGTCGTTGTTCGATAGGAAAG 1907
                                                                                                                                                                                                                                                                                                           In AAX87940. This DNA fragment comprises a Stul-Stul fragment of M. tuberculosis genomic DNA and contains an insertion sequence-like element and repetitive sequences. The DNA fragment is useful as a probe, especially for detecting or identifying M. tuberculosis in clinical isolates and body fluids e.g. sputum, cerebrospinal fluid, pleural fluid, urine, gastric lavage, bronchial lavage, pericardial or Lymph node aspirate (all claimed). It is also useful for restriction fragment length polymorphism analysis of M. tuberculosis of tuberculosis and M. tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 TrpCysHisProGlyTyrSerCysArgTyrTrpCys-------HisProArg*** 89
                                                                                                                                                                                                                                                                                       The present sequence represents an amino acid sequence deduced from the Mycobacterium tuberculosis specific DNA fragment provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SerGlyPro
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                                                                                                                                                                                                                                     New nucleic acid molecules, useful for detecting and identifying
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947 rProLeuThrThrLeuSerThrGluGlu------ProAsnThrThrProLysProLe 964
                                  2041 CTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGACAAATGGGGT
                                                                                                                                                                                           Mycobacterium tuberculosis specific DNA-encoded polypeptide
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                                                   GlyCys***SerHisArgArgArgPheArgCysArgGluCysCys 302
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| ArgProllePro------AlaArgProArgLeuPro 377
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(ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2067 GATGTCCACGCTGATTGTGCGCTGCAGATCGGGTTCGAACTCGATGTCACCACTCATAGC 2008
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125 ---ThrAlaGlyAlaLeuAspValValAsnAlaArgLeuGlnMetHisLeuGluValLeu 143
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164 LeuGlySerAsnGluAspLeuHisAsn---
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ΟŸ	1296 GTCGTCAAGCGATTT
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Qy	ATTTGTAGCCAATGCGTTGGCAAACTGTGCA
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Qy	TCACGGTTGGCCTTG
qq	le
Qy	TTG
q	:::     SluLeuLeuValHisAl
Qy	1080 TGCGAATGCTCTTTCCTCGGCACGCTTACGACCTATCACGTCAAGACGAGACCGCG 1021
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qq	393GlyalaGlnValThrGlyIleAlaGlyPhe402
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Qy	624 ACCTACAGAGCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGAT 565
qa	AlaThrIleLeuV

564 GAGGAAGTATTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTCTCC 505 :::	504 ATTTCTTTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTGCGCAGACGCTCCATCTC 445	444 GTCAGTGATACCCTTGAGCTGTCCTTCTTCCGTTACCTTCACGATCTTGCGCAG 385	384 ATACTTCACGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACC 325 :::::	324 ATCGCGCAGATAGTCGTGATCCAC	285 GATAGCACCGTATCCGCAGTGGTGGTTAAAGATCAGGCCCTGATCGGACAC 232   1	231 TGTGATACCGGTACATCCGCCACCGAAGATAACCACGGCATTGGCAATGGAATGGACTGTGTC 172		
Db 446	Oy 504 Db 465	Oy 444 Db 481	Oy 384 Db 499	Oy 324 Db 503	Oy 285 Db 523	Oy 231 Db 540	0v 171	

Search completed: May 16, 2003, 12:28:32 Job time : 165 secs

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US-08-860-886-2
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Sequence:

Scoring table:

## ALIGNMENTS

Sequence 28, Appl Sequence 295, App Sequence 6, Appli Patent No. 5200183

Appl i

Sequence 2, Sequence 28,

Sequence 2, Application US/09156836B
Patent No. 6742585;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stivastava, Ranjana
APPLICANT: Stivastava, Brahm Shanker
APPLICANT: Stivastava, Brahm Shanker
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
FILE REFERENCE: U 011876-4
CURRENT APPLICATION NUMBER: 08/99/156,836B
CURRENT FILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0 LOCATION: (54)
OTHER INFORMATION: amino acid has not been identified been identified been identified been identified been identified not not not not ORGANISM: Mycobacterium tuberculosis has has has has acid acid acid amino acid NAME/KEY: UNSURE
LOCATION: (4)
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NAME/KEY: UNSURE NAME/KEY: UNSURE RESULT 1 US-09-156-836B-2 LENGTH: 430 TYPE: PRT SEQ ID NO 2 FEATURE:

US-08-687-847-2 US-08-687-847-2 US-09-514-302-3 US-09-134-0012-5438 US-09-134-0012-5438 US-09-134-0012-2 US-09-134-0012-2 US-09-134-0012-5111 US-08-134-2 US-09-199-637A-295 US-07-854-596B-40 US-09-134-078-28 5200183-17 5223423-3 102 102 101.5 101.5 101 100.5 100.5 100 ບບ

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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262574 segs, 29422922 residues

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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL-frame+.n2p.model -DEV=x1p
-MODEL-frame+.n2p.model -DEV=x1p
-MODEL-frame+.n2p.model -DEV=x1p
-Q=ycgn2\_1/USPTO\_spool/US10008355/runat\_16052003\_110339\_9386/app\_query.fasta\_1.2311
-DB-Issued\_Patents\_AA -OPMT-fastan -SUFFTX=n2p.rai -MINWATCH=0.1 -LOOPCI.=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRR\_Mnan40.cdi
-LIST=45 -DOCALIGN=200 -THR\_SCORE=-ECC -THR\_MAX=100 -THR\_MN=0 -ALIGN=15
-USFR=-USI0008355\_eCGN\_1\_1\_33\_erunat\_16052003\_110339\_9386 -NCPU=6 -ICPU=3
-NOAPEXT=20 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Res C C .	Result No	Score 130 120 123 123 122 122 122 122 122 122 122 122	Match Match Match 33.22333.55	Ouery Match Length DB 3.5 430 4 3.4 883 2 3.4 430 4 3.2 1194 2 3.2 713 4 3.2 813 2 3.2 813 2 3.2 1181 2 3.2 1194 2	BG 408040000	US-09-156-836B-2 US-09-156-836B-2 US-08-993-492-2 US-08-997-897-2 US-08-08-940-18 US-08-488-940-4 US-08-488-940-3 US-08-488-940-1 US-08-488-940-1 US-08-488-940-1	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 53, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
O	11	119	3.0	2152	4	US-09-036-987A-3	Sequence 3, Appli
υ	12	119	3.0	2152	4	US-09-370-700-3	Sequence 3, Appli

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		CGATAGGAAAG     euTrpGly***	GAAGAGGTCGA	SerGlyPro	CTTCTCCAATACGCCCT        Cys***SerAraPro	ATATCCCTTGA		ACGTCCGGGGT	-HisProArg***		ysProCysCys	ATAGGCAT	;::    ysGlnHis***	CTGAATAGCGC		GATAGCCTTGG	Cys	CATGGCATGGA	sn***ThrGly	ACTCTTGTCGA	laGlyCysArg	TACATTCTTGA		CATGGCGGGCA	ArgCysTrpArgThr	CGATTTGAGGA		AAAACGAACCA	ly***SerArg	SGCCTTGGCTC		ACTCTTGCCGT	rgCysCysArg
352 37	-430)	-CCGTGATGTCGTTGGATAGGAAAG	GTTTTGGTGCG		ATCCTGCTTCTC	GTCCTGCGGTTC	 rgSerArgCys-	GCTCGGCAGAGC	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		rgCysCysSerC	CTTCTCAATGGC	II roCysCysSerC	CATCGCATCGGC	roSerSerArg-	CGGATCTTTCTC	-CysProSerLeuArg	TGGACTTGAGCATGGCA	 yrTrpCysProA	ATAAGGAACCAC	 yr***SerProA	TTTCTTGTCGAT	CysCys	TACAATATCGAG		CTTGTCGTCAAG	ysCysArg	GGCAAACTGTGC	-CysTrpGlnSerLeuGly***	CATCTCACGGTT	ysSerArg	SCCATAGACAGC	-ArgArgPheGlnAsnArgCysCysArg
Indels: Gaps:	56-836B-2 (1-	 ln**	ATAGCGACCATA	- :	ATCGCTCTTAGG	CAGGCAC	  ysArgAsp***A	GAAGTTGGCATC	rgTyrTrpCys-		rg***SerArgA	AAGACGCTTGCC	:: .rg***GlyCysP	DDL	::: lySerArgTyrP	AAGCTCTACTGC			rgCysGlnArgT	TODO	erArg***GlnT	GTCGCCTTTGAA	ysarg	GATACGCCGGCG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GTAGTCTTTGTA	ArgCys	AGCCAATGCGTT	CysT	GCTCAAATAAGT	SerArgSerArgArgCysSerArg-	AGACAATACATC	ArgA
3.49%	5-1 (1-2139) x US-09-1	CGAATACGGGGCTACCGGAGTTACCGCCCGTGATGTCGTTGTTCGATAGGA 	CGATATGGAGCTGACCGTTCTCGGCATAGCGACCATAGTTTTTGGTGCGGAAGAGGTCGA	IleGlySerGlyAspArgGluIleAspGlyGlu-	GGATATICICCTGTACGGCAAACTCATCGCTCTTAGGATCCTGCTTCTCCAATACGCCT	TGCCTGTCGTATGATAGTT	 	TGGAGCCGTAGCTCATACGCATGGTGAAGTTGGCATCGCTCGGCAGGCA	CysHisProGly	ACA	 SerCysArgCysTrpCysTyrArgA***SerArgArgCysCysSerCysProCysCy	-TCTCACGCAAACCGGCAAAGAAAAGACGCTTGCCCTTCTCAATGGCATAGGCAT			GlyCysArgTyrCysArgTyrProGlySerArgTyrProSerSerArg	GAGCAGCAGCTATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTTGG		CAAACTTTCCTTGTCCA	::: ArgArgPheArgCysProArg***ArgCysGlnArgTyrTrpCysProAsn***ThrGly	TTGT		ATACGAAGTCTGCATACTTCGTGTCGCCTTTGAATTTCTTGCGATTACATTCTTGA	ArgThrAlaArgCysArg-	ATATATCGGGGAGCTTGTCGGCAGGGATACGCCGGCGTACAATATCGAGCATGGCGGGCA	CysCys	GCACCTTACGGTCGAGGGAGGGAGGTAGTCTTGTACTTGTCGTCAAGCGATTTGAGGA		TACCGGCATGAGCATCAGGATTTGTAGCCAATGCGTTGGCAAACTGTGCAAAACGAACCA		CCTCGGTACCACCGAAGAGCGTCTCGCTCAAATAAGTCATCTCACGGTTGGCCTTGGCTC	ProArgSerA	CTTCCTTATAAGCCTTTTCGAGAAAAAAAAAAATACATCGCCATAGACAGCACTCTTGCGGT	
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οy	1096 TCTTACGGATCCAGTCTGCGAATGCTCTTTCCTCGGCACGCTTACGACCTATCACGT 1040	US-08-953-492
QQ	:::    241 SerArgGlyPheArg1leArgCysCysSerPhePro	; Sequence 2, ; Patent No.
Qy	1039 CAAGACGAGGAGACCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAG 980	GENERAL IN APPLICAN
Dp	253His***Ile 260	; APPLICAN ; APPLICAN
Qy	979 CATACTTGCTGGCATATTTGATACGGGTAGCCTGATCTGCGCTCATGGCTTCCTTC	; APPLICAN; TITLE OF
QQ	261 LeuArgCysPheHis	CORRESPO
ΟŊ	919 TGCCTTGCTTGATACCGCGAACTTCGATACGAGGATTGTTCTCGTTTTGGATACGATCTT 860	STREET
QQ	***SerCysArgArgCys	STATE
ογ	859 CCACACCCCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCAT 800 `	ZIP:
qq	275 275	; COMPOTER ; MEDIUM
Qy	799 AGTCGTCAGCCTTGTAGCCTTGCATGGATACGGCAGCGAAGTAAACGGGCTTATAGGGTT 740	COMPUT
QQ	275 275	CURRENT
οy	739 TATTGTCCTTGCTGTATTCGGCCGGCCGGCTTGTCGGCACGCGCATACACGCGGAATACGC 680	APPLIC
QQ	276CysProArgCysPheGlyCysArgGlyCysArg	; CLASS.
Qy	679 TGAAGTCGCCCGTGTGACGCGGCCACATCCAGTTGTCCGTATCGCCTCCGAACTTACCTA 620	FILING
Op	287CysGlnGlyCys***SerHisArgArgPheArgCysArgGluCysCys 302	; PRIOR AI
ογ	619 CAGAGCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGA 560	ATTORNEY
qq	302 302	REGIST
Oy	ATTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGAGTTGGTT	; REFERE
QQ	303 AsnCysArgCysTrpArgCysArgGluCysSerArgArgProGly 317	
Qy	499 CTT 497	INFORMATIC
QQ	]18 LeuProGlyArgAsp***ArgProValGlyHisArgLysIleProThrCysCysPheArg 337	LENGTH
ΟŸ	GGCATA	STRAN
qa	338 Cys***ArgSerProArgSerArgProAlaLeu***TrpProProGlySerCys***Thr 357	MOLECULE
δλ	454 GCTCCATCTCGTCAGTGATACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGA 395	•
qa	358 Asn	Pred. No.:
Qy	394 TCTTGCGCAGATACTTCACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAG 335	
QQ	362 CysCysProSer***SerArgProlleProAlaArgProArgLeuPro 377	Query Match:
Qy	334 AAACGAAACCATCGCGCAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATAGCACCGT 275	
Dp ·	:::::    378 GlyArgSerTyrArgTrpProPro	US-10-008-355
ó	TGGTAAAGATCAGGCCCTGATCGGACACTGTGA	Qy 574 GA1
. අ <u>අ</u>		Db 26 As
٥y	226 TACCGGTACATCCGCCACCGAAGATAACCACGGCATTGGCAATGGACGGCTTGT 173	Qy 610 CCC
QQ		46
δŏ	172 CGAAAC 167	670
<b>Q</b> Q .	422 ArgSer 423	ς C
		Ov 730 AAC

RESULT 2

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Oy 1666 GAGATGTAC 	Qy 1699 GCCAACTTG	1759	417	Qy 1819 GATGAGIT"     :::   Db 435 AspGlyTrp	RESULT 3 US-08-997-897-2 ; Sequence 2, Appli ; Patent No. 611451	; GENERAL INFORMATI ; APPLICANT: SRIV? ; APPLICANT: SURV? ; APPLICANT: SRIV?	; TITLE OF INVENT; ; FILE REFERENCE; ; CURRENT APPLICAT; ; CURRENT FILING I	NUMBER OF SEQ II SOFTWARE: Patent SEQ ID NO 2 LENGTH: 430		: LOCATION: (4) : FEATURE: : NAME/KEY: UNSUF	FEATURE: NAME/KEY: UNSUF LOCATION: (20) FEATURE:		: LOCATION: (54) : FEATURE: : NAME/KEY: UNSUF		; NAME/KEY: UNSUR ; LOCATION: (89) ; FEATURE: ; NAME/KEY: UNSUR	: LOCATION: (99) : FEATURE: : NAME/KEY: UNSUF : LOCATION: (114)		, NAME/KEY: UNSUF ; LOCATION: (129) ; FEATURE: ; NAME/KEY: UNSUF
GlyPheAsp 76 CCTCACT 846	AGTCGCGGT 906 ·	oLeuGlyArg 110	CAGATCAGGCTACC 954 :::         GluTyrAlaThr 126	SAATTCGATC 1011	GCGTGCCGAGGAAGA 1071 :::    -LysAlaYalarqLys 158	GTCTATGC 1119 ::: sileAsnTrp 178	NGGAGCCAAG 1164 NVAIGLUGIY 198	1188 .valAlaThr 218	TTTGCCAAC 1242	TGACGACAAGTAC 1302     .::    -AspProArgTyr 239	SCCGCCATG 1347     :::  Prolleval 259	-ATTGTACGCCGGCGT 1368     sileThrProAlaHis 279	rttcaaaggc 1428 NyalMetasn 299	*AGCGACAAG 1488    ::: Asparg 316	GAGAAAGAT 1548      GluileGly 331	1593  ThrGlyVal 351	-ATTCAGGCCGAT 1605 ::: nLeuAlaLysAsn 371	.GGTTTGCGT 1665
58 TrpAspThrThrLeuGlnAspIleIleIleArgGlnLysArgMetGlnGlyPheAsp 790 GCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACT 77	847 TCTTGGGGTGTGGAAGATGGAAAAGGAGAACAATCCTGGTATGGAAGTTCGCGT  11111:::111:::	GlnAlaLysValGluGluArgLeuArgGlyGluGlyIleSerArgTyrAspLeuGlyArg	ATCAAGCCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACC 	CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATC	GGTATGAACCGCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTGCGAGGAAAGA ::::::           ::: ThrLeuAspGluGJyLeuSer	GCATTCGCAGACTGGATCCGTAAGAACGCCAAGAGTGCTGTCTATGGC	GAT	GCCAACCGTGAGATGACTTATTTG	AGCGAGACGCTCTTCGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC       :::       ThtargProGluthrmetPheGlyAspVal	GCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTAC	AAAGACTACCTCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATG	CTCGAT	ATCCCTGCCGACAAGGTCCCCGATATATTCAAGAATGTAATCGACAAGAATTCAAAGGC	GACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAG	TTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGAT	CCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCT	ValValGluProArgLeuSerThrGlnTrpPheValLysMetAspGlnLeuAlaLysAsn	GCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGT     :::
0b 58 Qy 790	-		Oy 907 Db 1111	Qy 955 Db 127	Qy 1012 Db 147	Oy 1072 Db 159	Qy 1120 Db 179	Oy , 1165 Db 199	Oy 1189 Db 219	Qy 1243 Db 229	Qy 1303 Db 240	Qy 1348 Db 260	Oy 1369 Db 280	Qy 1429 Db 300	Oy 1489 Db 317	Qy 1549 Db 332	Qy 1594 Db 352	Qy 1606 Db 372

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-----GAT 1698 -
                                        ACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGC 1818
||||| :: :::: | |||:::
yrAsn-----AlaAspGlyGluMetTyrValGlyGluGluAlaProGluGly 434
           VASTAVA, RANJANA
AR, DEEPAK
YVASTAVA, BRAHM SHANKER
TYON: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
1: u011469-7
ATION NUMBER: US/08/997,897C
3. DATE: 1997-12-24
ID NOS: 7
ACCCCGGACGTGCTCTGCCGAGC-------
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TION:
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Db 74 TrpCysHisProGlyTyrSerCysArgTyrTrpCysHisProArg*** 89  Qy 1672 ACA	::: 90 SerCysArgCysTrpCysTyrArgArg***SerArgArgCysCysSerCysProCysCys	QY         1669        TCTCACGCAAACGAAAGAAAAGACCTTGCCCTTCTCAATGGCATAGGCATA         1616           .::  Db         110         ArgSerProCvs***SerArgArgArg***GlvCvsProCvsCv3SerCvsGlnHis***         129	1615TGGCCATCGCCTGAÀTAGCGC 1617TGGCCATCGCCTGAÀTAGCGC 130 Clurcalaramurducalaramurdacaluscalaramurdacasc	1588 GAGCAGCAGCTATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTTGG	146CysProSerLeuArgCys	Qy 1528 CARACTTTGCTCATGGACTTGAGCATGGGATGGGA1490 ::: 111   1111    1111    1111    11    11    11    11    1	OY 1489 ACTTGT	1456 ATACGAAGTCTGCATACTTCTTCGTGTCGCCTTTGAATTCTTGTCGATTACATTCTTGA	Db 192CysCys-rCysCys-r199	Qy 1396 ATATATCGGGGAGCTTGTCGGCAGGGATACGCCGGCGTACAATATCGAGCAGCGCA 1337	Db 200CysCysArgCysTrpArgThr 206	QY         1336         GCACCTTACGGTCGAGGGAGGTAGTCTTTGTACTTGTACTCGTCAAGCGATTTGAGGA         1277           DD         207	STGCAAAACGAACCA	213CysTrpGlnSerLeuGly***SerArg	Qy         1216         CCTCGGTACCACGAAGAGCGTCTCGCTCAAATAAGTCATCTCACGGTTGGCCTTGGCTC         1157           Db         222         ProArg	Length: 430  QY 1156 CTTCCTTATAAGCCTTTTCGAGAAGAAAAAAAGCAATACAATACAAGCAACTCTTGCGGTAAAAAAAA		Indels: 352 Qy 1096 TCTTACGGATCTACGGATGCTCTTTCCTCGCCACGCTTACGACCTATCACGT Gaps: 37	Db 241	Db 241 SerArgGlyPheArgIleArgCysCysSerPhePro	Db 241 SerArgG1yPheArgC1ySCysScrPhePro	Db   241 SerArgG1yPheArgC1ySCysScrPhePro	GTCGTTGTTCGATAGGAAG 1907  GY 1039 CAAGACGAGCGAGACCGGGTTCATACCGATCTACCATAGTTAGCACTCTGAG  All	CTGGTTGTTGGATAGGAAAG	GTGGTTGTTGGATAGGAAG 1907  GY 1039 CAAGACGAGCGAGCCGGGTTCATACCGATTCTTCCAATAGTTAGCATTCTGA  [1111]	CTGGTTGTTCGATAGGAAAG	GTGGTTGTTGGATAGGAAG 1907  GY 1039 CAAGACGAGCGAGCCGGGTTCATACCGATTCTTCCAATAGTTAGCATTCTGA  [11   1   1   1   1   1   1   1   1   1	CTGGTTGTTCGATAGGAAAG
LOCATION: (159) FEATURE: NAME/KEY: UNSURE	LOCATION: (169) FEATURE: NAME/KEY: UNSURE		LOCATION: (185) FEATURE: NAME/KEY: UNSURE				LOCATION: (291) FEATURE: NAME/KEY: UNSURE		LOCATION: (339) FEATURE: FORMERE:		NAME/KEY: UNSURE LOCATION: (356)	FEATURE: NAME/KEY: UNSURE LOCATION: (366)	FEATURE: NAME/KEY: UNSURE LOCATION: (410)		; LOCATION: (421) US-08-997-897-2		larity: 23.468 imilarity: 19.358	Query Match: 3.26% I DB: 3 G	100 to 00 00 00 00 00 00 00 00 00 00 00 00 00	768-766-80-80 X (8617-1) I-868-	-355-1 (1-2139) X US-U8-997-8997-8997-8997-8997-8997-8997-89	-355-1 (1-2139) X US-99/-899/-899/-CGAATACGGGGTACCGGAGTTACCGC	CGAATACGGGCTACCGGAGTTACCGC	CGAATACGGGGCTACCGGAGTTACCGCCCG'	CGAATACGGGGCTACCGGAGTTACCGC	CGAATACGGGCTACCGGAGTTACCGC	CGAATACGGGCTACCGGAGTTACCGC	1960 CGAATACGGGGCTACCGGGTTACCGC 1960 CGAATACGGGGCTACCGGGTTACCGC 1961

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	TATTGTCCTTGTGTTTCGGCCGGCCGGTTGTCGGCACCGGCATACACGCGGAATACGC 680	TGAAGTCGCCCGTGTGACGCGCCACATCCAGTTGTCCGTATCGCCTCCGAACTTACCTA	.::    CysGlnGlyCys***SerHisArgArgPheArgCysArgGluCysCys 302	CAGAGCTGGGAGGAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGA 560	302	AGTATTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTCTGCATTTT 500 :::            ASnCysArgCysTrp	9 CTT	  LeuproGlyArgAsp***ArgProValGlyHisArgLysIleProThrCysCysPheArg 337		GCTCCATCTCGTCAGTGATACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGA 395	AsnProlleArg 361	TCTTGCGCAGATACTTCACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAG 335	CysCysProSer***SerArgProlle	AAACGAAACCATCGCGCAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATACCACCGT	GlyArgSerTyrArgTrpProPro	ATCCGCAGTGGTGGTTGGTAAAGATCAGGCCCTGATCGGACACTGTGA :::	ThrLysSerGlyArgSerGlnAsnCysTrpHisArgSerSerGlySerArgThr 403	TACCGGTACATCGCCACCGA AGATAACCACGCATTGGCAATGGACGCTTGT	Argryt	CGAAAC	ArgSer 423	1 4 -488-940-18 	quence 10, Application US/U8488940 tent No. 585400000000000000000000000000000000000	MEAND INCOMPANION. PAPPLICANT: Reed, Guy L. TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE		ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street	CITY: Boston STATE: MA		PE	COMPUTER: ISEM FC COMPACTION OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS	LICATION DATA:	DITING DAME: 00 THE 100
	Oy 739		Db 287	Oy 619	Db 302	Oy 559 Db 303	Oy 49	Db 318	Qy 496 Db 338	0y 454	Db 358	Qy 394	Db 362				.98E qu		404		Db 422	RESULT 4 US-08-48	; Sequence 18, ; Patent No. 50	3	NUM			;;			CUR	

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718 ---AsnAsnLeuAspAlaPheGlylleMetAspTyrThrLeuThrGlyLysValGluAsp 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- ATCTTTACCAACCAC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCG------GGTCTTTCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 ValLysAsnArgGluGlnAlaTyrArgIleAsnLysLys------SerGly 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660 GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 HisProGlyTyrThrIleTyrGluArgAspSerSerIle------ValThrHisAsp 607
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133
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263
167
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
             NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REGISCOMCHOCKET NUMBER: 05433/009001
TELEPHONE: 617/542-5070
TELEPA: 200154
TELER: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 anino acids
                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           0.00188
127.50
35.05%
20.09%
3.34%
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Local Similarity:
Match:
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02110-2804
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ZIP: 021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1075 TTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1135 CTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTAT---TTGAGC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTAC 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 ileSerAsnGlnLeuSerGlyThrAlaValThrAlaLysGluArgTyrLysIleGluAla 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 AspileHisGlyAsnArgPheArgGlySerAla------ThrAla 394
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                                                                                                                                                                                                                                                               535 CCTTTCTATTCCAACAACGAATACTTCCTCATCGTC------TACGATGTATTCAAG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              832 GATCGCTACCTCACTTCTTGGGGT-----GTGGAAGATCGTATCGAAAACGAGAAAT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 AlaLysTyrLysGlyTyrTrpAspPheMetThrAspAlaThrLeuAspAsnLysTyrThr 304
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                                                                      156 IleProPheAspLysAsnLeuIleGluTyrLeuLysLysSerSerGluValValSerLys 175
                                                                                                                                                                                      475 GTATGCCAAGAACTGGCCAAAAAAAAAATGCAGACGAGAACCAACTCTGCATCGTAGAG 534
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                                                                                                            415 GTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAG 474
                                   355 CTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAG 414
                                                                                                                                                                                                            176 PheClualaGlnLysGlyGlyIleGluAsnAsnThrArgLeuThrHisLysAspLeuSer
                                                                                                                                                                                                                                                                                                  212 ThrGlnPheAlaGlnGluLysTyrLysGluLeuIleGluAsnAlaHisAspLysLysSer
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US-10-008-355-1 (1-2139) x US-09-059-584-53 (1-713)
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1429 GACACGAAGAAGTATGCAGAC---TTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGAC 1485
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                                                                                                                                                                                                                 (372 CCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGAC---AAGAAATTCAAAGGC 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1660 TIGCGIGAGAIGIACCCCGGACGIGCI-------CIGCCGAGCGAIGCCAACTIC 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1708 ACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTAC 1767
                                                                   CICCCCICGCICGACCGIAAGGIGCIGCCCCCCAIGCICGAIAITGIACGCCGGCGIAIC 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 LeuMetValAsnAspGluValIleValLysThrTyrGlyLysAsnPheGluTyrLeuLys 548
                                                                                                                                                                                                                                                                                                                                                                                                     476 PheThrLysLysGlnLeuAspAsnPheGlyAsnAlaLysLysLeuValLeuGlySerThr 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          549 PheGlyGluLeuSerValGlyAspSerHisSerValPheLeuGlnGlyGluArgThrAla 568
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433 ThraspaspasnLysLeuPheGlyValPheGlyAlaLysArgAspLysValGluLysThr 452
                                                                                                                                                                                                                                                                                 ------GlyThrPheAsnAsnThrAsnLysAlaThrThrPheThrPro 475
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Patent No. 5854049
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 Franklin Street CITY: Boston STREET STREET STREET STREET STREET STREET STREET MA
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COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 GURENT APPLICATION DATA: APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819 RREFERENCE/COCKET NUMBER: 05433/009001 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION OF 4: SEQUENCE CHARACTERISTICS: LENGTH: 800 amino acids TYPE: amino acids STRANDEDNESS: not relevant TOPOLOGY: linear MOLECULE TYPE: protein	Alignment Scores:  0.00432 Length: 800 Pred. No.: 122.50 Matches: 130 Score: 33.98* Conservative: 99 Best Local Similarity: 19.29* Mismatches: 254 Query Match: 2.1* Indels: 191 DB: 2	5-1 (1-2139) x US-08-488-940-4 (1-800)	GGTATCACAGTGTCCGATCAGGGCCTG	CACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGAT 324	GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCC 375 :::       :::       :::		ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495 ::: :::   ::: 	AAAGAA	30	TTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT 609	CCCAGCTCTGTAGGTAAGTTCGGA	70
COMPUTER READA MEDIUM TYPE: COMPUTER: II OCHRATING SY, SOFTWARE: PALICA FILING DATE: CLASSIETCATION RAME: FRASE REGISTRATION TELECOMMUNICAT TORONO TELECOMMUNICAT TORONO	Scores:		GGTATC? 	CACTGCG	GGTTTCC : AsnAsp]	GTGAAGT         Vallys	ATCACTC:::: LeuAsnG		AATC		o ·	
COMPUTER MEDIUM COMPUT COMPUT SOFTWA SOFTWA CURRENT APPLIC, FILING CLASSI ATTORNEY NAME TELECOMM TELEC	Alignment S. Pred. No.: Score: Percent Sim Best Local Query Match DB:	-008	223	265	325	376 231	436	496	502	559	610	649
-so	Aligni Pred. Score Perce Best Query DB:	US-10	Qy	Qy Db	Qy Db	Qy Dp	Oy Dp	δ, d	70	Qy Dp	Qy	Qy

qq	
Oy	GCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTT
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δy	769 GTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGT 828
qq	371Asp 371
Øγ	829 ACGGATCGCTACCTCATGG 852
qq	372 LysaspargTyrThrGluGluGluArgGluValTyrSerTyrLeuArgTyrThrGlyThr 391
δŏ	853 GGTGTGGAAGATCGTATCGAAAAGGAGAACAATCCTCGTATC 894
qq	392 ProileProAspAsnProAsnAspLysAsnAsnSerGlnLeuValValSerValAlaGly 411
δλ	TGGAAGGAAGCCATGAGCGCAGATCAGGCTAC
qq	412 ThrValGluGlyThrAsnGlnAspileSerLeuLysPhePheGluIleAspLeuThrSer 431
Οy	955 CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGG 999
QD	432 ArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAla 451
Qy	TCTCGCTCGTCTTGACGTGATAGGTCGTAA
qα	452 ThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeuLysAla 469
Qγ	()
qq	470 IleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPheGluValIle 488
Qy	TATAA
qq	489 AspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLys 508
Qy	1153 GAAGGAGCCAAGCCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACC 1212
q	509 AspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 527
Qy	1213 GAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCC 1272
qq	528 ValArgValArgTyrLysGluLysProileGlnAsnGln 540
Qy	1273 GGTATCCTCAAATCGCTTGACGAGAAC1302
qq	541 AlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp 558
Qy	1303 AAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTA 1359
q	559 AspAspPheArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaile 576
Qy	1360 CGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAA 1419
qq	577 GlyAspThrileThrSerGlnGluLeuLeuAlaGlnAlaGlnSerileLeuAsnLysAsn 596
Qy	GACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTA
QQ	597 HisProGlyTyrThrIleTyrGluArgAspSerSerIleValThrHis 612
Οy	1480 AGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATC 1539
QQ	613 AspAsnAspIlePheArgThrIleLeuProMetAspGlnGluPheThrTyrArgValLys 632
Qy	1540 GAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAG 1599
qa	633 AsnArgGluGlnAlaTyrArglleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsn 652
δλ	1600 GCCGATGCGATGCCTATGCCATTGAGAGGCAAG 1641

DB: 2 Gaps: 35	US-10-008-355-1 (1-2139) x US-08-488-940-3 (1-813)	Qy 223 GGTATCACAGTGTCCGATCAGGGCCTGATCTTTACCAACCAC 264	Db 190 GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 209	Qy 265 CACTGCGGATACGGTGCTATCCAGAGCACGGTGGATCACGACTATCTGCGCGAT 324	210 HisProGlyTyrThrlleTyrGluArgAspSerSerIleValThrHisAsp	GGTGA		Qy 376 GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGT 435	Db 244 ValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGly 258	Qy 436 ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495	Db 259 LeuAsnGluGluTleAsnAsnThrAspLeuIleSerGluLysTyrValLeuLysLys 278	Qy 496 AAAGAA 501	Db 279 GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr 298	Qy 502AATGCAGACGAGAGCCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATAC 558	Db 299 ValAspValAspThrAsnGluLeuLeuLysSerGluClnLeuLeuThrAlaSerGluArg 318	Qy S59TICCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT 609	Db 319 AsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyr 336	Qy 610 CCCAGCTCTGTAGGTAGGTTCGGAGGCGATACGGACAAC 648	Db 337AsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAsp 355	Qy , 649 TGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCGGTGC 708		Qy 709 AACCGGCCGGCCGAATACAGCAAGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCC 768	Db 370 LysargProGluGlyGluAsnAlaSerTyrHisLeuAlaTyr 383	Qy 769 GTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGGCAGT 828	Db 384Asp 384	Qy 829 ACGGATCGCTAC	Db 385 LysAspArgTyrThrGluGluGluArgGluValTyrSerTyrLeuArgTyrThrGlyThr 404	Qy 853 GGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATC	Db 405 ProlleProAspAsnProAsnAspLysAsnAsnSerGlnLeuValValSerValAlaGly 424	Qy 895 GAAGTTCGCGGTATCAAGCAAGCATCTGGAAGGCATGAGCGAGATCAGGCTACC 954	Db 425 ThrValGluGlyThrAsnGlnAspIleSerLeuLySPhePheGluIleAspLeuThrSer 444	QY 955 CCTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGG 999	Db 445 ArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAla 464	QY 1000 AAGAATTCGATCGCTATGAACCGCGGTCTCGTCGTCGTGATAGGTCGTAAGCGT 1059	Db 465 ThrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeuLysAla 482	Qy 1060 GCCGAGGAAAGAGCATTCGCAGACTCGATCCGTAAGAAC
Db 653 ThrAspLeulleSerGluLysTyrTyrValLeuLysLysGlyGluLysProTyrAspPro 672	Qy 1642	eThrIleLysTyrValA	Qy 1684 GCTCTGCCGAGGGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATC 1734	LysserG	1735 AAGGGATATGAACCGCAGGAGGTGCCTGGTACAAC	Db 713TyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGly 730	1771TATCATACGACAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGAT	731	Oy 1822 GAGTTGCCGTACAGGAGAATATCCTCGACTCTTCCGCACCAAAACTATGGT 1875	Db 740ValGluAspAsnH1sAspAspThrAsnArgIleIleThrValTyrMetGly 756	Qy 1876 CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTC 1911	Db 757 LysargProGluGlyGluAsnAlaSerTyrHisLeuAlaTyr 770	RESULT 7 US-08-488-940-3	: Sequence 3, Application US/08488940	GENERAL INFORMATION:	TITLE OF INVENTION: DASMIN-RESISTANT STREPTOKINASE	CORRESPONDENCE ADDRESS:	ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street	CITY: Boston STATE: MA	ZIP: 02110-2804	MEDIUM TYPE: Floppy disk	-Dos	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	AFFLICATION NUMBER: US/US/488,940 FILING DATE: 09-7UN-1995 CLASSTETCHION: 614	ATTORNEY INFORMATION: NAME: Fracer lante v	REFERENCE TO THE STATE OF THE S	TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070	TELEFAX: 617/542-8906 TELEX: 200154	z	LENGTH: 813 amino acids TYPE: amino acids	EDNESS:	YPE	Alianment Scores:		ercent Similarity: 33.98% Conservative: est Local Similarity: 19.29% Mismatches:	3.21% Indels:

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                                                     -----GGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGGAAAAGGCTTATAAG 1152
                                                                                                                           1153 GAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACC 1212
                                                                                                                                                                                                  .213 GAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCC 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                       1360 CGCCGCCTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAA 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                686 PheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGlu 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 AspGlySer---ValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHis 540
                                                                                                                                                                                                                                        .----LysProlleGlnAsnGln 553
502 AspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLys 521
                                                                                                                                                                                                                                                                                                                                                                      572 AspAspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeu-----AlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646 AsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              666 ThrAspLeulleSerGluLysTyrTyrValLeuLysLysGlyGluLysProTyrAspPro
                                                                                                                                                                                                                                                                                                            554 Ala-----LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1420 TTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTAT
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                                                                                                                                                                                                                                                                        1273 GGTATCCTCAAATCGCTTGACGACAAGTAC--------
                                                                                                                                                                                                                                      541 ValArgValArgTyrLysGlu------
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Patent No. 5894049
GENERAL INFORMATION:
APPLICANT: Reed, GUY L.
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325 GGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCG------GGTCTTTCC 375
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667 ValAspValAspThrAsnGluLeuLySSerGluGlnLeuLeuThrAlaSerGluArg 686
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130
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254
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TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
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|HisProGlyTyrThrIleTyrGluArgAspSerSerIle----
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                                                                                                                                                                                                                                                OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELECOMMUNICATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8006
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/488,940 FILING DATE: 09-JUN-1995 CLASSIFICATION: 514 ATTORNEY AGENT INFORMATION:
                                                             Richardson P.C.
                                                                                                                                                                                                                                 IBM PC compatible
                                                                              225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1181 amino acids
                                                                                                                                                                                                             Floppy disk
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122.50
33.98%
19.29%
3.21%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                             Fish &
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Best Local Similarity:
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TOPOLOGY: li
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                                                                                                      Boston
                                                             ADDRESSEE:
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                                                                                                                                                                                                                                   COMPUTER:
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::: Db 994 AspAsnAspIlePheArgThrIleLeuPro	Qy. 1540 GAGAAAGATCCGGCAGTAGAGCTTTCCAAC :::::	Qy 1600 GCCGATGCGATGCCCAATGCC   111   1:1:1:   111   1	Qy 1642	Oy 1684 GCTCTGCCGAGGGATGCCAACTTCACC	1735	1094TY	Oy 1771TATCATACGACAGGGAAGGG	Qy. 1822 GAGTTTGCCGTACAGGAGAATATCTCGAC	Qy 1876 CGCTATGCCGAGAACGGTCAGCTC ::	SUL	US-08-488-940-1; Sequence 1, Application US/08488940; Patent No. 5854049	; GENEKAL INVEWHATION; ; APPLICANT: Reed, Guy L. ; TITLE OF INVENTION: PLASMIN-RESIST ; NUMBER OF SEQUENCES: 20	CORRESPONDENCE ADDRESS:  ADDRESSEE: Fish & Richardson P.C STREET: 225 Franklin Street CITY: Boston	; STATE: MA ; COUNTRY: USA ; ZIP: 02110-2804 ; COMPUTER PEADALE FORM:	COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPUTER: SYSTEM: PC-DOS/MS-DOS	SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:  APPLICATION NUMBER: U.508/488,94	; FILING DATE: 09-JUN-1995 ; CLASSIFICATION: 514 ; ATTORNEY AGENT INFORMATION:	REGISTRATION NUMBER: 34,819 REFERENCE/DOCKET NUMBER: 05433/C	; TELECOMMOLICATION INFORMATION: ; TELEPHONE: 617/542-5070 ; TELEFAX: 617/542-8906 ; TELEX: 200154	; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 1194 amino acids ; TYPE: amino acid	; STRANDEDNESS: not relevant ; TOPOLOGY: linear
/ S59TTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT 609	610 CCCAGCTCTAGGTAAGTTCGGA	649 TGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATCCGCGTGTATGCCGGTGCCGAC	709 AACCGGCCGAATACACAGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCC	/38 LYSAIGPTOGIUGIYGIUASNAIASETTYTHISLEUALATYT 769 GTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGG	752Asp	/ 829 ACGGATCGCTAC	/ 853 GGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATC	895 GAAGTTCGCGGTATCAAGCAAGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACC  1	· 955 CGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATGG	813 ArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAla	<pre>/ 1000 AAGAATTCGATCGGTATGAACCGCGGTCTCGTCTTGACGTGATAGGTCGTAAGCTCT 1059 // 11</pre>	/ 1060 GCCGAGGAAGCATTCGCAGACTGGATCCGTAAGAAC	1099GGCAAGAGTGC     870 AspPheAlaSerAspAl	1153 GAAGGAGCCAAGGCCAA :::   ::: 890 AspGlyServalTh	1213 GAGGTGGTTGTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCTACAAATCCTCATGCTATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTATGCTCATGCTATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTATGCTCATGCTATGCTCAT	1273	922 AlaLysSerVa	/ 1303 AAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTCCCGCCATGCTCGATATTGTA 1359	/ 1360 CGCCGGCGTATCCCTGCCGACAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAA 1419     :::::::::::::    :::      958 GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuasnLysAsn 977	7 1420 TTCAAAGGGGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTAT 1479 11	1480 AGCGACAAGTTCCATGC
. 65 A	Oy Db	ò	3 6 6	å Å	QQ	9	Oy Dp	oy G	ò	g	S G	oy Ob	OY Db	oy B	yo 4	å å	qq	9 9	ç G	Oy Dp	δ

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AGAGCGTAATAGCTGCTGCTCGCGCTATTCAG 1599
                                                                      ysLysSerGlyLeuAsnGluGluIleAsnAsn 1033
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|roMetAspGlnGluPheThrTyrArgValLys 1013
                                                                                                                                                                TTGCCGGTTTGCGTGAGATGTACCCCGGACGT 1683
                                                                                                                                                                                   hrlleLysTyrValAspValAspThrAsnGlu 1073
                                                                                                                                                                                                                                                ::: ::: 1093
                                                                                                                                                                                                                                                                                    ----TGGTACAAC----- 1770
                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCTTCCGC----ACCAAAACTATGGT 1875
                                                                                                                                                                                                                            -----ATGCGTATGAGCTACGGCTCCATC 1734
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ysLeuLeuTyrAsnAsnLeuAspAlaPheGly 1111
                                                                                                                                                                                                                                                                                                                                               GCGTATTGGAGAAGCAGGATCCTAAGAGCGAT 1821
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|yrHisLeuAlaTyr 1151
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Percent	ent Similarity:	33.988	Conservative:	0000 1000 10000		qa	۵
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ු <b>අ</b> ධ	:::       ::: 608 AsnAspIlePheArgThrIle	::: .rgThr11e	::: LeuProMetAspG	:: -LeuProMetAspGlnGluPheThrTyrArg	624	අ <u>ධ</u>	۽ د
Qy	376 GTGAAGTATCTGC	GCAAGATCGTGAAGG	TAACGGACAAGGTAG	GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGT	435	δō	Α .
q	625 ValLysAsnArgG	  ValLysAsnArgGluGlnAlaTyrArgIleAsnLysLy	:: leAsnLysLys	SerGly	639	an a	Ω >
		TGGAGCGTCTGCGCA	ATCACTGACGAGATGGACGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAAC	TGGCCAA	0	α Δ	
		leAsnAsnThrAspL	euIleSerGluLysT	yrTyrValLeuLysLys	659	٥٨	γ
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	,	TCATCGTCTACGATG	TATTCAAGGACGTT	JULUSLA	509	Qy	у 1.
	AsnLeuAs	:::	AsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuT	s:::::::::::::::::::::::::::::::::::::	717	Δ	Db 1
ò	610 CCCAGCTCTGTAGGTAAGTTCGGA	GTAAGTTCGGA		GGCGATACGGACAAC	848	δλ	γ 1
	} ;		SINCE THE STATE OF	hrGlyLysValGluAsp	736	Ω	Db 1
δy	649 TGGATGTGGCCGC	GTCACACGGGCGACT	TCAGCGTATTCCGCG	TGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGAC	708	δλ	у 1
qa	737A	  snHisAspAspThrA		 alTyrMetGly	750	Δ	Db 1
Qy	709 AACCGGCCGGCCG	AATACAGCAAGGACA	ATAAACCCTATAAGC	AACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCC	768	ογ	
qq	   751 LysArgPro	:::! GluGlyGluA	:::      GluGlyGluAsnAlaSerTyrHisLeuAlaTy	 euAlaTyr	764	Δ	Db 1
Qy	769 GTATCCATGCAAG	GCTACAAGGCTGACG	ACTATGCCATGACCA	GTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGT	828	δŏ.	Α Τ
QQ	765			AspAsp	765	Δ ,	Op 1
Qy	829 ACGGATCGCTAC-			CTCACTTCTTGG	852	δο i	. у
qq		hrGluGluGluArgG	 LysAspArgTyrThrGluGluGluArgGluValTyrSerTyrLeuArgTyrThr	  euArgTyrThrGlyThr	785	<u>α</u> (	. DD
QY	853 GGTGTGGAAGATC	GGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATC	ACAATCCTCGTATC-		. 894		7 6
QQ	786 ProlleProAspA	\snProAsnAspLysA	rolleproAspAsnProAsnAspLysAsnAsnSerGlnLeuValValS	alValSerValAlaGly	805		90 7
Οy		NTCAAGCAAGGCATCI	GAGTTCGCGGTATCAAGCAAGCATCTGGAAGGAAGCATGAGCGAGGTCAGG	GCGCAGATCAGGCTACC	95	<u> </u>	DP 1
οg	806 ThrvalGluGlyT	hrAsnGlnAspIle£	erLeuLysPhePheG	ThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePheGluIleAspLeuThrSer	825	о <sub>у</sub>	y 1

ζ	935 CGIAICAAAIAIGC	
qq	826 ArgProAlaHisGlyGlyLysThrGluGlnGly	LeuSerProLysSerLysProPheAla 845
Οy	1000 AAGA	TTGACGTGATAGGTCGTAAGCGT 1059
qo	Db 846 ThraspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu	:::::  laAspLeuLeuLysAla 863
Qγ	1060	AC 1098
qa	Db 864 IleGluGluLeulleAlaAsnValHisSerAsnAs	ıı snAspAspTyrPheGluValIle 882
Qy	1099GGCAAGAGTGCTGTCTATGGCGATGT	ATTGTCTTCTCGAAAAGGCTTATAAG 1152
qq	883 AspPheAlaSerAspAlaThrIleThrAspAr	spLy
Qy	1153 GAAGGAGCCAA	GCGAGACGCTCTTCGGTGGTACC 1212
qq	903 AS	IngluPheLeuLeuSerGlyHis 921
Qy	1213 GAGGTGGTTCGTTTTGCACAGTTTGCCAACGCA	CTACAAATCCTGATGCTCATGCC 1272
qq	922	LysProlleGlnAsnGln 934
Qy	1273 GGTATCCTCAAATCGCTTGACGACAAGTAC	
qq	935 AlaLysSerValAspValGluTyrThrVal	GlnPheThrProLeuAsaProAsp 952
Οy	1303 AAAGACTACCTCCCTCGCTC	TGCCCGCCATGCTCGATATTGTA 1359.
qq	953 AspAspPheArgProGlyLeuLy	
Οy	Qy 1360 CGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAAAAAAA	TCAAGAATGTAATCGACAAGAAA 1419
qq	971 GI	laGlnSerIleLeuAsnLysAsn 990
ΟŸ	1420	TCGACAAGAGTGTGGTTCCTTAT 1479
QQ	Db 991 HisproGlyTyrThrIleTyrGluArgAspSerSerIleValThrHis	rgAspSerSerIleValThrHis 1006
Qy	1480	AGGAAAAGTTTGCCAAGGCTATC 1539
qq	Db 1007 AspasnAspIlePheArgThrIleLeuProMetAspGlnGluPheThrTyrArgValLys	IngluPheThrTyrArgValLys 1026
Qy	1540	TAGCTGCTCGCGCTATTCAG 1599
qq	Db 1027 AsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsn	lyLeuAsnGluGluIleAsnAsn 1046
Qy	1600	AGGGCAAG 1641
QQ	Db 1047 ThraspLeuileSerGluLysTyrTyrValLeuLysLySClyGluLysProTyrAspPr	::; ysGlyGluLysProTyrAspPro 1066
Oy	1642 -	TGCGTGAGATGTACCCCGGACGT 1683
qq	1067 PheAspArgSerHisLeuLysLeuPheThrIle	yrValAspValAspThrAsnGlu 1086
Qy	1684 GCTCTGCCGAGCGATGCCAACTTCACC	ATGCGTATGAGCTACGGCTCCATC 1734
QQ	1087 LeuLeuLysSerGluGlnLeuLeuThrAla	SerGluArgAsnLeuAspPheArgAspLeu 1106
QY	1735 AAGGGATATGAACCGCAGGACGGTGCC	ACAAC1770
QQ	1107TyrAspProArgAspLysAlaLy	IIIIII SLeuLeuTyrAsnAsnLeuAspAlaPheGly 1124
δy	1771TATCATACGACAGGCAAGGCGTATT	AAGCAĞ
QQ	1125 ileMetAs	1133
Οy	1822 GAGTTIGC	GCACCAAAACTATGGT 1875
Dp	1134ValGluAspAsnHisAspAspThr	[leI]
Qy	QY 1876 CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTC	CTTTC 1911

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571 GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591 HisProGlyTyrThrIleTyrGluArgAspSerSerIle------ValThrHisAsp 607
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                                                                                               Sequence 17, Application US/08488940
Fatent No. 5854049
GENERAL INFORMATION:
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish 6 Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORY disk
COMPUTER READABLE FORM:
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130
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254
191
35
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,940
FILING DATE: U9955
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/009001
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
Db 1151 LysargProGluGlyGluAsnAlaSerTyrHisLeuAlaTyr 1164
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
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33.98%
19.29%
3.21%
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Best Local Similarity:
Query Match:
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US-08-488-940-17
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	qq	099	  GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr	619
	οy	502	GACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAA	558
	qq	680	las	669
	Qy	559	TTCCTCATGGTCTACGATGTATTCAAGGACGTTGGTATTTGCTCCT	609
	Dp	700	AsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyr	717
	Οy	610	CCCAGCTCTGTAGGTAAGTTCGGA	648
	qq	718	eMetAspTyrThrLeuTh	736
	Οÿ	649	rgrggccg	708
	qq	737	AsnHisAspAspThrAsnArgIleTleThrValTyrMetGly	750
	٥y	709	AACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCC	768
	Db	751	 LysargproGluGlyGluAsnalaSerTyrHisLeuAlaTyr	764
	Qy	169	CCATGCAAGGCTACAAGGCTGACGACTATGCCATG	828.
	qq	765	ASP	765
	Qy	829	)	852
	Db	992	ј дтугт	785
	Οy	853	GGTGTGGAAGATCGTATCGAAAACGAACAATCCTCGTATC	894
:	QQ	786	:::     ProlleproAspAsnProAsnAspLysAsnAsnSerGlnLeuValValSerValAlaGly	805
	٥y	895	GAAGTTCGCGGTATCAAGCAAGCCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACC	954
	qq	908	ePheGluI	825
	Qγ	955	ATCAAATATGCCAGCAAGTATGCTCAGAG	666
	Dp	826	gProAlaHisGlyGlyLySThrGluGlnGlyLeuSerProLys	845
	0y 1	000	AAGAATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGT	1059
	QQ	846		863
	Qy 1	090	GCCGAGGAAAGAGCATTCGCAGACTCGAAACGAAC	1098
	qq	864	AspAspTyrPheGluValIl	882
	0y 1	660	GGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAG	1152
	qa	883	AspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLys	902
	Qy 1	1153	GAAGGAGCCAAGGCCAACCGTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACC	1212
	qq	903	.::	921
	Qy 1	213	3CT	1272
	Dp	922	ValArgValArgTyrLysGluLysProlleGlnAsnGln	934
	Qy 1	273	ATCCTCAAATCGCTTGACGACAAGTAC	1302
	QQ	935	AlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp	952
	0γ 1	1303	AAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTA	1359
	Db	953		970

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1360 CGCCGCCGTATCCCTGCCGACAAGCTCCCCGATATTCAAGAATGTAATCGACAAGAA 1419
                                                                       1420 TICAAAGGCGACACGAAGAAGTAIGCAGACTICGIAIICGACAAGAGIGIGGTICCIIAI 1479
                                                                                                HisProGly------TyrThrlleTyrGluArgAspSerSerlleValThrHis 1006
                                                                                                                                            1480 AGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATC 1539
                                                                                                                                                                   1540 GAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAG 1599
                                                                                                                                                                                                                                                        1027 AsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsn 1046
                                                                                                                                                                                                                                                                                                                   ------CGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGT 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1087 LeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeu 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1822 GAGTITGCCGTACAGGAGAATATCCTCGACCTCTTCCGC-----ACCAAAACTATGGT 1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1684 GCTCTGCCGAGCGATGCCAACTTCACC-----ATGCGTATGAGCTACGGCTCCATC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGly 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TATCATACGACAGGCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGAT 1821
                                                                                                                                                                                                                                                                                                                                                                                           1067 PheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGlu
                                  971 GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn
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                                                                                                                                                                                                                                                                                            1600 GCCGATGCGATGCCCATTGCCATTGAGAAGGGCAAG------
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1125 IleMetAspTyrThrLeuThrGlyLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes FOI TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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US-09-036-987A-3
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2034 TTCGAACTCGATGTCACCACTCATAGCTTCCCAGTTGCCATCGAAAGCAAGACCGATCAG 1975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1974 ACGGCCGTTCTTATCGAATAC-----GGGGCTACCGGAGTTACCGCCCGTGATGTCGTT 1921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2079 GAGAACGTAGCGGATGTCCACGCT-----GATTGTGCGCCTGCAGATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1435 ValArgIleAlaMetArgAlaAlaGlyValAsnPheArgAspAlaLeuIleAlaLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1496 ProLeuAlaValAlaAspHisArgMetValThrArgIleProAlaGlyTrpSerPheAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1821 -------ATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCTTGCCTGTCGTATG
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1536 GlyLeuArgProGlyGluSerLeuLeuValHisSerAlaAlaGlyGlyValGly-----
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
  US/09/036,987A
                                                                                            NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                     09-MAR-1998
                                                                                                                                                                                                                                                                                                         : 2152 amino acids
amino acid
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119.00
30.96%
19.10%
3.01%
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MOLECULE TYPE: protein
APPLICATION NUMBER:
FILING DATE: 09-MAR
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                         LENGTH:
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Sun May 25 15:40:16 2003

AlaSerLeuArgMetLeuProArgGlyGlyArgPheLeuGluLeuGlyLysThrAspVal 
CTTGTCGATTACATT CTTGAATATATCGGGGAGCTTGTCGGCAGGGATACGCCGGCG
TACAAT
CAGCACCTTACGGTCGAGCGAGGGAGGTAGTTTGTACTTGTCGTCAAGCGATTT :::        :::
GAGGATACCGGCATGAGCATCAGGATTGTAGCCAATGCGTTGGC
AAACTGTGCAAAACGAACCACCTGGTACCACCGAAGAGCGTCTCGCTCAAATA :::
AGTCATCTCACGGTTGGCCTTGGCTCCTTATAAGCCTTTTCGAGAGAAGACAATAC
ATCGCCATAGACAGCACTCTTGCCGTTCTTACGGATCCAGTCTGCGAATGCTCTTCCTC
GGCACGCTTACGACCTATCACGTCAG :::        SerLeuThrValGluArgLeuAspGlnValLeuArgProLysValAspGlyAlaArg
ACGAGCGAGACCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAGCATA
CTTGCTGGCATATTGATACGGGTAGCCTGATCTGCGCTCATGGCTTCCTTC
TTGCTTGATACCGCGAACTTCGATACGAGGATTGTTCTC
<b>AlaGluHisGlyMetAlaSerThrL</b> euArgGluAlaGluGlnAspArgLeuAlaArgSer
GTTTTGGATACGATCTTCCACACC
GlyLeuLeuProIleSerThrGluGluGlyLeuSerGlnPheAspAlaAlaCysGlyGly
CCAAGAAGTGAGGTAGGGATCGGTACTGCCGGGAAACCGATGGTCATGGCATAGTC :::        :::    :::    :::     :::

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1941 AlaHisThrValValAlaProValArgPheSerArgLeuSerAspGlyAsnAlaIleLys 1960
                                                                                                                                                                                                                                                                          1970 ----- ProHisArgValAsnLysAlaAlaThr
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                                                                                                                                                                                                                                                                                                                                                                   1979 -----AlaAspAspAluSer 1984
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                                                 795 GTCAGCCTTGTAGCCTTGCATGGATACGCCAGCGAAGTAAACGGCCTTATAGGGTTTATT 736
                                                                                                                                       735 GTCCTÜGCTGTATTCGGCCGGCCGGTTGTCGGCACCGGCATACACGCGGAATACGCTGAA 676
                                                                                                                                                                                                                              675 GTCGCCCCGTGTGACGCGCCCACATCCCAGTTGTCCCTTCCCGAACTTACCTACAGA 616
                                                                                                                                                                                                                                                                                                                       615 GCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGAAGTA 556
                                                                                                                                                                                                                                                                                                                                                                                                           555 TICGTIGITGGAATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTCTGCATTTTCTTT 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 CAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATAGCACCGTATCCGCAGTGGTGTT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 -----GAGCGTAAAGCCGAGCTTCGATCCAG 115
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APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
TILE REFERENCE: 50489 DIVI
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
FEARLIER APPLICATION NUMBER: US/09/370,700
FEARLIER APPLICATION NUMBER: US/09/36987
FEARLIER PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                 1969
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US-09-370-700-3
; Sequence 3, Application US/09370700
; Patent No. 6274350
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			ATCATGAA 2080 ::      spGlyGlu 1434	NGATCGGG 2035 :::     aLeuGly 1454	CCGATCAG 1975	erGluGly 1466	ATGTCGTT 1921 	186	  aPheGly 1495	1822	erPheAla 1515	STCGTATG 1774	spLeuAla 1535	CTCATACG 1714	ly 1553	AAACCGCC 1654	::: laSerGlu 1573	1654	hrCysAsp 1593	TCGGCCTG 1597	-ValValLeu 1611	TTCTCGAT 1537	Phealaasp 1620	1507	hrAspVal 1640	1507	heAspThr 1660
	Length: 2152 Matches: 161 Conservative: 100 Mismatches: 274 Indels: 308 Gaps: 33	3 (1-2152)	TTAGATCAACTTCAGCTCTTGGATGAGAGGGGCACTGACCCCATTTGTCATCATGAA 	GAGAACGTAGCGGATGTCCACGCTGATTGTGCGCTGCAGATCGGG 	TTCGAACTCGATGTCACCACTCATAGCTTCCCAGTTGCCATCGAAAGCAAGACCGATCAG	-TyrProGlyValAlaSerLeuGlySerGluGly	ACGGCCGTTCTTATCGAATACGGGCTACCGGAGTTACCGCCCGTGATGTCGTT    ::::::    	TTCTCGGCATAGCGACCATAG	::    ::  ArgValMetGlyWetIleProLysAlaPheGly	SCAAACTC	 ProLeuAlaValAlaAspHisArgMetValThrArgIleProAlaGlyTrpSerPheAl	-ATCGCTCTTAGGATCCTGCTTCTCCAATACGCCCTTGCCTGTCGTATG	ArgAlaAlaSerValProlleValPheLeuThrAlaTyrTyrAlaLeuValAspLeuAla	ATAGTTGTACCAGGCACCGTCCTGCGGTTCATATCCCTTGATGGAGCCGTAGCTCATACG	AlaAla	CATGGTGAAGTTGGCATCGCTCGGCAGAGCACGTCCGGGGTACATCTCACGCAAACCGGC	MetalaalaileGlnLeualaargHisLeuGlyalaGluValTyralaThrAlaSerGlu		${\tt AspLysTrpGlnAlaValGluLeuSerArgGluHisLeuAlaSerSerArgThrCysAs} \\$	-AAAGAAAAGACGCTTGCCCTTCTCAATGGCATAGGCATTGGCCATCGCCATCGGCCTG	!	AATAGCGCGAGCAGCAGCTATTACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGAT	- [di	CTTGGCAAACTTTTCCTTGTCCATGGA	SerLeuArgMetLeuProArgGlyGlyArgPheLeuGluLeuGlyLysThrAspVa		$\tt ArgAspProValGluValAlaAspAlaHisProGlyValSerTyrGlnAlaPheAspThr$
ver. 2.0 polyspora spinosa	0.0213 119.00 30.96% 19.10% 3.01%	$9) \times US-09-370-700-3$	CAGCTCTTGGATGAGACGGG     :::         AlaLeuValAspGluProT	GAGAACGTAGCGGATGTCCACGCT	GTCACCACTCATAGCTTCCC		ATCGAATACGGGGC :::    ValGluTbrG]vProGlvV3	AGCGATATGGAGCTGACCG1	  ArgVa	GCGGAAGAGGTCGAGGATATTCTCCTGTACGGCAAACTC-	  AlaAspHisArgMetValT	ATCGCTCTTAGGATCCTGCT	valProlleValPheLeuT	CCAGGCACCGTCCTGCGGTTCAT	  GlyGluSerLeuLeuValHi	GGCATCGCTCGCAGAGCAC	:::!!!!! :GlnLeuAlaArgHisLeuG]		AlaValGluLeuSerArgG	ACCCTTCCCTTCAATGC	PheGluGlnGlnPheLeuGlyAlaThrGlyGlyArgGlyValAsp	AGCAGCTATTACGCTCTTGC	.GlyGlu	CTTGGCAAAC1	MetLeuProArgGlyGlyAı		.GluvalAlaAspAlaHisPı
E: Patentin 3 3 : 2152 PRT 5M: Saccharo	ment Scores: No.: int Similarity: Local Similarity: Match:	-008-355-1 (1-213	39	2079 GAGAACGTAGCG:::    	2034 TTCGAACTCGAT	1455 Met	1974 ACGCCGTTCTTATCGAATAC-    :::::     1467 AlaglvValValValGluthrG		1485	1860 GCGGAAGAGGTC	1496 ProLeuAlaVal	1821	516 ArgAlaAlaSer	1773 ATAGTTGTACCA	536 GlyLeuArgPro	1713 CATGGTGAAGTT	1554 Metalaalaile	1654	1574 AspLysTrpGln	1653AAAGAAAAG	1594 PheGluGlnGln	596 AATAGCGCGAGC	612 AsnSerLeuAlaGlyGlu	536 AGC	1621 AlaserLeuArg	507	1641 ArgAspProval
; SOFT ; SEQ 1 ; LEN ; TYF ; ORC US-09-3	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	us-10-(	Qy 21 Db 14	Qy 2(	0y 2(	Dp 17	Oy 19		Dp 14	0y 18	Db 14	Qy 18	Db 1	0y 17	Db 15	0y 1.	Db 1	0y 10	Db 1.	0y 1(	Dp 1	0y 1	Dp 1	Qy 1.	Db 1	Oy 1	Dp 1

Oy	1506	TGGAACTTGTCGCTATAAGG
- qa	661	::: :::
Qy	1449	
qq	1681	:::         uProLeuProValThrAlaTrpAspValArgGlnAlaPro
Qy	1416	SAATATATCG
QQ	1701	ArgHisLeuSerGlnAlaArgHisValGlyLysLeuValLeuThrMetProP
Qy	1359	ATCGAGCATGGCGGG
Db	1721	oAlaAlaGlyThrValLeuValThrG
Qy	1338	TCGAGCGAGGGAGGTAG
QQ	1741	
Qy	1281	GAGGATACCGGCATGAGCATCAGGATTTGTAGCCAATGCGTTGGC 1237
QQ	1761	oAlaAlaSerGlyAlaAlaGluLeuValAlaGlnLeuThrAla
ογ	1236	3GT
qq	1781	rLeuGlnAlaCysAspValAlaAspArgGluThrLeuAlaLysVa
Oy	1182	AGTCATCTCACGGTTGGCCTTGGCTCCTTATAAGCCTTTTCGAGAGAAGACAATAC 1123
qa	1797	
Oy	1122	īčc
QQ	1807	ThralavalvalHisalaAlaGlyValLeuAspAspGlyValSerGlu 1822
Qy	1062	GGCACGCTTACGACCTATCACGTCAG 1036
ΩD	1823	
δy	1035	ACGAGCGAGACCGCGGTTCATACCGATCGAATTCTTCCAATAGTTAGCACTCTGAGCATA 976
Dp	1842	AsnLeuLeuGluLeulleAspProAspValAlaLeuValLeuPheSerSerValSerGly 1861
Qy	975	CTTGCTGGCATATTTGATACGGGTAGCCTGATCTGCGCTCATGGCTTCCTTC
qq	1862	valLeuGlySerGlyGlyGlnGlyAsnTyrAlaAlaAlaAsnSerPheLeuAspAla 1880
QY	915	TTGCTTGATACGGGAACTTCGATAGGAGATTGTTCT 877
QQ	1881	LeualaGlnGlnArgGlnSerArgGlyLeuProThrArgSerLeuAlaTrpGlyProTrp 1900
Οy	877	
qα	1901	GluHisGlyMetAlaSerThrLeu
οy	876	GTTTTCGATACGATCCACACC 853
đ	1921	GlyLeuLeuProIleSerThrGluGluGlyLeuSerGlnPheAspAlaAlaCysGlyGly 1940
QY	852	CCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCATAGTC 796
. qa	1941	AlaHisThrValValAlaProValArgPheSerArgLeuSerAspGlyAsnAlaIleLys 1960
Qy	795	GTCAGCCTTGTAGCCTTGCATGGATACGCCAGCGAAGTAAACGGCCTTATAGGGTTTATT 736
qq	1961	PheSerVal 1969
Qy	735	TTGCTGTATTCGGCCGGCTGTCGGCACCGGCATACAÇGCGGAATACGCT
qa	1969	. 1969
Oy	675	GTCGCCCGTGTGACGCGGCCACATCCAGTTGTCCGTATCGCCTCCGAACTTACCTACAGA 616

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2048
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2005 ValArgMetHisValAlaAlaValLeuGlyPheAlaGlySerGlnGluIleThrAlaAsp 2024
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2092 AsnLeuProThrLeuAlaArgAspGluAlaThrArgAlaGlnIleThrThrArgLeuGln 2111
                                                                                                                                                                                                                                                                                                                                     --- ACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGCAGATACTT 379
                                                                                                                                                                                                                                                                                                                                                                                                                              CACGGAAAGACCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACCATCGCG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 GGTAAAGATCAGGCCCTGATCGGACACTGTGATACCGGTACATCCGCCACCGAAGATAAC 199
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                                                                                                                                                                                                                                                                                                                                                                             2025 GlyThrPheLysValLeuGlyPheAspSerLeuThrValValGluLeuArgAsnArgIle
                                                                                                                                                       555 TTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTCTGCATTTTCTTT
                                                                                                                                                                                                   1985 LeuArgLysArgLeuGlyArgLeuProAspAlaGluGlnHisArgIleLeuLeuAspLeu
                                                                                                                                                                                                                                               495 TTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTGCGCAGACGCTCCATCTCGTCAGTGAT
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                                                              615 GCTGGGAGGAGCAAATACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGAAGTA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2045 AsnGlyAlaThr------
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: California
RY: United States of America
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Patent No. 5962643
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 5962643e1
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 43
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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ADDRESSEE: Pretty, S
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2112 AlaIleLeu 2114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
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996 TTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGA 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CCAACGCATTGGCTACAAATCCTGATGCTCA 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TATGGCGATGTATTGTCTTTCTTCTCTCGAAAAGGCTTATAGGA 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           762 CGCTGCCGTATCCATGCAAGGC----TACAAGGCTGACGACTATGCCATGACCATCGG 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816 TTTCCCGGGCAGTACGGATCGCTACCTCATTGGGGTGTGGAAGATCGTATCGAAAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 eAlaProAsnAspGlyGluCysHisLeuSerProLysGlyGluTyrThrHisSerThrLe 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 uGlnAspTyrProSerIleSer----GlnIleAsnGlnLysValLysAspAsnAlaIl 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936 GAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTA 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 eAsnIleIlePheAlaValThrAlaSerGlnLeuSerValTyrGluLysLeuValGluHi 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 GGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GTTCGTTTT---GCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 uValGlnThrSerLysCysAspAsnLeuLysGluGlyGlnGlnValSerPheThrAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                        282 GlyAsnLeuAsp-----AlaProGluGlyGlyPheAspAlaIleMetGlnAlaIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                           702 TGCCGACAACCGGCCGGCCGAATACAGCAAGACAATAAACCCTATAAGCCCGTTTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1269 TGCCGGTATCCTCAAATCGCTTG-----------
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119
66
201
211
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                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                    Indels:
Gaps:
 8717
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 33:
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 846 amino acids
TYPE: AMINO ACID:
STRANDEDNESS: single
                                                                                                                                                                                                                                 0.0227
115.50
30.998
19.938
                                                                                                                                                            linear
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Best Local Similarity:
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NERAL INFORMATION:

1291	TOTAL THE STATE OF	
Oy 1292	Yourdaniltoolyoeliledlylytolinalolinaldansiiselojsselolyilolinaldansiiseloja	
Db 527	: hrSerMetCysGlyIleCysAsnCysAspAspSerTyrPheGlyAsnLysCysGluCysS 547	
Qy 1296 Db 547	CAAGTACAAAGACTACCTCC	
1323	CGACCGTAAGGTGCTGCCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGACAA 1382	
Qy 1383 Db 587		
Oy 1422 Db 607	CAAAGGCGACACGAAGAAGTATGCAGA 1448 :::    :::::	
Qy 1449 Db 627	CTTCGTATTCGA	
Qy 1494 Db 647	TGCCATGCTCAAGTCCATGGACAAGGAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGC 1553 [	
Qy 1554 Db 660	AGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGAT 1610	
Qy 1611 Db 665	GGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTCTT	
Qy 1671 Db 685	GTACCCCGGACGTGCTCTGCCGAG	
Qy 1707 Db 704	CACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGC 1760 :::               ::	
Qy 1761 Db 722	CTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGA 1820     -  -  -  -  -  -  -  -  -  -  -  -	
Oy 1821 Db 741	1821 TGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTA 1880	
Qy 1881 Db 755		•
Oy 1927 Db 775		
Oy 1974 Db 790	TCTGATCGGTCTTCGATGCCAACTGGGAAGCTATGAGT 2016    :::           -LeuValGlyLeuAla11eLeuLeuTrpLySLeuLeuThr 803	
RESULT 14		

; Sequence 33, Application US/08938085A ; Patent No. 6339148

US-08-938-085A-33

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354 uClnAspTyrProSerIleSer-----GlnIleAsnGlnLysValLysAspAsnAlaIl 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| |||||| :::
282 GlyAsnLeuAsp-----AlaProGluGlyGlyPheAspAlaIleMetGlnAlaIleAla 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 GGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGG 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       702 TGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAAACCCTATAAGCCCGTTTACTT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 CysArgSerGlnIleGlyTrpArgGluGlnAlaArg------ArgLeuLeu 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  762 CGCTGCCGTATCCATGCAAGGC-----TACAAGGCTGACGACTATGCCATGACCATCGG 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 TITCCCGGGCAGTACGGATCGCTACCTCACTTGGGGTGTGGAAGATCGTATCGAAAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      936 GAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTA 995
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert,
TITLE OF INVENTION: A No. 6339148el Integrin Beta Subunit and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346
119
56
201
211
26
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A
FILING DATE: 26-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
RFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 846 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0227
115.50
30.99%
19.93%
3.02%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
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Local Similarity:
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Db 685 CysPro	QY 1707 CACCAT		1761	727	UY 1821 16AGTT 	1881	755	1927		Qy 1974 TCTGAT	Db 790 -Leuva	RESULT 15 US-08-484-105-14	; Sequence 14, A	GENERAL INFOR	; APPLICANT: ; APPLICANT:	; APPLICANT:	; APPLICANT: ; APPLICANT:	; APPLICANT: ; APPLICANT: . ADDITCANT:	TITLE OF IN	CORRESPONDE ADDRESSEE ; STREET:	CITY: Sai	ZIP: 941.	COMPUTER NEE  COMPUTER:  COMPUTER	SOFTWARE:	; APPLICATION ; FILING DATE	; CLASSIFICA ; ATTORNEY/AGI . NAMF: OCT	STR	TELECOMOUNI	TELEFAX: TELEFAX:	O H	; TYPE: am.; STRANDEDNI; TOPOLOGY:
:::		stleglnGlySerSerAlaAlaLysLeuAsp	1056 GCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGACTGCTGC 1113	403AsnAspSerAsnValVa 409	1114	409 lGluLeuValLysGluGluTyrArgLysIleSerSerSerValGluMetLysAs 427	1155 AGGAGCCAAGGCCAACGTGAGATGACTTATTGAGCGAGAGGCTCTTCGGTGGTACCGA 1214	427 pAsnAlaThrGlyAspValLysIleThrTyrPheSerSerCysLeuSerAsnGlyProGl 447	GGTGGTTCGTTTGCACA	uValGInThrSerLysCysAspAsnLeuLysGluGlyGlnGlnValSerPheThrAlaGl	1233 GTTG		 487 erProValGlyIleAsnGluValMetGlnIleGlnLeuThrMetLeuCysSerCysProC 507	1291 1291	507 ysGluAsnProGlySerIleGlyTyrGlnValGlnAlaAsnSerCysSerGlyHisGlyT 527	1292ACGA 1295	527 hrSerMetCysGlyIleCysAsnCysAspAspSerTyrPheGlyAsnLysCysGluCysS 547	1296 CAAGTACAAAGACTACCTCC	547 eralathráspLeuthrSerLysPheAlaAsnAspThrSerCysArgAlaAspSerThrS 567	1323 CGACCGTAAGGTGCTGCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGACAA 1382	1383 GCTCCCCGATATATCAA	587 ArgProAsnProlleGluIleIleSerGlyLysHisCysGluCySAspAsnPheSerCys 606	1422 CAAAGGCGACACGAAGAAGTATGC		::: ::: 627 CysLysCysLysProGlyTrpThrGlySerAsnCysGlyCysGlnGluSerAsnAspThr 646	1494 TGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGC 1553	647 CysMetProProdlyGlyGlyGlyGlulleCysSerGlyHis 659	1554 AGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCGCGTATTCAGGCCGATGCGAT 1610	111C}scTacAs	1611 GGCCAATGCCTATGAGAAGGCAAGGCTTTTTTTTTTTGCGGTTTGCGTGAGAT 1670 	1671 GTACCCCGGACGTGCTGCCGAG
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TGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGC----- 1760
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                                                                                                                                                                                                                                                                                                                                                                                                     -----ATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCG 1973
                                                                                                                                   ACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGA 1820
                                                                                                                                                                                                                          TTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTA 1880
                                                                                                                                                                                                                                                                                                                                      || ||||::||||||:::
|uGlnGlyGluLeuHisValTyrAlaGlnGluAsnLysGluCysProAlaLysVa 775
o---ThrCysSerGlyArgCysGlnGluLeuLysAspCysValGlnCysGlnMet 703
                                                                                       sThrGlyGluLeuLys-----AsnGlyAspAspCysAlaArgAsnCysThrGln 721
                                                                                                                                                            hePheAspGluAspAspCysLysPheMetPhe-------LysTy 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCNALLY, Francis J
LADRENSON, Patricia
LADRENSON, Patricia
LI, Joachim J
GAVIN, Kimberly
SAVIN, Kimberly
NEURINION: ORIGIN OF REPLICATION COMPLEX GENES
SECTION OF SEPLICATION COMPLEX GENES
SERVENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400 san Francisco California USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         etLeuGlyIleValMetGlyValIleAlaAlaIleVal-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **EADABLE FORM:

*YPE: Floppy disk

?: IBM PC compartible

&: SYSTEM: PC-DOS/NS-DOS

E: Patentin Release #1.0, Version #1.30

PPLICATION DATA:

**LION NUMBER: US/08/484,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DALE.

PAGENT INFORMATION:
OSMAN Ph.D., Richard Aron
RATION NUMBER: 36,627
NCE/DOCKET NUMBER: A-59032/DJB/RAO
UNICATION INFORMATION:
ONE: (415) 494-8701
310 277299
N FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08484105
89341
RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STILLMAN, Bruce
BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERISTICS:
885 amino acids
amino acid
NNESS: single
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FOSS, Margit
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TYPE:	protein	0y	84
		함 ·	29
0.0264	Length: Matches:	Oy	8
Percent Similarity: 30.618 Best Local Similarity: 18.188 Query Match: 3.018		d y	31, 93
1 0-2120	Gaps: 34	qa	33
		QY	
rgArgArgGlyA	outemorm.com.com.com.com.com.com.com.com.com.co	qa	
CTCTACAGTTTC	GTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGG 209	δ O	
rgLeuTyrProG	 	ag :	
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lyGluPheTyrG	GlnLeuAspGlyGluPheTyrGluThrAsnLysGluLysGlyAspLys-PhePheGluGl 124	^0	
TCTCGCACGATGC    :::::::: SerGlnSerIle1	TGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAA 380 :         :::::::::           uThrPheAlaSerGInSerIleLysAsnGluLeuTyrLeuThrAlaGluLeuSerGluI 144	. 점	
TATCTGCGCAAGATCGTGAAG 	4	<u>ک</u> ۾	
eTyrLeuArgAspLeuGInPheVaLAlaAsn	IleLy		
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Qy	843	CACTTCTTGGGGTGTGGGAACATCGTATCGAAAACGAGAACAATĆCTGGTATCGAA 897 ::: aAsnAlaSerSerSerAspSerAspGluGluPheGluAspTyrGlnSerAlaGluGluLe 314
οy	868	GTTCGCGGTATCAAGCAAGGCATCTGGAAGGA 92
Dp	314	 
δy	930	CCATGAGCGCAGATCAGGCTACCCG
QQ	332	oLeuGlnProSerAlaValHis
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δλ	- 2	CGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAA 11
QQ	360	::::::    ::: ::: ::: :::
ΟŸ	1104	
QΩ	377	sIleProAspLeuAsnAspIlePheGlnArgHisAsnAsnAspLeuAspIleAlaAlaLe 397
Qy Db	1137	7 CGAAAAGGCTTATAAGGAAGGACCAACCGTGAGATGACTTATTGAGCGAGAC 1196
δý	1197	GAGGTGGTTCG 12
qa	412	:::   :: nSerLysGluGluIleValLy 43
δλ	1224	ATTGGCTACAAATCCTGATGCTCATGCC
qq	432	pPheAspAsnTyrLeuProAlaArgGluAsnGluPheAlaS
δλ	œ	
qq	452	erLeuTyrSerAlaileGluAlaGlyThrSerThrSerIleTyrIleAlaGlyThrPr 47
ΟŊ	1291	GACGACAAG
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ý 6	1326	ATGCTCGATATTGTACGCG 1
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ος δ	i i	CGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAA 14
aa	215	AlaserAspserTyrGluValPheTrpGlnLysIleSerGlyGluLysLe 528
δo d	1419	AAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTA 14
2 2	070	III SELGIJALAAIAMELGILUSEI LEUGILUKHEIJ/FPHEASHLJSVALFIO 343
δ		AGUGALAAGITICCAIGCCATGCICAAGICCAIGGACAAGGAAAAGITIIGCCAAGGCIAI 15 
qq	546	
δλ	1539	GAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGC
QΩ	547	sLysArgProlleValValLeuLeuAspGluLeuAspAlaLeuValSerLysSerG
Qy	1599	GATGCGATGCCAATGCCTATGCCATTC
QQ	267	AspValMetTyrAsnPhePheAsnTrpAlaThrTyrSerAsnAlaLysLeu
Qy	1650	GTTTGCGTGAGATGTACCCGGACGTGCTCTGC
3 :	) c	TATESTANDO NO NECESTANDO NO NECESTANDO NA CONTRA CO
γ̈́ο	1697	CGATGCCAACTTCACC

q	909	 606 rarglleGlyPheThrArglleMetPheThrGlyTyrThrHisGluGluLeuArgThrIl	626
Qy	1711	ATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGG	1757
QQ	626	elleAsnLeuArgLeuLysTyrLeuAsnGluSerSerPheTyrValAspProGluThrGl	646
Qy	1758		1817
qq	646	ySerSerTyrMetIleSerProAspSerSerThrIleGluThrAspGluGluGJuLysAr	999
Qy	1818	CGATGAGTTTGCCGTACAGGAGAATATCCTC	1848
QQ	999	666 gLysAspPheSerAsnTyrLysArgLeuLysLeuArgIleAsnProAspAlaIleGluIl	989
oy .	1849	ACCAA	1865
qq	989		206
0y	1866	AAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTT	1910
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ΟÝ	1948	AGCCCCGTATTCGATAAGAACGCCCGTCT	1976
Db	746		166
Qy	1977	GATCGGTCTTCGATGGC	1998
QQ	166	:       ::        766 eSerGlyLeuSerPheSerGlyLysLeuPheLeuTyrAlaLeuIleAsnLeuIleLysLy 786	786
Oy	1999	999AACTGGGAAGCTATGAGTGGTGGAGTTCGAACCCGATCTGCAGCGCACAT	2054
qq	786	sLysGlnThrAspValGlnLeuGlyAspIleValGluGluGluHetArgLeuLeuIleAspVa	908
ογ	2055	CAGCGTGGACATCCGCTACGTTCTC 2079	
QQ	806	806 lAsnGlyAsnAsnLysTyrIleLeu 814	٠

Search completed: May 16, 2003, 12:39:14 Job time: 73.5 secs

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Sequence 3, Appli
Sequence 4, Appli
Sequence 1382, A
Sequence 1384, A
Sequence 1384, A
Sequence 103, Appli
Sequence 1013, Appli
Sequence 1015, Appli
Sequence 1016, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 25, Appli
Sequence 21, Appli
Sequence 23, Appli
Sequence 1068, Appli
  sequence 5,
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Bonbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTON: Dipeptidylpeptidases And Methods Of Use
FILE REFRENCE: 235.00440101
CURRENT ERPPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATON NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            712
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US-10-142-515-11

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US-10-034-623-62

US-10-136-935A-2

US-10-196-935A-2

US-09-945-917-57

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US-09-945-917-57

US-09-945-917-918

US-09-909-567B-44

US-09-909-567B-426

US-09-815-242-11918

US-09-815-242-11918

US-09-810-238-426

US-10-100-049-23

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US-10-28-388-1068
                                                                                                            0 US-09-801-368-108
0 US-09-815-242-13382
0 US-09-815-242-13684
0 US-10-008-355-18
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0 US-09-920-5301-1012
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0 US-09-920-328A-6
2 US-10-036-328A-6
2 US-10-036-328A-6
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US-10-111-311-83
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US-10-99-930-984-6
US-10-997-340-4
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
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100.00%
100.00%
97.36%
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110
110
110
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Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
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LENGTH: 712
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-MODEL-frame+.n2p.model.-DEV=xlp
-Q-Acgn2_1/USPTO_spool/US10008355/runat_16052003_110341_9460/app_query.fasta_1.2311
-Q-Acgn2_1/USPTO_spool/US10008355/runat_16052003_110341_9460/app_query.fasta_1.2311
-Q-Acgn2_1/USPTO_spool/US10008355/runat_16NFIX=n2p.rapb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -SGRAT=1 -END--1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX.CO.
-THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OOTFMT—pcb -NORM-ext -HEAPSIZE=500
-MAXLEN-200000000 -USER=CS10008355_@CGN_1_1_25_@runat_16052003_110341_9460
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NG_SCORES=0 -WAIT -LONGLOG
-DEV_INMEOUT=120 -WARN_TIMEOUT=90 -THRESDEXT=7 -XGAPDF=10 -XGAPDFT=0.5 -FGAPOP=6
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Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                       APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Benbula, Agnieszka
TITLE OF INVENTION: Dipeptidyleptidases And
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
GlnCysProArgLeuIleGlnGluLeuLysLeuIle
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; Sequence 8, Application US/10008355
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; GENERAL INFORMATION:
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Patent No. US20020164759A1

GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Botempa, Jan S

APPLICANT: Banbula, Agniteszka
TTILE OF INVERTION: Dipptidylpeptidases And Met
FILE REFERENCE: 235.00440101

CURRENT APPLICATION NUMBER: US/10/008,355

CURRENT FILING DATE: 2001-11-08

PRIOR FILING DATE: 2000-11-08

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.0

SEQ ID NO 9
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421 LeuGlnGlyAsn---AspAlaSerAla----ArgLysGluAlaIleAspLysIleArg 437
                                           438 ThrargTyrSerLysPheAlaAsnLysAspTyrSerAlaGluValAspLysLysValAla
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TyrAlaAspArgSerGlyArgMetProValAlaPheCysAlaThrThrHisThrThrGly
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APPLICANT: Travis, James
APPLICANT: Botempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
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LysAlaAlaLeuAlaAlaGlyAsnAspProPheLysArgThrThrAlaLeuGluThr 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ATT---CCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AlaGlyProAsnAlaArgIleTyrValLeuGluGlnIleThrAspValThrAlaGlnAla 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 GAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 PheSerPheAlaGlyGlyAsnThrTyrArgValPheLysAsnLeuGluIleLysAspVal 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCAAATGAAATTAAAAAGTATTCTTCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG
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Matches:
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/2
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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Best Local Similarity:
Query Match:
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TYPE: PRT
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1780 ACAGGCAAGGCGTATTGGAG    Qy	Oy 1954 GTATTCGATAAGAACGGCCGTC    1	; Sequence 5, Application US/10; Patent No. US200201647591 ; Patent No. US200201647591 ; Patent No. US200201647591 ; APPLICANT: Travis, James APPLICANT: Potempa, Jan S APPLICANT: Potempa, Jan S APPLICANTON: Dispeption; TITLE OF INVENTION: Dispeption; CURRENT APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-11-01; PRIOR PILING DATE: 2001-11-01; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: PatentIn version 3	; SEQ ID NO 5 ; TYPE: PRT ; TYPE: PRT ; ORGANISM: Shewanella putrefi US-10-008-355-5 Alignment Scores: 7 62e-6 Score: 7 62e-6 Score: 7 884.50 Percent Similarity: 48.58 Best Local Similarity: 31.91% Query Match: 23.15%	US-10-008-355-1 (1-2139) x US-10 QY 6 AATGAAATTAAAAGTATTCTT
831 274 891 288 933 308	1053 348 11101 368 1161 1221	403 1269 423 1293 443 1335 460	1377 475 11425 495 500	515 1605 535 1665 555 1719 1779
772 TCCATGCAAGGCTACAAGGCTGACGATTATGCCATGACCATCGGTTTCCCGGGCAGTACG   1   1   1   1   1   1   1   1   1	994 TATTGGAAGAATTCGATGGTATGACGGGGTCTCGCTGGTTGACGTGATAGGTCGT 111111111111111111111111111111111	erdlyvalile ATGCTCAT        spalaGlnArg AATCGCTTGAC          sysGlnMetGlu	CTGCC laalalleAsp	501
772 TCCATGCAAGGCTACAAGGCTGACGATGACCATGACCATGCGTTCCGGGCAGTACG   1	994 TATTGGAAGAATTGGATGGATGAACCGGGTCTGGTCGTTGACGTGATAGGTCGT 994 TATTGGAAGAATTGGATGGATGAACCGGGTCTGGTCGTTGACGTGATAGGTCGT 11111		1336	1501
TATGCCATGAC ::: PhevalMetva GAAGATCGTATAl PheLysAsnLe AAATATGCCAG AAATATGCCAG AAATATGCCAG AAATATGCAG	994 TATTGGAAGATTCGATGGATGAACCGCGGTCTCGCTCGTTTGAC 994 TATTGGAAGATTCGATGGATGAACCGCGGTCTCGCTCGTTTGAC 111111111111111111111111111111111111	LeuGlyGln GCT AlaIleGluArGC ProThrIleGl CTCGACCGTAA :::      :	GATATTGTACGVally:	ASIALIAASPAr STAATAGCTGC STATATAGCTGC STATATAGCTGC STATATAGCTGC STATATAGCTGC STGCCGAGGCG STGCCGAGGCG STGCCGAGGGCG STGCCGAGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGG
772 TCCATGCAAGGCTACAAGGCTGACGACTATGCCATG [1] [1] [1] [1] 255 SerAspGlnProLeuGlyAspGlyAspPheValMet 832 GATCGCTACCTCACTTCTGGGGTGGAAGATCGT ::        275 AsnArgTyrAlaLeuVal	TCGTATGAC		CCGCCATGCTC	LeuLysTrpPhe LeuLysTrpPhe CTTTCCAAGAGC ::: ::: ::: Tyralavalala InTGCCATTGAG ::: ::: GlyGluLeuLeu :::       ::       ::         :: 
SCAAGGCTACA   	AAAGAATTCGA                   LysAsnPhea   CCCGGGGAAN   SerGluGluT   CCTGTCTATG	AASnGlnAspA rCCACAGTTG [1] [AlavalAsnL. rccacagagagagagagagagagagagagagagagagaga	461 GluTyrasnLysLeuPro 11 1  461 GluTyrasnLysLeuPro 378GACAAGG 476 ValTrpLeuGlyAspGly 426 GGCGAACGAAGATATV 11 1  476 SerSerGluGluArg 486 AAGTTCCATGCCATGCTC	SGCTCCATCA SGCAGTAGAGC' AlalleargT' SGCCAATGCCT' STACCCC' SANLySSETH
772 TCCATC   11   255 SerAsg   832 GATCGC   ::	994 TATTGGAR 994 TATTGGAR 1054 AAGCGTGG 1102 AAGAGTGC 1102 AAGAGTGC 1102 AAGAGTGC 1102 AAGAGTGC	385 Lysalaass 1222 CGTTTGC. 404 Glyvalal. 1270 424 GlualaGl. 1294 GACAAGTA(	1336 461 GluTyr 1378 476 ValTrg 1426 GGCGAC 496 SerSer 1486 AAGTTC	501 1546 GATCCGCC
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GAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAG 1839 CACCAAAAACTATGGTCGCTATGCCGAGAAC-----GGT 1893 ATGGGGTCAGTGCCCCCGTCTCATCCAAGAGCTGAAGTTG 2133 ACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTAC 2073 614 : |||:::||| sAlaLysSerTyrAlaAsnLeuAlaAspGlnArgIleGly 634 TCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGG 245 GGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAAT 125 TCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCAT 185 || :::::::||| :: rpglnProHisGlnLeu---ProAlaMetAlaAspValLe 51 |||| ::: |||| aLys---AsnThrGlyValGluProPheAspSerProLys dylpeptidases And Methods Of Use 1 734 247 129 280 1118 25 Length:
Matches:
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g O	71	tAsnAlaValIleSerLeuGlyGlyCysThrAlaSerPheValSerProLysGl 89	
λ	246	CCTGATCTTTACCAACCACCACTGCGGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGA 305	
g G	68	yLeuValValThrAsnHisHisCysAlaTyrGlySerIleGlnTyrAsnSerThrProGl 109	
λ Q	306	TCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGAT 362 : :::	
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3 8	129	aProGlySerArgValTyrValThrGluAspValThrAsnValThrGluArgValLysAl 149	
ά	423	GACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCA :::	
අු	149	aGlyLeuGluAsnLysThr·················GlyArgGluPheTyrGl 161	
λ 2	483	AGAACTGGCCAAAAAAGAAATGCAGACGAGAACCAACT 521   ::	
οy	522		
q	181		
λα	583	CAAGGACGTTCGTATTGGTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATAC 641	
a D	201	eArgAspValArgLeuValTyrAsnProAlaGlySerValGlyLysTyrGlyGlyAspVa 221	
à á	642	GGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGG 701	
2	777	~	
oy O	702	TGCGGACAACCGGCGGCGAATACAGCAAGGACAATAAACCCTATAAGGCCGTTTACTT 761	
δy	762		
q	261		
λα	822	GGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAACATCGTATCGAAAA 875	
Q Q	787		
λ G G	301	CGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG	
δy	936	99	
. q	319	aProGluGlySerAspGluArg11eLySTyrGluSerGlnIleAlaGlyLeuAlaAsnTy 339	
Oy G	966		
3 8	, ,	, ,	
A Q	359	GCGTGCCGAGGAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGT 1112 ::::	
ογ	m	CTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	
qq	379	sTyrGlyLysThrLeuAlaGluLeuAspAlaLeuIleAlaLysSerLysAlaHisGl 398	
QY DP	1173 398	TGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGT 1220 :	
οy	1221	TCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCT 1280	
QQ	416		

Οy	SCTTGACGACAAGTACAAAGA	
QQ		10
οy	1309 ************************************	37
qq	. III IAspLysAlaValL	10
ογ	38 GCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCCCGACAAGCTCCCGGATATAT 13	97
qq	465 uPheAspMetLeuLysArgTyrAlaAlaLeuProGluAlaGlnArgLeuPro 48	~
ōλ	AGAATGTAATCGACAAGAA :::	37
Dp		0
δλ	B -AAGTAIGCAGACIICGTAIICGACAAGAGIGIGGIICCIIAIAGGGACAAGIICCA 14	
QΩ	500 aLysThrLeuAspLysMetTyrAlaLysThrGluLeuGlyAsnLysAspValArgLeuAl 520	0
δλ	1494 TGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAAAAAAACTCCGGC 1553	
qq	ysSerValAspAspPheLysAlaSerLysAspPrc	w
δλ	1554 AGTAGAGCTTTCCAAGAGCGTA 1575	7.5
Dp	536 eIleGinPheAlaValAlaMetTyrAspThrAsnMetSerGluGluLysLysGluLysGl 556	w
ΟŊ	76ATAGCTGCTGCGCGCTATTCAGGCCGATGGGATGCCAATGCCTA 16	22
g	556 uLeuAspGlyGluLeuMetLysValArgProGlnTyrMetAspAlaIleIleAlaTy 575	ιΩ.
Qy	23 TGCCATTGAGAAGGGCAAGGGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACG 16	82
a		47
Qy	83 IGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGATA 17	4
QQ	585AlaAspAlaAsnSerSerLeuArgValThrValGlyHisValLysGlyTy 601	-
Q Q	1743 TGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGGCAAGGGCGTATTGGACAA 1802	02
δy	1803 GCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCAC 1862	62
Op	621 sAspThrGlyIleAspProPheAspAlaProLysGlnGlnLeuGluLeuIleLysGl 640	0
Qy	1863 CAAAAACTATGGTGGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATC 1916	16
QQ	IleAspSerValProValAsnPheLeuS	0
ōλ	17 GAACAACGACGCGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCT 197	92
Ωρ	60 rThrLeuAspThrThrGlyGlyAsnSerGlySerProThrLeuAsnGlyArgAlaGluLe 6	0
δy	1977 GAICGGICITGCITTCGAIGGCAACIGGGAAGCIAIGAGIGGIGACAICGAGITCGAACC 2036	36
Ωp	680 uValGlyLeuLeuPheAspGlyValTyrGluSerIleIleGlyGlyTrpAlaPheAspAs 700	0
δλ	37 CGAICTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGACAAATG 20 ::::::     :::                   ::::::	96
QQ	700 nGluIleAsnArgSerIleHisValAspSerArgTyrMetLeuTrpValMetLysTyrLe 720	0
Οy	2097 GGGTCAGTGCCCCGTCTCATCCAAGAGCTGAAGTTGATC 2136	
QΩ	720 uAspHisAlaAspAsnLeuLeuAlaGluMetGluIleVal 733	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGlyLeuGlyTyrCysThrAlaSerPheValSerProGlnGlyLeuValValThrAsn 78
                                                                                                                                                                                                                                                                                                                                                                                     GlnTrpGlnProTyrGlnMet---ProSerIleAlaAspLysLeuSerAlaArgGlyIle 40
                                                                                                                                                                                                                                                                                                                                           21
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TyrTyrLeuIleLysGlnLeuMetIleArgAspValArgLeuValTyrAlaProProGlu
                                                                                                                                                                                                                                                                                                                                    142 ACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 GATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerValGlyGlyTyrGlyGlyAspIleAspAsnTyrGluTyrProArgHisSerGlyAsp
                                                                                                                                                                                                                                                                                                                       ATTCTTCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGGGGTAGCCAAAGCCGACAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AspIleProAlaAspLysLeu-----AlaAspLeuThrSerTyrProMetAsnAlaVal
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                 APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
ATLE CON INVENTO: Dipeptidylpeptidases And Methods Of
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 20001-11-08
PRIOR FILING DATE: 20001-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3:0
SEQ ID NO 6.
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Mismatches:
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; ORGANISM: Shewanella putrefaciens
US-10-008-355-6
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           APPLICANT: Travis, James
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Query Match:
DB:
GENERAL INFORMATION:
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                                  1642 CGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG--
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APPLICANT: Banbula, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Met
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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Indels:
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Best Local Similarity:
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US-10-008-355-3
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LENGTH: 52
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US-10-008-355-1 (1-2139) x US-10-008-355-3 (1-52)

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APPLICANT: BOGGET, Thierry
APPLICANT: Boggert, Thierry
APPLICANT: Boggert, Thierry
APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: OCNTROL CELL, BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: DHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/945,917
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3
97 SerGlyAsnLeuGlyAlaValLeuGlnLeuLeuPheLeuLeuSerThrTyrLysGlnLys 116
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61 LysArgLeuAlaLysIleThrSerAsnLeuAspGly---LeuGluThrCysLeuAspTyr 79
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                                                                                                   1990 TTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGC
                                                                                                                              1 PheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArg
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                    US-10-008-355-1 (1-2139) x US-09-945-917-3 (1-1528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09945917
Publication No. US20030042381A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Caenorhabditis elegans
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Sun May 25 15:40:17 2003

δ	628	GACAACTGGATGTGGCCGCGTCACGGGCGACTTCAGCGTATTC 68	7
qq	136	oproAlaValSerLys141	·
Oy Dp	142	CGCGTGTATGCCGGTGCCGAAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTAT 747 :::	
ç G	748	AAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATG 807	
oy Dp	808	ACCATCGGTTTCCCGGCAGTACGATCGCTACCTCACTTGGGGTGTGGAAGATCGT 867	
yo 4			
3 6	904		4 IV
q :	211		
<u>2</u> 5	231	SSerLeuGluSerSerSerThrTyrSerSerIleSerAsnLeuAsnArgProThrSerGl 251	
Oy Dp	943	GATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAG 1002   1::::::	
oy Og	1003	AATTCGATCGGTATGACCGCGGTCTCGCTCGTCTTGACGTGATAGGT 105 	00
Oy Db	1051	CGTAAGCGTGCCGAGGAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCT 1111	01
oy O	310	GTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAGGAAGG	0,
ۇ مۇ	330		0 0
Qy Db	1231 343	CAGTITGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTT 129 ::: rLyslleAlaAla	06
oy Dp	1291 354	13	50
oy Qq	1351 373	GATATTGTACGCCGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATC 1410 :::	10
oy Db	1411	GACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAA 146 	
Oy Dp	1464	GAGTGTGGTTCCTTATAGCGACAAGTTCCATGCTCAAGTCCATGGACAAGGA 1520   1	03
Oy Db	1521 426	AAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAG 1571	
οy	1572	CGTAATAGCTGCTCGC 1590	

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APPLICANT: BOGGET, Thierry
APPLICANT: BOGGET, Thierry
APPLICANT: Wandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: CONTROL CEL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
FILE REFERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 ATCACAGTGTCCGATCAGGGCCTGATC---------TTTACCAACCACCACTGC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LysargleualaLyslleThrSerasnLeuAspGly---LeuGluThrCysLeuAspTyr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 LeuLysAsnLeuGlyLeuAsp------CysSerLysLeuThrLysThrAspIleAsp 96
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Matches:
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                                                                           ; Sequence 4, Application US/09945917; Publication No. US20030042381A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Caenorhabditis elegans
446 rileValThrAlaileArg 452
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1583
TYPE: PRT
                                        RESULT 9
US-09-945-917-4
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                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
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À À	ACCATCGGTTTCCCGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGT 867         :::    :::    :::    :::   - ProGinSerArgileSerLysileAspSerSerLysileGlyileLysProLysTh 191	
A-	A	
9 E	GGTATCAAGCAAGGCATCTGGA	
i vi	sSerLeuGluSerSerShrTyrSerSerIleSerAsnLeuAsnArgProThrSerGl 251	
ಶ − ಾ	GATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAG 1002  :::::	
<b>∢∵</b> ∾ છ	AATTCGATCG-:GTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGT 1050 	
0 – 7	CGTAAGCGTGCCGAGGAAAGAGCATTCGCAGATCCGTAAGAACGGCAAGAGTGCT 1110   .::::           :::   LysthrileGlyAlaLysGlnGluProAspAsnSerGlyGlyGlyGlyGlyGlyGlyMetLe 310	US-09 Aligni Pred.
0 <b>–</b> 5	GTCTATGGCGATGTATTGTCTCTCGAAAAGGCTTATAAGGAAGG	Score Percei Best Query
0-4	CGTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTGGT	DB: US-10
O H	CAGTTTGCCAACGCATTGGCTACAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTT 1290 	ф 
0 0	GACGACAAGTACAAAGACTACCTCCCCTCGGTCGACCGTAAGGTGCTGCCCGCCATGCTC 1350 :::::            sproprothsSerLysLeuGlySerAlaThrSerMetSerLysLeuCysThrProLy 373	
0 0	GATATTGTACGCGGCGTATCCCTGCCGACAGCTCCCGGATATATTCAAGAATGTAATC 1410 :::	δ 40
0 – 4	GACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAA 1463 	yo aa
1464 (	GAGTGTGGTTCCTTATAGCGACAAGTTCCATGCTCAAGTCCATGGACAAGGA 1520 	YO OY
521	AAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAG 1571     :::  :                  :::	VQ -
1572	CGTAATAGCTGCTCGC 1590	QV
£ " ≥ 1 ≥ 1	SSULT 10 -09-801-368-108 Sequence 108, Application US/09801368 Sequence 108, OS20020128250A1 GENERAL INFORMATION: APPLICANT: Busby, Robert	40 60 P
7	VT: Cali, Brian	_

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APPLICANT: Hedutzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Madden, Kevin
APPLICANT: Madden, Kevin
APPLICANT: Madden, Kevin
APPLICANT: Mator
APPLICANT: No. US20020128250Alman, Thea
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Summers, Eric
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440

SOSTWARE PREPARENTIN VERSION 3.0
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111 111 111
508 SerSerAlaProValProThrProSerSerThrThrGluSerSerSerAla---- 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 CCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAA 124
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Matches:
Conservative:
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Gaps:
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DRGANISM: Saccharomyces cerevisiae
9-801-368-108
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LENGTH: 1367
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TGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGGTTCGGAGGCGATACGGACAACTGGATGTTGTTTGT	SerSerThrThrGluSerSerThrProValThrSerSerThrThrGluSerSerSer GGCCGTATCCATGCAAGGCTAAGGCTGACGACTATGCCATGACCATGA II II III III III III III III IIII II	GTTTCCGGGCAGTACGGATCGCTACCTCTTGGGGGGGGGAAGATCGTATCGAAA	ThrGluserSerSerAlaProValThrSerSerThrThrGluserSer TGAGGGCAGATCAGGCTACCCGTATCAATATGCCAGCAAGTATGCTCAGAGTGCTAACT	ATTGGÄAGAATTCGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTA	AGCGTGCCGAGGAAAGAGCATTGGCAGACTGGATCC	AGAGTGCTGTCTATGGGGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	AGGCCAACCGTGAGATGACTTATTGAGCGAGGCGTCTTTCGGTGGTAGTACCGAGGTGGTTC	GTTTGCACAGTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCA 	AATCGCTTGACGACAAGTACAAAGACTACCTCCCTCGCTCG	CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAGCTCCCCGATA	TATTCAAGAATGTAATGGAGAAGAAATTCAAAGGGGACACGA	AGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCG	ACAAGTTCCATGCCATGCTCAAGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA	AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG	Gluser	ATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGC
596 526 656 541 716	559 764 579	815 599 875	619 935 636	995	1055 667	1103 687	1163	1223	1283	1343	1394	1436 804	1484 819	1544	833	1604
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1715 GTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCT------ 1762
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                                                                                                                                                                                                                                                                                                                                                                                                                          1002 CysSerProLysThrIleThrThrValProCysSerThrSer-----ProSer 1018
                                                              1664 GTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACT-----TCACCATGC 17.14
                                                                                                                                                                                                                                               1763 ------GGTACAACTATCATACGACGCCAAGGCCTATTGGAGAAGC 1804
                                                                                                                                                                                                                                                                                                                                                                1910 TCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACG 1969
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                                                                                          -----SerIleProPheSerSerThr 888
                                                                                                                                                                                                                                                                        889 ThrGluSerPheSerThrGlyThrThrValThrProSerSerLysTyrProGlySer 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                         949 AsnSerAlaGlyGluThrThrSerGlyCysSerProLysThrValThrThr------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yemmonto, Pobert T.
APPLICANT: Yemmonto, Robert T.
APPLICANT: Yemmonto, Robert T.
APPLICANT: Yemmonto, Robert T.
APPLICANT: Yemmonto, Robert T.
APPLICANT: Au Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 100000103-21
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/205,727
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                              875 IleThrSerSerAlaProSer------
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER OF SECTION NUMBER OF SECTION NOS:   SOFTWARE: FastSEQ for	4.0	133.00 Matches: 104 13.07 Matches: 104 13.07 Conservative: 65 20.35% Mismatches: 166 14.29 176 10 Gaps: 24 187 188 Gaps: Db 300 188 Mismatches: 176 199 1429 100 1429	Oy 1489	352	372	1666 383	1699	954 QY 1759 126 Db 417	CGTATCAAATATGCCAGCAAGTATGCTCAAGTGCTAACTATTGGAAGAATTCGATC 1011	RE 1071 US 158 ;	; G 'AACGGCAAGAGTGCTGTCTATGGC 1119 ;    :::    :::   LyTrpIleTyrArgGlyGluPheIleIleAsnTrp 178 ; ;		TATUTICAGCGAGACGGTCTTCGTGGGTACCGTGGTTGGTTTGTTGTACAACAGTTTTGACAAC 1242 CURRENT PPITTNG
M M D C C C C C C C C C C C C C C C C C	TION NUM DATE: 20 ID NOS: tSEQ for 2 reptococ		574 GATGTATTC		730 AAGGACAATAAACCCTATAAGCCCGTTT		847 TCTTGGGGTGTGGAAGATCGTATCGAAA        ::   :: 91 GlnAlaLysValGluGluArgLeuArgG		955 CGTATCAAATATGCCAGCAAGTATG         27 ThrileLysGluGlnTrpGlyLysMetG				1183 TATTTGAGCGAGACGCTCTTCGGTGGTACC

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CCATGCTCAAGTCCATGGACAAGGAAAGTTTGCCAAGGCTATCGAGAAAGAT 1548
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| yrAsn-----AlaAspGlyGluMetTyrValGlyGluGluAlaProGluGly 434
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|adsnGlnAspThrGluAspLys------Val 382
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-----AspProArgTyr 239
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Ohlsen, Kari L.
Zyskind, Judith W.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamanoto, Robert T.
Yu, H. Howard
WENTION: Identification of Essential Genes in WENTION: 1 dentification of Essential Genes in VENTION: 104
LICATION NUMBER: 105/09/815, 242
LING DATE: 2001-03-21
CCATION NUMBER: 60/191,078
GG DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: ::::: :::||
|leSerArgGlnLeuTrpTrpGlyHis-----
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020061569A1
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955 CGTATCAAATATGCC---AGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATC 1011
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Matches:
Conservative:
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Indels:
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFWARE: FastSEQ for Windows Version 4.(
SEQ ID NO 13684
                                                                                                                                                                                                                                                                       ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13684
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127.00
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ORGANISM:
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                                                       1183 TATTTGAGCGAGGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC
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                                                                                                                                      GCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTAC
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.004401011
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
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PRIOR FILING DATE: 2000-11-08
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Patent No. US20020164759A1
GENERAL INFORMATION:
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US-10-008-355-18
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TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                   Version #1.30
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                                                                                                                                           Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/10/192,584
FILING DATE: 11-Jul-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/077,098
FILING DATE: 19-May-1998
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: JP97
APPLICATION NUMBER: JP97
FILING DATE: 19-SEP-1997
                                                                                                                                                                                                          US-10-008-355-1 (1-2139) x US-10-008-355-18 (1-26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: KORNBAU, Anne M.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TOKUNAGA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10192584
Publication No. US20330027987A1
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
SAKAGUCHI, Masashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCE CHARACTERISTICS:
LENGTH: 2042 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     MATSUO, Kazuo
HAMADA, Fukusaburo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                              ORGANISM: Porphyromonas gingivalis US-10-008-355-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
         SOFTWARE: Patentin version 3.0 SEQ ID NO 18 LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                         CGTGAGCTCGGCTTTACG 144
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96.15%
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Best Local Similarity:
NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                       Alignment Scores:
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US-10-192-584-6
                                      LENGTH: 20
TYPE: PRT
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-----PheAlaGluGlyLysSerSerlleAlalleGlyThrAspLysIleSerGly--- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 AlaLysSerAla-----GlyAsn-----GlnSerValSerLeuGlyGlnAsnSerTrp 217
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|GlyTyrGlyAlaThrAsnAspArgSerAlaThrGlyAlaIleAlaLeuGlyVal----- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TATGCCATGACCATC 813
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73 LeuGluValTyrSerSerSerValLysLeuSerThrValSerAlaGlnSerAsnSerVal 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 HisAsnThrAlaPhePheGlnProLeuPheThrLysCysThrTyrLeuAlaLeuLeuIle 55
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Matches:
Conservative:
Mismatches:
Indels:
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                      MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-192-584-6
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1118.50
36.038
22.228
3.10%
TOPOLOGY: linear
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Best Local Similarity:
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----AACTTCACCATGCGTATG 1719
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                                                                                                              -- 1437
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                                                                                                                                                                                        -----GTATTCGAC 1461
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                                                                                                                                      358 ---GlyLeuArgSerPheValAla-----LysAspAlaValGlyGlyThrAlaIleGly 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 AsnAlaGlySerMetAlaTyrGlyTyrLysAlaLysAlaValGlyAlaGlyAlaIleAla 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 IleLysLysThrAlaThrThrAspSerSerAlaGlyGlyGlyLysAsnAlaIleAlaIle 509
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                                   1339 CCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTC
                                                           375 GluGluSerArgThrPheAlaLysAspSerValAlaIleGlyAsnLysThrGluAlaSer
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                                                                                                            1399 AAGAATGTA---ATCGACAAGAAATTCAAAGGC------GACACGAAG-----
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US-09-920-552-103
; Sequence 103, Application US/09920552
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APPLICANT: Griffiths, David J.
APPLICANT: Weiss, Robin A.
APPLICANT: Weiss, Robin A.
APPLICANT: Weiss, Robin A.
APPLICANT: Weiss, Partrick
TITLE OF INVENTION: Material and Methods Relating to a No. US20020094576Alel Retro
FILE REFERENCE: Abbott Labs
CURRENT APPLICATION NUMBER: US/09/920,552
CURRENT FILING DATE: 1099-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-37
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nLeuValAspGlnVal-------LeuGlnAspProMetGluGlyIleGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGA 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACGATGTATTC-----AAGGACGTTCGTATGGTATTTGCTCCTCCAGCTCTGT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: ::: ::: IIIIIII :: rGlnGluAlaTyrValGlyGluHaGluGluGluGluGlyThrSerProProArgGluMe 176
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162
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Matches:
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Patent No. US20020094576A1
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-920-552-103
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Best Local Similarity:
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CAAGGCTGACGACTATGCCATGGCTTTCCCGGGCAGTACGGATGGCTACCTCAC :	TICTIGG	CGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTC	GAAGGAAGCCATGAGCGCAGATACCCGTATC			GAAGAATTCGATCGGTATGAACGCGGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCG ::::::::::::::::::::::::::::::::::	TGCCGAGGAAAGGCATTCGCAGACTCGTTTT-	yLeulleProGluArgAsnLeuValLysAlaValLeuGl	GGCGATGTATTGTCTTCTCGAAAGGCTTATAAGGAAGGAGGCCAAGCCG	TGAGATGACTTATTTGAGCGAGGCTCTTCGGTGGTACCGAGGTGGTT	rLysGlnAsnTyrGlnAlaGlyAsnGlnAlaTrpAspGluGluMetLeuIleGlyGluGl	-CGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCT	CAAATCGCTTGACGACAAGTACAAAGACTACCTCCCTCGCTCG		CGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAA :::  ::            ::: :::		GAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTGGTA :::	TTCGACAAGAGTGTGGTTCTF	gLeuMetGluAlaAlaGlyAsnIlePheGluThrValGluGluAlaMetProLeuValAr	TATAGCGACAAGTTCCATGCTCAAGTCCATGGACAA	gArgLeuAlaTyrGluGln-AlaAsnLysThrCysArgGluAlaLeuArgProTrpGlnH	GGAAAAGTTTGCCAAGGCTATCGAGAAAGATCGGCAGTAGAGCT	TTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGCCTA	lySerHisAlaAlaValAlaValThrArgGlnPheArgGlnAsnMet	TGCCATTGAGAAGGGCAAGCGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACG	TGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGATA
786	846	876	924	259	961	666	1059	317	332	1173	351	371	1281	381	1341		1401	1456	428	1477	448	1518	1563	488	1623	1683
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521	1743	534	1785	547	1818	267	1845	587	1857	607	1863	627	1914	647	1968	667	2028	687
qq	Qy	qq	ογ	QΩ	οy	ф	Qy	qq	δλ	qq	Qy	qq	QY	qq	QY	qa	QY	qa

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mucin 3 - human (f	probable membrane	microbial collagen	a-aqqlutinin core	hypothetical prote	DNA helicase (EC 3	hypothetical prote	hypothetical prote	1,4-alpha-glucan b	glycogen branching	hypothetical prote	hypothetical prote		glutamate synthase	transferrin-bindin	Lactobacillus phag	penicillin-binding	DNA helicase II UU	valy1-tRNA synthet	mucin - rat	hypothetical prote	hypothetical prote	mucin 2 precursor,	hypothetical prote	related to trichod	hypothetical prote	probable phage tai	hypothetical prote	translation elonga	exiT protein - Myc	cell polarity prot
PC4395	S59310	A36866	A41258	T34434	D69103	T21460	T33813	F98228	AH3057	T25174	F72308	T19168	H83865	S70660	AC1647	AD1617	D82883	C95066	S24169	T25173	T02345	A43932	T33369	T51214	T29634	AF0258	T34369	C82332	T14180	T40866
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3.4	3.4	3.4	3.3	3.3	3.3	3.3	3.3	3.3	3,3	3,3	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.5	3.0	3.2	3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.1
131	129.5	129	127.5	127	126.5	126.5	125	124.5	124.5	124.5	123	123	123	122.5	122.5	122	122	122	120.5	120.5	120.5	120.5	120	119	119	119	118.5	118	117.5	117
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May 16, 2003, 12:22:51; Search time 79.5 Seconds

- protein search, using frame\_plus\_n2p model

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1 atgcaaatgaaattaaaaag..........aagagctgaagttgatctaa 2139

US-10-008-355-1 3820

Title: Perfect score:

Sequence:

hypothetical protein XF1887 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C; Accession: G82627
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID: 20365717; PMID: 10910347
A; Note: for a complete list of authors see reference number A59328 below

A; Accession: G82627

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-16 <SINA; Cross references: GB: AE004008; GB: AE003849; NID: 99106961; PIDN: AAF84693.1; GSPDB: GN
A; Experimental source: strain 9a5c
R; Simpson, A.J. G.; Reinadh, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junquelra, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.A.; de Oliveira, A.A.; Sawa
A; Authors: da Silva, A.C. R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
A; Reference number: A59328
A; Reference number: A59328

A; Contents: annotation C; Genetics:

Length: Matches: Conservative: 7.33e-54 907.50 49.21% · Percent Similarity: Alignment Scores: Pred. No.:

716 239 135

ALIGNMENTS

Command line parameters:
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-MODEL-frame+.nZp.model.-DE-xIp
-Q-/cgn2\_1/USPTO\_spool/US10008355/runat\_16052003\_110338\_9364/app\_query.fasta\_1.2311
-Q-/cgn2\_1/USPTO\_spool/US10008355/runat\_16052003\_110338\_9364/app\_query.fasta\_1.2311
-DB-PTR\_73 -QFWT-fastan -SUFFIX-nZp.rpr -MINMATCH-0.1 -LOOPCL-0 -LOOPEXY=0
-UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN-200 -THR.SCORB-PTR\_ANX=100 -THR\_MIN-0 -ALIGN=15 -MODE-LOCAL
-USER-US10008355\_6CGN\_1\_1111\_@runat\_16052003\_110338\_9364 -NCPU-6 -ICPU-3
-NO\_XILXY -NO\_MANP -LARGEDURY -RG\_CCRES-0 -WAIT -LONGLOG -DEV\_TIMBOUT-120
-WARN\_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

283224 segs, 96134422 residues

Searched:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

**BLOSUM62** 

Scoring table:

Jatabase :

pir1:\*
pir2:\*
pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	hypothetical prote	probable membrane	gastric mucin (clo	qlucan 1,4-alpha-q	C30C11.4 protein	hypothetical prote	HKR1 protein precu	alpha-2-macroglobu	mucin 5AC (clone J	mucin MUC5B, trach	alpha-amylase (EC	valine-trnA liqase	probable pts pep p
	TD OIL	G82627	T02345	S25345	147141	S48478	S44784	T11678	S69703	A53102	\$53362	T45025	A60999	D97933	C71528
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	Nuery Match Length DB	716	1.791	1609	528	1367	176	948	1802	4543	477	3570	1104	883	571
æ	Query Match	23.8	4.1	4.0	3.9	3.8	3.8	3.7	3.7	3.6	3.6	3.6	3.5	3.5	3,3
	Score	907.5	156	154.5	149	145	143.5	141	139.5	139	138	137	133.5	133	132.
	Result No.		2	٣	4	S	9	7	80	σ	10	11	12	13	c 14

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-----GCCGGTATCCTCAAATCGCTTGAC 1293 1294 GACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTG-------1335 ------GACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAA 1425 1426 GGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGCTTCTTATAGCGAC 1485 1486 AAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAA 1545 1546 GATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTĠCTGCTCGCGCTATTCAGGCCGAT 1605 1840 AATATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAAC----GGT 1893 ------CTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCC----- 1377 1606 GCGATGGCCAATGCCTATGCCATTGAGAAGGCAAGCGTCTTTTCTTTGCCGGTTTGCGT 1665 1666 GAGATGTACCCC-----GGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATG 1719 1720 AGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACG 1779 1780 ACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAG 1839 AAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTT 1221 ::: ||||||||||| :::||||||||| 44 ------ArgArgTyrLeuPhcOGluMetAspArgGlnMetGlnGInTyrTrpLeuThr 460 111 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 424 GlualaGlyTyrGlnGluArgAspLeuProThrIleGluGlyAsnLeuLysGlnMetGlu 443 ||| :::||| 476 ValTrpLeuGlyAspThILeProAlaThrLeuLySArgLeuGlyAspThrLysLeuSer 495 ||||||||||::
516 AspProAlaIleArgTyrAlaValAlaIleMetProAlaLeuLeuGluIleGluArgGln 535 404 GlyValAlaValAsnLeuTyrArgLeuAlaIleGluArgThrLysSerAspAlaGlnArg 423 536 AsnLysIleArgThrGlyGluLeuLeuLysAlaArgProlleTyrLeuGlnAlaLeuAla 555 ||| :::|||||||::: ||| ::: 596 ThrLeuGlnGlyValMetAlaLys---AsnThrGlyValGluProPheAspSerProLys 614 ..... 111 369 GluAlaLeuAlaAlaHisGlnThrLeuValAspLeuThrGluGlnTyr-------1222 CGTTTTGCACAGTTTGCCAACGCATTGGCT-----ACAAATCCTGATGCTCAT---496 SerSerGluGluArg------------1054 AAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGCC-349 1162 1336 1378 Ωp g δλ qq ò qq δy q δ g ò Q δλ g δ ò g οχ Dp ò Q ò g δy QQ δ Dp δ ò Db ò q ογ q

Db 702ArgGlySerArgSerSerProGluProLysThrLysSerArgThrProProArgArg 720 Qy 498 AGAAAATGCAGAACCAACTCTGCATGCAGGGCCTTTCTATTCCAACAA 551	QY 579 ATTCAAGGACGTTCGTATGCTCCTCCCAGCTCTGTAGGTAAGTT 629	QY 690 CGTGTAÏGCCGGTGCCGACAACCGGCCGAATACAGCAAGGACAATAAACCCTATAA 749  111   111	OY 810 CATCGGTTTCCCGGGCAGTACGGTACCTCACTTCTTGGGTGTGGAAGATCGTAT 869	Oy 930 AGCCATGAGCGCAGATCAGCCTATCAAATATGCCAGCAA 974	1035 TCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAGAGCATTCGCAGACTGGATCCG	OY 1134 TCTCGAAAAGGCTTATAAGGAAGCAGCCAACCGTGAGATGACTTATTTGAGCGA 119  OY 1134 TCTCGAAAAGGCTTATAAGGAAGCAGCCAACCGTGAGATGACTTATTTGAGCGA 119  11	1224 955 1284	DO 905 IGAIGSERAIGSERAIGSERAIGSERAIGSERAIGSERAIGSERAIG DE 905 IGAIGSERAIGSERAIGSERAIGSERAIG DE 908 1344 CATGCTCGATATTGTACGCCGGCGTATCCTGCCG
Qy         1954         GTATTCGATAAGAACGCCGTCTGATCGGTCTTGCATGGCAACTGGGAAGCTATG         2013           III	Db 695 ValGInTrpIleMetThrGluValAlaProAlaPrOHisLeuLeuLySGluLeuAsnLeu 714  RESULT 2  T02345  hypothetical protein KIAA0324 - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Dacces(inn: m07345) Esequence_revision 05-Mar-1999	Rilicke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.; re; J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998 A.; Description: Sequencing of human chromosome 16p13.3 A; Reference number: Z14664 A. Accession: T02345 A; Settininary; translated from GB/EMBL/DDBJ A. Molecule, type: DNA	A; Residues: 1-1791 <ric> A; Coss-references: EMBL:AC004493; NID:g2996648; PIDN:AAC08453.1; PID:g2996650 C; Genetics: A; Map position: 16 A; Introns: 1610/2; 1706/2 A; Note: KIAA0324</ric>	Alignment Scores: 0.0236 Length: 1791 Score: 156.00 Matches: 184 Percent Similarity: 34.42% Conservative: 81 Best Local Similarity: 23.90% Mismatches: 276 Ouery Match: 2 Gaps: 35 Bis: 1.71-2130, v.m0244, 71-1701	OY 27 TCTCGGAGCAGCCTGCTTGGGTGCTTCAGGGGTAGCCGAAAGCCGACAAGGCATGTG 86	Db 624 SerProArgArgSerArgSerSerProGluValLysAspLysProArgAlaAla 643  Oy 147 CCCGTTGGATTCGTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT 206	SerGlySerAsp GGTGGATCACGA         ProAlaProArg	Db 668 SerArgSerGlySerSerLysGlyArgGlyProSerProGluGlySerSerThr 687  Qy 381 GTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAGGCAGCAGCTCAAGGGTATCAC 440  Db 688 GluSerSerProGluHisProProLysSerArgThrAlaArg 701  Qy 441 TGACGAGATGGAGGGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAA 497

A; Residues: 1-1609 < FRO> A; Cross-references: EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227; MIPS:YCR089 C; Genetics: SGD:FIGS A; Gene: SGD:FIGS A; Gene: SGD:FIGS A; Genes: SGD:S0000685; MIPS:YCR089w A; Map position: 3R C; Keywords: transmembrane protein F; 4-20/Domain: transmembrane #status predicted <tmi>F; 1592-1609/Domain: transmembrane #status predicted <tmi>F; 1503-1609/Domain: transmembrane #status pred</tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi>	Alignment Scores: 0.0285 Length: 1609 Pred. No.: 154.50 Matches: 153 Score: 35.18% Conservative: 101 Best Local Similarity: 21.19% Mismatches: 254 Query Match: 4.04% Indels: 214 DB: 2 Gaps: 28	Qy         74 ACAAAGGCATGTGCTCCAACGAACTCAATCAGGAGAATCTGGATGGTGAGC         133                   : :	Oy 254 TTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATC 307  Db 818 SerSerThrValLeuSerSerThrValSerGluGlyAlaLysAsnProAlaAlaSerGlu 837  Qy 308 ACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCATCCGGATTCCGG 367  Db 838 ValThrIleAsnThrGlnValSerAlaThrSerThr	Oy 428 TCAAGGGTATCACTGACGAGAGGGTCTGGGCAAAGCTCAGGAGGTATGCCAAGAAC 487 :::::	Qy         602 TTGCTCCTCCAGCTGTAGGTAAGTTCGAGGCGATACGGACACTGGATGGCCGC 661
1437 1024 1491 1038	qy 1536 TATCGAGAAAGATCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGG 1589  ::           ::	1710   CTATCGTACGGCTCCATCAAGGGATATGAACGCAGGACGGCGGGCCTGGTACAA	1890 CGGTCAGCTCCATACCTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAG  1800 CGGTCAGCTCCATACGCTTTCCTATCGAACAACTCAGGGCGGTAACTCCGGTAG  1140 laLeuAsnSerSerArgMetSerCysPheSerArgProSerMetSerProThrProLeuA  1950 CCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTCGATGCAACG  1160 sp	Oy 2064CATCCGCTACGTTCTTCATGATGACAAATGGGGTCAGTGCCCCGTCT 2114	ul-2000 s cerevisiae chr 254.1; PID:91907

Sun May 25 15:40:18 2003

991	931	1011	991	1051	1017	1111	1030	1171	7007	1231	1291	1065	1342	1079	1402	1095	1462	1113	1522	1576	1511	1636	1677	1177	1723	1196	1783	1216	1843	1236	1903
::: :::::: :::::::::::::::::::::::::::		ThrProPhe	CCATGAGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTA	ACTATTGGAAGAATTCGATCGGTATG		GTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTG	SerGluMetSerThrPheSerValSerThrGlnSerL	TCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAG		s discontant in the fact of th	AGTTTGCCA			::    :::        ::	CCATGCTCGA	)PheSerSerGlyTyrSerLeuProSerSerThrProSerGlnTyr	ATGTAATCGACAAGAAA	SerLeuSerThrAlaThrThrThrIleAsnGlyIleLysThrValTyrThrT	3 AGAGTGTGCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGAAA	AGTITGCCAAGGCTATCGAGAAAGAICCGGCAGTAGAGCTITCCAAGAGCGTAA	servatasparyknevatserseruyskroserserbergererunrnrse	7 TAGCTGCTGCTCGCGCTATTCAGGCCGATGCCCAATGCCCTATGCCATTGAGAGG 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCAAGCGTCTTTT	:::      ::: :::     3 laThrThrThrIleSerGlyLeuLysThrValTyrThrThrTrpCysProLeuThrS		:::       ::: :::         ::::::	1 ACGCTCCATCAAGGGATATGAACCGCAGGACGGTGCTGGTACAACTATCATACGACAG	SerAlaSerSerAlaThrSerThrSerIleSerLeuSerThrSe		7 SerSerGlyTyrLeuSerLysGlyValCysSerGlyThrGluCysThrGlnAspValPro	1 TCCTGGACCTCTTCGGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATA
972	881	992	932	992	1017	1052	1018	1112	1 6	1043	1232	1049	1292	1066	1343	1080	1403	1096	1463	1523	777	1577	1637	1158	1678	1177	1724	1197	1784	1217	1844
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Gastroenterology 106, 200, 1994
A;Title: Pig gastric mucin: isolation and characterization of a cDNA clone with a nov A;Reference number: I47141; MUID:94102478; PMID:7506218
A;Accession: I47141 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rolecule type: mRNA
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A;Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
A;Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
B;Cruner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, J.T.
Biochem. J. 308, 89-96, 1995
A;Title: Isolation and characterization of cDNA clones encoding pig gastric mucin.
A;Reference number: S55315; MUID:95275264; PMID:7755593
A;Status: preliminary gastric mucin (clone PGM-2A) - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 03-Nov-2000 C;Accession: 147141; S55115 R;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, J.T. 2065 2066 TCCGCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125 ::: 1312 AlaThrAlaValSerSerSerThrPheIleAlaSerSerLeuProLeuSerSerLysSer 1331 1237 ThrGlnSerSerSerProAlaSerThrLeuAlaTyrSerProSerValSerThrSerSer 1256 1946 GTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGG 2005 ::: |||||||| 1292 ThrSerLeuLeuSerThrSerLeuProSerProAlaPheThrSerSerThrLeuProThr 1311 . 128 GTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTG 187 68 AAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGC 127 248 TGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATC 307 308 ACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGG 367 17 ---ThrThrSerValGInSer------SerSerSerSerVal 28 ------ ProSerSer 41 A;Molecule type: mRNĀ A;Residues: 1-528 <TU2> A;Cross-references: GB:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208 C;Superfamily: pig submaxillary mucin 2006 AAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACA 188 CCAATGCCGTGGTTATCTTCGGTGGCGGGATGTACCGGTATCACAGTGTCCGATCAGGGCC 1904 TCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACT----Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: |||:::||| 29 ProlleProSerThrThrSerValGln------US-10-008-355-1 (1-2139) x 147141 (1-528) 0.0419 149.00 34.228 21.518 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: 52 Score: ò Db ŏ q qq δy Dp Dp δ g ŏ QQ δy δy Ω ò

λ	368	GTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGC 4	127
ą	53		69
λλ	428	TCAAGGGTATCACTGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAAC 4 ::111	487
ą	9	ProProlleSerSerThr	65
<u>ک</u> ج	488	TGGCCAAAAAAGAAAATGCAGGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCA 5	547
3 ,	3 .		- !
<b>≿</b> 8	548	ACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTC 6         ::     ThrThtSerThrThrSer	607 84
χ̈	608		299
q	85		96
λý	668		700
ą	66		118
<b>,</b>	701	GTGCCGACAACCGGCCGGCCGATACAGCAAGGACAATAAACCCT 7	745
q	119		138
à	746		805
ą	139		154
۲	806	CTTCTTGGGGTGTGGAAGATC	865
æ	155		167
λλ	866	GGTATCAAGCAAGGCATCTGGA	925
ą	168	erSerAlaProThrThrSerAlaThrSerValGlnProSerSerSerSer	186
2,	926		985
ą	187	SerProPro1leSerSerThrValSerValGlnThrSerSerSerSer 2	203
ζ	986	GTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCTTGACGTGA 1	1045
ą	204		215
λ	1046	TAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGA	1105
æ	216	SerSerSerValProThrThrSerAlaThrSerValArgSerSerSer 2	232
λ	1106	GTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGCTTATAAGGAAGG	1165
ą	233		252
γ̈	1166	CCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTT	1225
ą	253		266
⋩	1226	CATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAAT	1285
ą	267		282
λ̈́	1286	CGCTTGACGACAAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGCTGCCGCCA 1	1345
ð	283		301
λ̈́	1346	TGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATG 1	1405
q	302		312

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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR01
C;Specias: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: S48478; A26877; B26877; S27281; JC6123
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1406 TAATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGA 1465
                                                                                                                                                                                            1526 TTGCCAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAAȚAGCTGCTG 1585
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                           313 ---SerSerSerProThrThrSerThrThrSerValGlnProSerSerSerGlySer 331
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                                                                                                                     32 AlaProThrThrSerAlaThrSerValGlnProSerSer------Ser
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R;Rowley, K. submitted to the EMBL Data Library, October 1994 A;Reference number: \$48478 A;Accession: \$48478

A. Molecule type: DNA
A. Residues: 1-1367 <ROW>
A. Residues: 1-1367 <ROW>
A. Cross-references: GB 24.7047; EMBL: Z38061; NID:g603997; PID:g763364; GSPDB:GN00009;
A. Cross-references: GB 24.2-2149, 1987
J. Bacteriol. 169, 2142-2149, 1987
A. Title: Gene fusion is a possible mechanism underlying the evolution of STA1.
A. Reference number: A91831; MUID:87194600; PMID:3106330

A; Molecule type: DNA A; Residues: 1-242 <YAM>

014.1; PID:g 015.1; PID:g menez, A. STA2 and SG		CITICIALICCAACAACGAATACTICCICATCGTCTACGATGTATTCAAGGACGTICGTA
A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552 R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Precorius, I.S. Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996 A;Title: Mucl. a mucin-like protein that is regulated by Mss10, is critical for pseudohy A;Reference number: JC6123; MUID:96323237; PMID:8710886 A;Status: nucleic acid sequence not shown A;Status: nucleic acid sequence not shown	oy da oy	6 CGGCCGAATACAGCAAGGACCATAAAGCCCGTTTAGTTCG
Residues: 1-1367 <lam> Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387 Genetics: Genetics: Genetics: Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458 Cross-references: MIPS:YIR019c; SGD:S0001458 Cross-references: MIPS:YIR019c; SGD:S0001458 Supe position: SR glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein 5-21/Domain: transmembrane #status predicted <tm1> 1350-1366/Domain: transmembrane #status predicted <tm2></tm2></tm1></lam>	67 67 67 67	GTTTCCCGGGCAGTACGGATCGCTACCTCTTGGGGTGTGGAAGATCGAAGAAAAAAAA
: 0.118 Length: 1367 145.00 Matches: 160 ty: 33.69% Conservative: 95 arity: 21.14% Mismatches: 354 Indels: 148 (1-2139) x 548478 (1-1367)		995 ATTGGAAGAATTCGATCGCTATGAACCGCGGTCTCGTCTTGACGTGATAGGTCGTA 1054  647 GluserSerSeralaProValProThrProSerSerThrThrGluserSerSerAla 666  1055 AGCGTCCCGAGGAAAGAGTCGATCGCAGATGACTCGTAAGAACGGCA 1102  111   11
CCAAGCCGACAAAGCCATGTGGCTCCTCAACGAACTCAGGAGAATCTGGATCGA 124	90 OY COY COY	ThrThrGluSerSerslaprovalThrSerSerThrThrGlüSerSerSeralaPro AGGCCAACCGTGAGATGACTTATTGAGCGAGAGCGTTTCGGTGCTACCGAGGTGGTTC        ValProThrProSerSerSerThrThrGlüSerSerSerAlaProvalPro GTTTTGCAGAGTTGCCAACGCATTGGCTACAAATGCTGATGCTGATGCCGGTATCCTCA  ### Proposes of the content of the
ValProThrProSerSerSerThrThrGluserSerAlaProvalThrSerSerThr 414  ATCAGGGCCTGATCTTTACCACCACCACCACGGGGTGTATCCAGAGCCAAAGCA 298  :::	OY OY	AATGGTTGACGACAAGTACAAAGACTACCTCCCTCGCTCG
ThrSerSerThrThrGluSerSerSerAlaProvalThrSerSerThrThrGluSerSer 454  CGATTCCGGGTCTTTCCGTGAAGDATCTGCGCAAGATCGTGAAGGTAACGGACAAGG 415	Qy Db Qy	TATTCAAGAATGTAATCGACAAGAAATTCAAAGGGAACGAGAATTCAAAGGGAACGA   11
	QY Db Qy	1484 ACAAGTTCCATGCCATGCTCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA 1543

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US-10-008-355-1 (1-2139) x S44784 (1-776)
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S44784
C30C11.4 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 29-Sep-1999
C;Accession: S44784
R;Favello, A.D.
submitted to the EMBL Data Library, January 1993
A;Description: Sequence of the C. elegans cosmid C30C11.
A;Reference number: S44782
A;Reference number: S44784
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-776 <FAV>A;Coss references: EMBL:L09634; NID:g156220; PIDN:AAA27967.1; PID:g156223
C;Genetics:
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                                  -----GGTACAACTATCATACGACAGGCCAAGGCCGTATTGGAGAAGC 1804
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                                                              835 SerSerValProValProThrProSerSerThrThrGluSerSerAlaProVal
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C; Superfamily: heat shock protein 91
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21.57%
3.76%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 893 TCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773 CCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    833 ATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTA 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 lulleglu------IleValGlyGlySerSerArgIleProMetIleArgG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTATGCCAAGAACTGGCCAAAAAAGAA--------AATGCAGACGAG---- 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....AlaIleLysAspThrGlnProTyrArgIleArgLeuSerT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 ITGCICCICCAGCICIGIAGGIAAGIICGGAGGCGAIACGGACAACIGGAIGIGGCCGC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCACACGGGCGACTTCAGC----GTATTCCGCGTGTATGCCGGTGCCGACAACCGGC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgAspGluValProPheSerLysLeuValSerLeuLeuArgSerGlyProPheAsnValG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 CGGCCGAATACAGCAAGGACAAT---AAACCCTATAAGCCCGTTTACTTCGCTGCCGTAT 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ProGluGluIleAspG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 AGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGG 472
                                                                                                                                                                                                                                                                                                                                                                            291 uCysPheMetGluAspLysAspValThrGlyLysMetGln-ArgGlnGluPhe----- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GluAspLeuAlaAlaProIlePheAsnArgIleLysGlnValLeuIleA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --------AACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAAT 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GTTCGTATGGTAT 601
ATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCG 172
                                                                                                                                         GTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGGATGGTTTCGTTTCTC 337
                                                                                                                                                                                                                                                 ---------GGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleTrpPheAsp------AlaLeuIleArgGluHisPheArgLysGluPheLys
                                                                                                          ACAAGCCGTCCATTG--------CCAATGCCGTGGTTATCTTCGGTGGCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::::|||||||
482 alLysvalArgValAsnProAspGlyIlePheThrIleAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GlyGlyAsnGlnLysVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 ACTTCCTCATCGTCTACGATGTATTCAAGGAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:::|||:::||||
| SolieuPheAlaAspGlyValSerIleLys---
                                                                                                                                                                                                                                                                                                                                                                                                                                             338 GCACGAIGGGIGAGGAGCIICCGAIICCĢ-
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Db 54 LeuAspSerAsnThrThrSerAlaSerValGlnThrIleAlaIleSerGlnThrAspAsn 73	Qy 560 TCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTC 607 ::::::	Qy 608 CTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGC 661 ::	OY 662 GTCACACGGCGACTTCAGCGTATTCCGCGGTGTATGCCGGTGCCGACAACCGGCCGG	Qy 722 AATACAGCAAGGACAATAAACCCTATAAGCCGGTTACTTCGCTG 766	Qy 767 CCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATGGGTTTCCGGGCA 826	Qy 827 GTACGGATCGCTACCTCACTTCTTGGGTGTGGAAGATCGTATCGAAAACGAGAACAATC 886	Qy 887 CTCGTATCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAA	OY 947 AGGTACCGGTATCAAATATGCCAGCAAGTATGCTCAGAGGTGCTAATTGGAAGAATT 1006	QY 1007 CGATCGGTATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGG 1066	Qy 1067 AAAGAGCATTCGCAGACTGGATCCGTAAGAACGCCAAGAGTGCTGTTATGGCGATGTAT 1126	OY 1127 TGTCTTCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATT 1186 :::	Qy 1187 TGAGCGAGACGCTTTCGGTGGTACCGAGGTGGTTTGCACAGTTTGCCAACGCTT 1246	Qy 1247 TGGCTACAAATCCTGATGCTCATGCGGTATCCTCAAATCGCTTGACGACA 1297 :::  Db 267 ThrlleAspSerSerSerPheThrSerSerThrProValSerLeuThrSerSerThr 286	Qy 1298 AGTACAAAGACTACCTCCCTCGACGTAAGGTGCTGCCGCCATGCTCGATATTG 1357	Qy 1358 TACGCCGCGTATCCCTGCCGACAAGCTCCCGGATA	1394	Qy 1418 AATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGATATTCGACAAGAGTGTGCTTCTT 1477	QY 1478 ATAGCGACAAGTTCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTA 1537
Db 505 alGluGluValProAlaGluAlaMetGluValAspGlyAspAlaLysThrGluAlaProA 525	Qy 1073 CATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGT 1129	OY 1130 CTTCTCCGAAAGGCTTAT	Qy 1150AAGGAAGGAGCCAACGCGACCGTGAGATGACTTATTTGAGCGAGACGC 1198 ::	OY 1199 TCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTA 1252	OY 1253 CAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGTACC 1312	QY 1313 TCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCC 1372 :::   :::    ::: Db 622 lyGluAspAlaGluArg	OY 1373 CTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAGAAATTCAAAGGCGACA 1432  Db 635SerGluLeuLysAlaValGlyThrProValValGluArgTyrArgGluSerGluT 653	OY 1433 CGAAGAAGTATGCAGACTTCGTATTCGAGAAGAGTGTGGTTCCTTATA 1480	Oy 1481 GCGACAAGTTCCATGCCATGCTCAAGGCAAGGAAAAGT 1525	Oy 1526 TIGCCAAGGCTATCGAG 1542              Db 693 alileAsnAlaileGlu 698	RESULT 7 T11678 hypothetical protein SPBC21D10.06c - fission yeast (Schizosaccharomyces pombe)	C.Species: Schizosaccharomyces pombe C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 C.Accession: T11678 R.Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.	Submitted to the EMBL Data Library, September 1998 A;Reference number: 217313 A;Accession: T11678 A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Residues: 1-948 (SEE> A;Cross-references: EMBL:AL031536; NID:e1319499; PID:e1319505 A;Experimental source: strain 972h(-)	C; Venetics: A; Map position: IIR A; Note: SPBC21D10.06c		airly: 22.04* mishaciles: 3.69* indels: 2 Gaps:	US-10-008-355-1 (1-2139) x T11678 (1-948) Qy 503 ATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACT 559

A; Note: séquence extracted from NCBI backbone (NCBIN:144110, NCBIP:1444111 C:Genetics: A;Gene: SCD:HKR1 A;Cross-references: SGD:SO002828; MIPS:YDR420w A;Map position: Approach prosition: A;Map position: A;		CGAATGCGTGAGCTCGGCTTTACGCTCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG  ::: The list of the second of the secon	241 CAGGGCCTGATCTTACCAACCACCACTGCGGATACGGTGCTATCCGAAGCCAAAGC	0y         412 AAGGTAGAAGGACTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAG         471           10         98 ThrThrGlnThrSeTAspThrMetSerSerValLysLysSerThr         112           0y         472 GAGGTATGCCAAAACTGGCCAAA
Qy 1538 TCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCGCGCTATTC 1597	1832	Oy 1871Argarcarangecaaacgarcacacararcacaracaacaca 1924  Oy 1871Argarcacaracacacacacacacacacacacacacacaca	1985 TTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAACCCGATC ::::::::::::::::::::::::::::::::::::	RESULT 8  S69703  HKR1 protein precursor - yeast (Saccharomyces cerevisiae)  N; Allernate.names: protein YDR420w C; Species: Saccharomyces cerevisiae C; Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001 C; Accession: S69703; A53382  R; Dietrich, F.S. Submitted to the EMBL Data Library, August 1995 A; Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 98: A; Reference number: S6955 A; Accession: S69703 A; Moccession: S69703 A; Moccession: S69703 A; Moccession: S69703 A; Moccession: S69703 A; Riasabhara, S.; Yamada, H.; Mio, T.; Shiratori, Y.; Miyamoto, C.; Yabe, T.; N Bacteriol. 176, 1488-1499, 1994. A; Title: Cloning of the Saccharomyces cerevisiae gene whose overexpression over A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: 1-581, A', 583-593, A', 595-1802 < KAS> A; Residues: Residues: Kashara &

Page 11

οy	754	GTTTACTTCGCTGCCGTATCCATGCAAGGCTGAGGCTGACGACTATGCCATGACCATC 813	
Q D	181	GlyThrLeuAlaGln	
οy.	814	GGTTTCCGGGGCAGTACGGTACCTCACCTCTTGGGGTGTGGAAGATCGTATCGAA 873	
g G	198		
ζ S	874	92	
a C	218	ernralaataserintileaspolyrneserseroiuserinroininrasprneseras 23	
٥٧ م	e (	AGCCATGAGGGGAGATCAGGGTACCAAATATGCCAGGAAGTATGCTCAGAGTGC 98	
a ,	238	nThrValSerPheGluAsnSerValGluGluGluTyrAlaMetSerLysSerGlnLeuSe 258	
δ δ	990	TAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	
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70 4	1050	TCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGC 11	
3 2	1110	yeruser miranasp====	
g q	282	olleThrSerPheSerSerTyrSerGlnThrThrSerThrGluThrSerGluSerSe 302	
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<u>2</u>	302	coledadargacriatrascc	
٥y	1224	TTTTGCACAGTTTGCCAACGCATTGGCTACAATCCTGATGCTCATGCCGGT 1275	
qq	322	:::   IPheSerMetSerGluValGluLeuSerThrTyrTyrAspLeuSerAlaGlyAsnTyrPr 342	
Οÿ	1276	ATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCTC 1319	
QQ	342		
οy	1320		
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δλ	1380		
e G	371		
ΟŊ	1431		
qq	390	erAspThrValValSerThrSerSerThrAsnThrValProTyrSerSerValHisSerT 410	
ΟŊ	1470	GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCCAAGGTCCAAGGAAAAGTTTG- 1528	
qq	410		
Qy	1529	CCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGC 1580	
Db	426	yrSerSe	
ΟÝ	1581	TGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGC	
QQ	443		
ΟŊ	1641	GCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGC 1700	
QQ	450		
οy	1701	CAACTICACCAIGCGIAIGAGCIACGGCICCAICAAGGGAIAIGAACCGCAGGACGGIGC 1760	
οgα	463		
Οÿ	1761	CIGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCA 1805	

Nilternate names: CD91: LDL receptor related protein 1; low density lipoprotein rece C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: O4-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 22-Jun-1999
C; Accession: A53102
R; Nimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.
J; Biol. Chem. 269, 212-219, 1994
A; Title: The somatic cell-specific low density lipoprotein receptor-related protein o A; Reference number: A53102; MUID:94103212; PMID:7506255 C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-bind C; Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glyco F;1-17/Domain: signal sequence #status predicted <SIG> F;18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K> F;18-3942,3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <MAT> F;29-66/Domain: LDL receptor ligand-binding repeat homology <LDLL> F:74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2> A;Molecule type: mRNA A;Residues: 1-4543 <NIM> A;Cross-references: GB:X74904; NID:g438006; PIDN:CAA52870.1; PID:g438007 C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-assoc ------GCTACGTTCTCTTCATGATTGACAAATG 2096 1806 GGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAA 1865 -----ATAT 1904 1992 CGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCAC 2051 1932 GGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTT 1991 503 hrTyrThrSerSerProSerAlaProValAlaValSerSerThrTyrThrSerSerPro5 523 583 lalleSerSer-----ThrTyrThrSerSerProSerValProValAlaValS 599 563 erProSerAlaProvalAlaValSerSerThrTyrThrSerSerProSerAlaProvalA <YW05><YW06> <YW08> <YW09> < X W 0 3 > < X W 0 4 > <YW07> homology <EG4> receptor ligand-binding repeat homology <LDL3> receptor ligand-binding repeat homology <LDL4> in: LDL receptor 11gand Dinding repeat nomology <LDLZ
in: EGF homology <EG1>
in: EGF homology <EG2>
in: LDL receptor WTD-containing repeat homology <YW
in: LDL receptor Ingand-binding repeat homology <YW
in: LDL receptor Ilgand-binding repeat homology <YW
in: LDL receptor Ilgand-binding repeat homology <YW
in: LDL receptor ligand-binding repeat homology <UD
in: LDL receptor ligand-binding repeat homology <UD 1866 AAACTATGGTCGCTATGCCGAGAACGGTCAGCTCC---pha-2-macroglobulin receptor precursor - chicken 2097 GGGTCAGTGCCCCGTCTCATCCAAGAGC 2125 619 erProSerAlaProValAlaValSerSer 628 2052 AATCAGCGTGGACATCC----A;Status: preliminary A; Accession: A53102 F:893-929/Domain: F;74-110/Domain: I F;117-150/Domain: 156-190/Domain: F;200-241/Domain: :242-283/Domain: F;294-336/Domain: :337-380/Domain: ;381-422/Domain: 480-521/Domain: :573-615/Domain: :616-661/Domain: 713-754/Domain: 5-840/Domain: 852-888/Domain: 423-470/Domain: :662-712/Domain: 5-797/Domain δ òy Db ò Db δλ g őλ g δ ò

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F;4421-4443/Domain: transmembrane #status predicted <TMM>
F:4444-4543/Domain: intracellular #status predicted <INT>
F:116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1
3488,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covale F:68,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F:2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrLysGlySerHisValCysSerCysAlaLysAsnPheMetLysThrAspAsnMetCys 3858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysAlaGluGlySerGluHisGlnIleLeuTyrIleAlaAspAspAspAsnLysIleArgSer 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyLeuLysMetProArgGlyIleAlaValAspTrpValAlaGlyAsnIleTyrTrpThr 3974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGTTTCTCGCACGATG---GGTGAGGAGCTTCCG---ATTCCGGGTCTTTCCGTGAAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGAC 588
                YWTD-containing repeat homology <YW45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: |||||| |||:::|||
MetThrAsnThrThrMetCysGlyAspGluAlaGlnCysIleGlnAlaGlnSerSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCTG-------CGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAAGCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrCysThrCysArgArgGlyPheGlnLysValProAspLysAsnSerCysGln-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCGTATGGTATTTGCTCCTCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------GluProAla-----PheGlnGlyAspGluAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrAlaSerAsnArgAsnArgArgGlnIleAspGlyGlyValThrHisLeuAsnIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCCGCGTCACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4543
139
69
196
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-008-355-1 (1-2139) x A53102 (1-4543)
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                                                                                            homology
homology
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                    LDL EGF 1 EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                        F;4235-4266/Domain: B
F;4217-4302/Domain: B
F;4307-4338/Domain: B
F;4313-4373/Domain: B
F;4315-4408/Domain: B
F;4421-4443/Domain: E
                                                        F;4150-4181/Domain:
F;4199-4230/Domain:
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| P. 934-969/Domain: LDD | P. 934-969/Domain: LDD | P. 934-1009/Domain: LDD | P. 91013-1009/Domain: LDD | P. 91013-1009/Domain: LDD | P. 91013-1009/Domain: LDD | P. 91013-1138/Domain: LDD | P. 91013-1139/Domain: LDD | P. 91013
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nucin gene MUC5AC: a consensus cysteine-rich d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGCCAACTTCACCATGCGTATGAGCTAC 1725
                                                                                                                                                                                       7-Feb-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGTCCATGGACAA:----GGAAAAGTT 1526
:::||| :::|||
GluValSerIleGluHisLeuGlyGlnVal 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGCTTTCCAAGAGGGTAATAGCTGCTGC 1586
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:::
.rgCysGlnTyrGlnGlnCysPheAsnTyrC 4311
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33374; PIDN:CAA84031.1; PID:9563375
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                                                                                                   GGTGCCTGGTACAACTATCATACGAC 1781
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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2963 AlaThrMetSerThrIleHisProSerSerThrProGluThrThrHisThrSerThrVal 2982 281 CTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGATGGTTTCGTTTCTC 337 11:::		395 TCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGC 454 3008	455 GTCTGGGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAAGAAAATGCAGACGAGA 514	515 ACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACG 574 :::	575 ATGTATTCAAGGACGTTC	617 CTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGC 661	662 GTCACACGGGCGACTTCAGCGTATTCCGCGTGTGCGGTGCCGACAACCGGCCGG	3107 ThrSerSerLysalaThrProSerSerSerFroGlyThrAlaThrAlaLeuProAlaLeu 3126 782 GCTACAAGGCTGACCATGACCATGGCTTTCCCGGGCAGTACGGTTCCCTACA 3127 ArgSerThrAlaThrThr	842 TCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAG 898 11	SerThralaThrProSerSerThr	Throadhisthreecanoratests——askediscipacing to a control of the con		AGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAAGAG ThrThrGlyPheThrAlaThrProSerSerSerProGlyThrAlaLeuThrProProVal	1109 CIGTCTATGGCGATGTATTGTCTTCTCTGAAAGGCTTATAAGGAAGG	1169 ACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTG 1228	1229 CACAGTTGCCAACGCATTGGCTACAAATCCTG
DP Qy DP	Oy Dp	Qy	Qy	QY	Qy	Oy Op	ov ov	DP Qy DP	o do	q o	oy o	ପ୍ର ଓ	Qy Db	Oy Op	QY	oy Db
Db 125 lyCysProValThrSerThrProValThrAlaProSerThrProSerGlyArgA 143 Oy 1752 GGACGGTGCTGGTACAACTATCATACGACAGGCAAGGCGTATTGGAGAA 1802 Db 143 laThrSerProThrGlnSerThrSerSerTrpGlnLysSerArgT 158	OY 1803 GCAGGATCCTAAGAGCGATGAGTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCAC 1862 :::	OY 1863 CAAAAACTATGGTCGCTATGCCGAAACGGTCACTCCATATCGCTTTCCTATCGAACAA 1922	OY 1923 CGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCG 1973	<pre>Qy 1974 TCTGATCGGTCTTCGATGGCAACTGGGAAGCTATGAGTGACAT 2024</pre>	<pre>Qy 2025 CGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTTCAT 2084</pre>	<pre>Qy 2085 GATTGACAAATGGGGTCAGGCCCCGTCTCATCCAAGAGC 2125</pre>	RESULT 11 T45025 mucin MUC5B, tracheobronchial [imported] - human (fragment) C;Species: Homo sapiens (man) C;Species: 1-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000	R.Dessayn, J. L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A. J. Biol. Chem. 272, 3168-3178, 1997 J. Biol. Chem. 272, 3168-3178, 1997 J. Biol. Chem. 272, 3168-3178, 1997 A.Fitle: Human mucin gene MC5B, the 10.7 kb large central exon encodes various alternat A.Reference number: 222899; MUID:97166151; PMID:9013550 A.Accession: T45025	A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1.3570 < DES> A.Cross-references: EMBL:272496; NID:91834502; PIDN:CAA96577.1; PID:91834503 C.Genetics:	A:Gene: MUCSB Alignment Scores: 0.631 Tenorh: 3570	re: 137.00 represents 137.00 recent Similarity: 33.29% rt Local Similarity: 20.67% rry Match: 3.59%	Gaps:. (1-3570)	Qy 65 CCAAAGCCACAAAGGCATGTGGCTCCTCAACGAACTCAGGAGAATCTGGATCGAA 124	Oy 125 TGCGTGAGCTCGGCTTTACGCTCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCA 184	Oy 185 TIGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCG	

0y 1262

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A;Title: The nucleotide sequence of an alpha-amylase gene from an alkalopsychrotrophin, A;Reference number: A60999
A;Accession: A60999
A;Accession: A60999
A;Molecule type: DNA
A;Residues: 1-1104 <KIM>A;Residues: 1-1104 <KIM>A;Residues: 1-1104 <KIM>A;Residues: 1-104 <KIM>A;Residues: 1-104 <KIM>A;Personces: GB:X55799; NID:g296762; PIDN:CAA39321.1; PID:g296763
C;Function: A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Perhmay: glycogen/starch degradation
A;Perhmay: glycosidase; hydrolase; polysaccharide degradation
F;1-32/Pomain: signal sequence #Status predicted <SIG>F;33-1104/Product: alpha-amylase #Status predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1051 CGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCT 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 ArgAsnMetLysIleMetValAsp------ValValVal 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::|||
491 TyrProSerAspAlaAspArgAlaArgPheSerAspLeuLeuArgGlnGlyAlaAspVal 510
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531 AsnValArgLysGlnIleIleAsp---TrpGlnThrAspTrpIleGluLysAlaThrThr 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 ValGluAsnIleLysTyr------AspValArgTyr 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluThrSerGluProTyrTyrGlyTyrHisGlyTyrTrpAlaAsnAsnPheGlyGluLeu 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    943 GATCAGGCTACCCGTATCAAATAT------GCCAGCAAGTATGCTCAGAGTGCT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 TTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGG-----ATG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         655 TGCCCGCGTCACACGGGCGACTTCAGCGTATTCCGC---GTGTATGCCGGTGCCGACAAC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           712 CGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 CAAGAACTGGCCAAAAAAAAAATGCAGAGAGAACCAACTCTGCATCGTAGAGCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 TATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 TCCATGCAAGGCTAC----AAGGCTGACGACTATGCCATGACC-----ATCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::: |||
550 GluAsnGlyAsnThrIleAspTyrPheArgValAspThrValLySHisValGluAspAla
                                                                                                                                                                                                                                                                                                       1104
1138
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Sun May 25 15:40:18 2003

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GluAlaGluAla	GTCTATGGGGATGTATTGTCTTCTCTCGAAAGGCTTATAAGGAAGCC	AAG	ACCTCTTCGGTGGTACCCAGGTGGTTCTTTTGCACAGTTT	GCCAACGCATTGCTACAAAT	:::::        ::: LeuHisSerLeuAlaGlyAspLysGlyLysLeuGlnValAlaAlaThrLeuGlnAlaThr		GACTACCTCCCTCGCTCGACCGTAAGGTGCTCCCCCCCCATGCTCGATATTGTACGCCGG ::: AsnAsnTyrProGlnTyrAspAsnArgTyrAspPheAlaTrpAsp	CGTATCCTGCCGACAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAA ::::::::::::::::::::::::::::::	GGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGAC	AAGTTCCATGCCATGCTCAAGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAA	GATCCGGCAGTAGATTTCCAAGAGCGTAATAGCTGCTGCTGCTATT ::	CAGGCCGATGCGATGCCATGCCATTGAGAGGGCAAGCGTCTTTCTT	GCCGGTTGCGTGAGTGTACCCCGGACGTGCTGCTGCCGAGCGATGCCAACTTCACCATG ::	CGTATGAGCTACGGCTCCATCAAGGGA	LeuvalProGluAsnAsnIleArgIleHisTrIvsArgGluAspAsnValTvrIvsAsn	TATCATACGACAGGCGAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCC	GTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAG 1.	AACGGTCACGTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGT :::    :::	AACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGGC :::::!
590	1111	1162	1195	1237	661	1258	1306	1366	1426	1486 751	1546	1597 790	1654	1714	1741	1771	1831 879	1888	1939 916
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C. Accession: D97933
R. Hoskins; J. A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Dellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A; Tille: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                            valine-tRNA ligase (EC 6.1.1.9) [imported] - Streptococcus pneumoniae (strain R6) C.Species: Streptococcus pneumoniae C.Date: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-883 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99296.1; PiD:g15458063; GSPDB:GN00174
C;Genetics:
1999 AACTGGGAAGCTATGAGTGGTGAC-----ATCGAGTTCGAACCC---GATCTGCAGCGC 2049
                                                                            111 GluserPhereuThrLysValTrpGluTrpLysAsp------GluTyrAlaThr 126
                      846
                                                                                                             956 Asn---ThrValArgIleHisTyrThrArgGluAlaValAspTyrAspAspPheGlyIle 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------AAGGACGTTCGTATGGTATTTGCTCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610 CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGCGTCACACG 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          730 AAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               847 TCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGT 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGAGATCAGGCTACC 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 TrpAspThr---ThrLeuGlnAspIleIleIleArgGlnLysArgMetGlnGlyPheAsp 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    883
104
65
166
24
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: vals
C;Superfamily: valine-tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                574 GATGTATTC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.647
133.00
33.078
20.358
3.488
                                                                                                                                                          2092 ---AAATGGGGT 2100
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: D97933
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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B.S.

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Sun May 25 15:40:18 2003

οy.		CGTATCAAATATGCCAGCAAGTATGCTCAGACTGCTAACTATGGAAGAATTCGATC 1	1011
g D	127 Th:		146
οy	1012 GG	GGTATGAACCGCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGA 1 :::::       :::	1071
QQ	147 Th:		58
οy	1072 GC		1119
ф	159 Va	ValbheValAspLeuTyrLysLysGlyTrplleTyrArgGlyGluPhelleIleAsnTrp 1	178
٥y	1120 GA		1152
Op	179 AS <sub>1</sub>	   AspProAlaAlaArgThrAlaLeuSerAspIleGluValIleHisLysAspValGluGly	198
οy	1153		1182
Ωp	199 Ala		218
Qy	1183 TA	TATTIGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC 1	1242
90 0	219 Th		228
ογ	1243 GC		1302
Ωp	229 AL	::          ::      AlaIleAlaValAsnProGluAspProArgTyr	239
٥y	1303 AA	ტ.	1347
qq	240 LY	LysAspLeuIleGlyLysAsnValIleLeuProIleAlaAsnLysLeuIleProIleVal 2	259
٥y	1348 CT	CTCGATAITGTACGCCGGCGT 1	368
qq	260 Gly	GlyAspGluHisAlaAspProGluPheGlyThrGlyValValLysIleThrProAlaHis 2	279
οy	1369 AT	O	1428
Dp	280 As	AspProAsnAspPheLeuValGlyGlnArgHisAsnLeuProGlnValAsnIleMetAsn 2	299
٥y	1429 GA(	GACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAG	488
QQ	300 AS		316
ò	1489 TT	CATGCCATGCTCAAGTCCATGG	548
QQ	317 Ph		331
δy	1549 CC	CCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCT1	.593
qq	332 AL		151
λ̈́O	1594	ATTCAGGCCGAT	1605
Db	352 Va	::: ValValGluProArgLeuSerThrGlnTrpPheValLysMetAspGlnLeuAlaLysAsn 3	371
δλ	1606 GC		1665
QQ	372 Al		382
Qy	1666 GA		1698
QQ	383 G1		402
Ο̈́Υ	1699 GC	ATCAAGGGATATGAACCGCAGGACGGT	1758
Dβ	403 Tr	::: ::::: :::!!  pValIleSerArgGlnLeuTrpTrpGlyHisGlnIlePro	416
δy	1759 GC		1818
QQ	417 Al		34

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probable pts pep phosphotransferase - Chlamydia trachomatis (serotype D, strain UW3/C C; Species: Chlamydia trachomatis C; Date: 13.5ep-1998 #sequence_revision 13.5ep-1998 #text_change 21-Jan-2000 C; Accession: C71528 Rstephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia the A:Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001306; GB:AE001273; NID:g3328748; PIDN:AAC67931.1; PID:g332 A;Experimental source: serotype D, strain UW-3/Cx C;Genetics: A;Gene: pts1
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I F;17-565/Domain: phosphotransferase system enzyme I homology <PTl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1428 GCCTTTGAATTTCTTGTCGATTACATTCTT---GAATATATCGGGGAGCTTGTCGGCAGG 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1635 CTTCTCAATGGCATAGGCATTGGCCATCGCATCGGCCTGAATAGCGCGAGCAGCAGCTAT 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1575 TACGCTCTTGGAAAGCTCTACTGCCGGATCTTTCTCGATAGCCTTGGCAAACTTTTCCTT 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GCCATGGAACTTGTCGCT 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1479 ATAAGGAACCACACTCTTGTCGAA-----TACGAAGTCTGCATACTTCTTCGTGTC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ATTTGTAGCCAATGCGTTGGC 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LysAsnAlaGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 ThralaThrargValAspArgValGlnAspIleHisAspIleSerAsnArgValIleGly 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LeuGluLysGluAlaLysGlyLysGlnGlyTyrGlnGluIleAlaSerIleLeuGlnAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||| :::
52 GluHisGluIleSerArgTyrTyrLysAlaLeuLysArgSerArgSerAspLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1311 GTAGTCTTTGTACTTGTCGTCAAGCGATTTGAGGATACCGGCATGAGCATCAGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1236 AAACTGTGC-----AAAACGAACCACCTCGGTACCACCGAAGAGCGTCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571
115
88
186
185
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 IleValProGlyIleGlyLeuGlyLysAlaLeu----
1819 GATGAGTTTGCCGTACAGGAGAATATCCTCGAC 1851
                       US-10-008-355-1 (1-2139) x C71528 (1-571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1515 GTCCATGGACTTGAGCAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.628
132.00
35.37%
20.03%
3.33%
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A;Molecule type: DNA
A;Residues: 1-571 <ARN>
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                              RESULT 14
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Sun May 25 15:40:18 2003

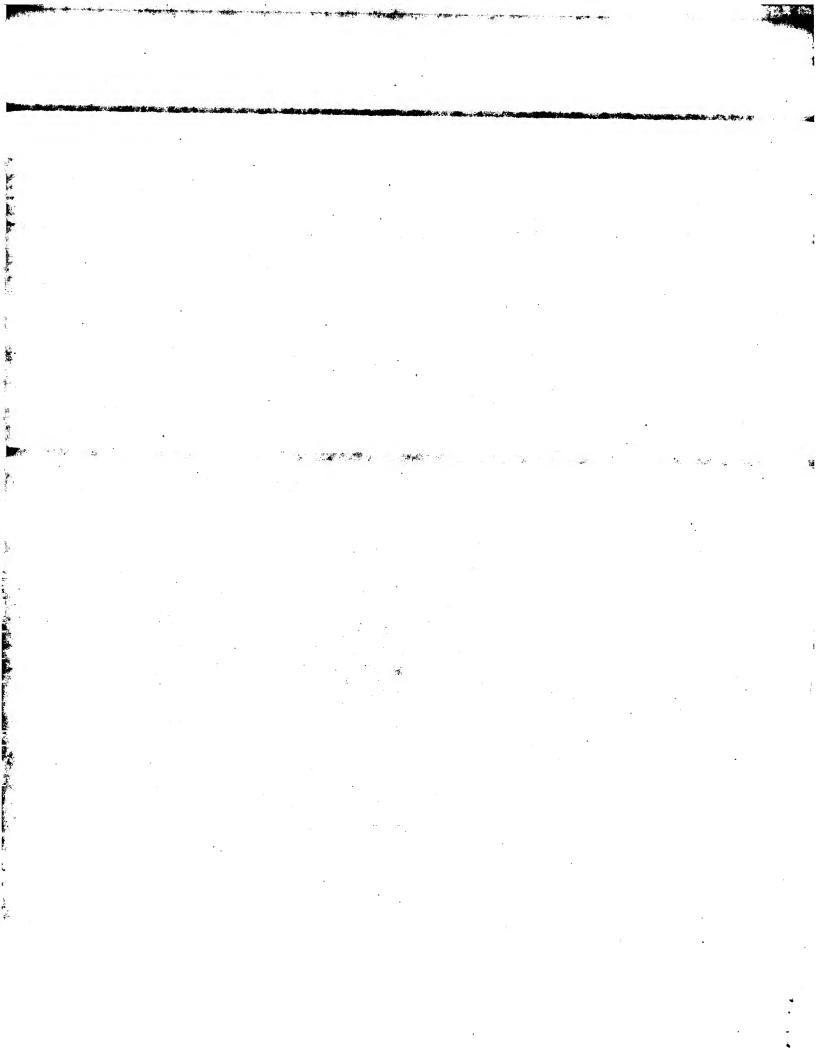
QQ	178	SerGluGluLeuThrProSerGluAlaAlaAsnAlaAsnProGluTyrIleArgGlyPhe 197	
oy P	1191		
3 6	,		
à é	212	AGCCTTTTCGAGAGAGACACATACATCGCC	
ò	1116		
qq	232		
Οy	1065	CTCGGCACGCTTACGACCTATCACGTCAAGACGAGC 1030	
qq	252		
Οý	1029	GAGACCGCGGTTCATACCGATCGAATTCTTCCAATAGCTAGC	
Q.	272	ProvalGlnValGlnThrGlyLysAsnLeuProLeuIleSer-LeuSerAla 288	
οy	696	GGCATATTTGATACGGGTAGCCTGATCTGCGTCCTTCCTT	
Ор	289		
οy	606	GATACCGCGAACTICGATACGAGGATTGTTCTCGTTTTCGATACGATCTTC 859	
QQ	299	eGluArgGluSerProGlyThrSerValGlyLeuPhe311	
οy	828	CACACCCCAAGAAGTGAGGTAGCGATCCGTACTGCCCGGGAAACCGATGGTCATGGCATA 799	
QQ	312	.:: 	
οy	798	GTCGTCAGCCTTGTAGGCTTGCATGGATACGGCAGCGAAGTAAACGGGCTTATAGGGTTT 739	
g	318		
δ	738	AT	
qq	338	InPheGlnCysSerAspIleHisValLeuArgLeuPheAspPheGlyGluAspLysGluC 358	
οy	735	GICCITGCTGTATTCGGCCGGCCGGTTGTCGGCACCGGCATACACGCGGAATACGCTGAA 676	
Op	358		
οy	675	GTCGCCCGTGTGACGCGGCCACAT CCAGTTGTCCGTATCGCCTCCGAACTTACCTAC 619	
Q	374	GlnGluLysValLeuLysGluGlnLeuGlnAlaIleAlaIleValSer 389	
oy Db	618 390	AGAGCTGGGAGCAAGTACCATACGAACGTCCTTGAATACATCGTAGACGATGAGGAA 559	
οy	558	GTATTCGTTGTTGGAATAGAAAGGCTCTACGATGCAGAGTTGGTTCTCGTCTGCATTTTC 499	
qq	407	::: :::    :::       :::      :::     :::      :::	
ογ	498	TTTTTGGCCAGTTCTTGGCATACCTCCTGAGCTTTGCGCAGACGCTCCATCTCGTCAGT 439	•
Op	425	SerGluAsnileLeuTrpGlySerMetileGluIleProSerAlaValTrpMetileGlu 444	
ò	438	GATACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGCAGATACTT 379	
qq	445	:::     :::     ::::::	
οy	378	CAGGGAAAGACCGGGAAGCTCCTCACCCATGGGGGAAACGAAACCATCGCG 319	
QQ	465	LeuGlyThrSerArgGluArgSerLeuLeuGlyGluArgSerArgValProHisProSer 484	
۶ ج د	318	CAGATAGTCGTGATCCACCGTGCTTTGGCTCTGGATAGCACCGTATCCGCAGTG 265	
3	n	ValileArgmetileHisHisValValGinGinAlaLySGinLySASnValProValSer 504	

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date 10 -Nov-1997 #sequence_revision 10 -Nov-1997 #text_change 08-Oct-1999
C; Accession: PC4395 #sequence_revision 10 -Nov-1997 #text_change 08-Oct-1999
R; Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Ein Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A; Title: Nolecular cloning of human MUC3 CDNA reveals a novel 59 amino acid tandem re A; Reference number: PC4395; MUID:97445141; PMID:9299468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-648 <VAN>
A;Cross-references: DDBJ:AF016692; NID:g2454614; PIDN:AAB71685.1; PID:g2454615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 CTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATG---TATTCAAGGACGTTC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 Val-------------ThrSerSerGluAlaSerThrProSerThr 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 GCG--------TGTATGCCGGTGCCGACAACCGGCCGGCCGAATACA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728 GCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACA 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LeuAspSerThr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 ------CGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           788 AGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GTATCGAAAACGAGAACA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ATCCTCGTATCGAAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593 GTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental. source: intestine
F;1-59,60-118,119-177,178-236,237-295/Region: repeat
F;296-565/Region: semi-unique #status predicted
F;566-582,583-599,600-616,617-633,634-647/Region: repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
264 GTGGTTGGTAAA-----GATCAGGCCCTGATC 238
                                              ||| |||:::
505 ValCysGlyGluMetAlaGlyAspProAlaLeuLeu 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-008-355-1 (1-2139) x PC4395 (1-648)
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131.00
34.148
22.658
3.438
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Best Local Similarity:
Query Match:
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Pred. No.:
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ó	962	AATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGA 1018	
qq	80		
δy	1019	ACCGCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCG 1078	
QQ	292	SerThrThrProValThrArgPhe	
δý		CAGACTGGATCCGTAAGAACGCCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCG 1138	
QQ	311	SerIleProSerValTyrThr 323	
οy	1139	AAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGC 1198	
Q	324		
δλ	1199	TCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACGCTTGCCAACGCATTGGCTACAAATC 1258	
QQ	327	GlySerThrLeuGluGly 336	
Οy	1259	CTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCT 1318	
QQ	337	ThrThrThrMetProMetSerThrThrSerGlu 347	
οy	1319	CGCTCGACCGTAAGG1357	
Dp	348	:::  ArgSerThrLeuLeuThrThrValLeuIleSerProIleSerValMetSerProSerGlu 367	
ΟŊ	1358	TACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAA 1408	
Dp	368	::: :::	
oy.	0	. C	
ΩQ	382	SerThrLysAlaGlySerPheSerIleProAlaGluValThrThrIleArgIleSerIle 404	
Qγ	1445	CAGACTICGIAITCGACAAGAGIGIGGIICCIIAIAGCGACAAGIICCAIGCCAIGCA 1504	
Dp	405	ThrSerGluArgSerThrProLeuThrThrLeuLeuValSerThrThrLeuProThrSer 424	
Οy	1505	AGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGC 1561	
අ <u>ධ</u>	425	PheProGlyAlaSerIleAlaSerThrPro	
ΟŊ	1562	TTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCT 1621	
qq	434	434	
ΟŅ	1622	ATGCCATTGAGAAGGGCAAGCGTCTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGAC 1681	
qq	435		
δy	1682	rgcg	
Dp	446	ThraspThralaSerThrProThrIleProValAlaThrThrIleSerValSerVal 464	
QY	1742	ATGAACCGCAGGACGTGCTGGTACAACTATCATACGACAG 1783	
qq	465	IleThrGluGlySerThrProGlyThrThrIlePheIleProSerThrProvalThrSer 484	
δy	1784	GCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA 1843	
QQ	485		
θy	1844	TCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCC 1900	
QQ	503	Ë	
οy	1901	ATATCCTTTCCTATCGAACAACGACATCACGGCGGTAACTCCGGTAGCC 1951	
g	517	ThrThrThrSerPheSerThrThrLysGluPheThrThrProAlaMetThrThrAlaAla 536	

2011	542	2071	261		
1952 CCGTATTCGATAAGAACGCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTA 2011	537 ProLeuThrTyrValThr 542	2012 TGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCT 2071	543MetSerThrAlaProSerThrProArgThrThrSerArgGlyCysThrThrSerAla 561	2072 ACGTTCTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125	A]
1952	537	2012	543	2072	562
Οy	QQ	δλ	Dp	Qy	Ωp

Search completed: May 16, 2003, 12:38:15 Job time : 131.5 secs



19	A. (tina char. nt o ope G. G.	This SWISS-PROT entry is between the Swiss Institute European Bloinformat use by non-profit ins modified and this statem modified and this statem entities requires a lice or send an email to lice.  EMBL, \$\$5920, \$\$1504.  PIR: \$\$1504, \$\$1554.  PIR: \$\$25345, \$\$25345.  SGD: \$\$000685; FIG2.  SGUENCE 1609 AA: 166  ignment Scores: 0.016  or send Similarity: 21.19
Ge Copyright (c) Otein search, us May 16, 2003, 1 US-10-008-355-1 3820 1 atgcaaatgaat 1 atgcaaatgaat Xgapop 10.0, x Ygapop 10.0, x Fgapop 6.0, E Fgapop 6.0, E Delop 6.0, E	Post-processing: Minimum Match 0%  Maximum Match 100%  Listing first 45 summaries  Command line parameters:  -WODEL-frame+ n2p.model -DEV-xlp  -0~/cgn2_1/USPTO_spool/US10008355/runat_16052003_110337_9320/app_query.fasta_1.2311  -0~/cgn2_1/USPTO_spool/US10008355/runat_16052003_110337_9320/app_query.fasta_1.2311  -0~/cgn2_1/USPTO_spool/US10008355/runat_16052003_110337_9320/app_query.fasta_1.2311  -1.CST-45 -DOCALIGN-200 -THR_ARTRIX=blosum62 -TRANS-human40.cdi  -1.CST-45 -DOCALIGN-200 -THR_ARCRIX=1 - MATRIX=blosum62 - TRANS-human40.cdi  -1.CST-45 -DOCALIGN-200 -THR_ARCRIX=1 - MATRIX=0 - MAILEN=200000000  -USER-US10008355_ecGN_1_1_47_erunat_16052003_110337_9320 - NCPUe_3  -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 - MAILEN=200000000  -VGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -EVELEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=7  -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=7  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=0.5  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=0.5  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -YGAPEXT=0.5  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5  -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5  -YGAPOP=10 -YGAPEXT=0.5  -YGAPO	154.5 4.0 1609 1 FIG2_YEAST 143.5 3.8 776 1 AMYH_YEAST 143.5 3.8 1802 1 HKR1_YEAST 139 3.6 4543 1 LRP1_CHICK 137.5 3.8 1802 1 WR6_YEAST 132 3.3 571 1 PT1_CHLTR 127.5 3.3 772 1 ASA_YEAST 126.5 3.3 3778 1 YS99_CAEEL 127 3.2 1104 1 COLA_CLOPE 128 3.2 1104 1 COLA_CLOPE 128 3.2 1104 1 COLA_CLOPE 138 3.1 1024 1 HLYA_ECOLI 117.5 3.1 1024 1 HLYA_ECOLI 117.5 3.1 1147 1 TEA1_SCHPO 116.5 3.0 1169 1 YK82_YEAST 116 3.0 652 1 IRGA_VIBCH 116 3.0 652 1 TOP1_STRCO

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	: cdps		_	9	. gTOT
US-10	US-10-008-355-1 (1-2139) x FIG2_YEAST (1-1609)	(6	_	;	1112
Qy	74 ACAAAGGCATGTGGCTCCTCAACGAACTCAAGGAGAATCTGGAATGCGTGAGC	GGAGAATCTGGATCGAATGCGTGAGC 133		S &	1031
Db		GluCysThrPro 798		3 8	1172 (
οy	Ċ			r d	1043
qq			_	οy	1232 /
οy	194 CCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGCCCTGATCT			qq	1049
Ср	812 ProLeuLeuSerThr	Ser		δλ	1292
ολ	254 TTACCAACCACTGCGGTAACGGTGCTATCCAGAGCCAAGCACGGTGGTTC	GCACGGTGGATC		QQ	1066
q	818 SerSerThrValLeuSerSerThrValSerGluG			٥y	1343
οy	308 ACGACTATCTGGGGGATGGTTTGTTTGTCGCATGGGTGAGGAGCTTCCGATTCCGG	GATGGGTGAGGAGCTTCCGATTCCGG 367 :::		ОÞ	1080
q				οy	1403
ολ	368 GTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGC		_	qa	1096
g	854	Ser.854		QY	1463
ογ	428 TCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAAC			Ωþ	1114
qq	855 ThrGlnValSerAlaThr			Qγ	1523
οy	488 TGGCCAAAAAAGAAAATGCAGACGAGCAACTCTGCATCGTAGAGCCTTTCTATTCCA			Q	1132
qq	861SerAlaThrAlaThrAla	ThrSerGlnVal		ογ	1577
٥٨	548 ACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTC			QQ	1151
QQ	876 SerThrAlaSerGluThrIleSerThrLeuGlyThrGlnAsnPheThrThrThrGlySer	hrGlnAsnPheThrThrThrGlySer 895	_	οy	1637
Οy	602 TIGCICCICCCAGCICIGIAGGIAAGIICGGAGGGGATACGGACAACIGGATGIGGCCGC			qq	1158
q	-	detileAsnThrThrValValSerArg 913		ογ	1678
οy	662 GTCACGGGCGACTTCAGCG	GCGTATTCCGCGTGTATGCCGGTGCCGACA 709		qq	1177
QQ	914 LysThrLeullelleSerThrGluValCysSerHisSerLysCysValProThrValll	HisserLysCysValProThrVallle 933		ò	1724
ογ	710 ACCGGCCGGCCGAATACAGCAAAAAAACCCTATAAGCCCGTTTACTTCGCTGCCG	CCTATAAGCCCGTTTACTTCGCTGCCG 769		අධ	1197
qq	934.ThrGluValValThrSerLysGlyThrProSerAsnGlyHisSerSerGlnThr	ProSerAsnGlyHisSerSerGlnThr 951		ò	1784
0y	770 IAICCAIGCAAGGCIACAAGGCIGACGACIAIGCCAIGACCAICGGIIIICCGGGGCAGIA	CCATGACCATCGGTTTCCCGGGCAGTA 829		o Q	1217
qq	952 LeuGlnThrGluAlaValGluValThrLeuSerSerHisGlnThrValThrMetSerThr	SerHisGlnThrValThrMetSerThr 971		δλ	1.844
δy	830 CGGATCCCTACTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGA-	ATCGTATCGAAAACGAGA 880		qq	1237
Ор	972 GluValCysSerAsnSerIleCysThrProThrValIleThrSerValGlnMetArgSer	ValileThrSerValGlnMetArgSer 991	•	ò	1904
0y	881ACAATCCTCGTATCGAAGTTCGCG	-ACAATCCICGIAICGAAGITCGCGGIAICAAGCAAGGAAGGAAG 931		연	1257
qq	992 ThrProPheProTyrLeuThrSerSerThrSerSerSerSerLeuAlaSerThrLysLys	SerSerSerLeuAlaSerThrLysLys 1011		0	1946
ò	932 CCATGAGCGCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTA	ATGCCAGCAAGTATGCTCAGAGTGCTA 991		7 A	1277
qq	1012Serser	SerSerLeuGluAlaSer 1017		ò	2006
ογ	992 ACTATIGGAAGAATICGAICGGTAIGAACCGCGGICICGCICGTCTIGACGIGAIAGGIC			qq	1292
qq	1017	1017	_	Qy	2066

Qy Db	1052 (	GTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTG	1111
Qy	1112	TCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	1171
Db	1031	ProLeualaPheThrCysProLeualaPheThrCysArgSerThr	1042
Qy	7	GTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCAC	1231
Q	1043	ThrservalserGinTrp	
οy	7	AGTTTGCCAACGCATTGGCTACAAATCCTGATGCCTCATGCCGGTATCCTCAAATCGCTTG	5 5
qq	1049	SerAsnThrValLeuThrAsnThrIleMetSerSerSerSerAsnValle	9
δλ	2	ACGACAAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGCTGCCGG	34
QQ	w .	SerThrAsnGluLysProSerSerThrThrSerProTyrAsn	5 6
δλ		CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGA	1402
og ,		TOTAL THE ADDITIONAL DESIGNATION OF THE ADDITIONAL DESIGNATION OF THE ADDITION	1462
5 6	1096	AIGIDALCGACANGAGAILEANNOCCONTACHAILEANNOCCHAIGE SEE SEE SEE SEE SEE SEE SEE SEE SEE S	1113
3 8	, ,	<ul><li>Aをおびかりできます。</li><li>Aをおびかりできます。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかります。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびかりまする。</li><li>Aをおびがりまする。</li><li>Aをおびがりまする。</li><li>Aをおびがりまする。</li><li>Aをおびがりまする。</li><li>Aをおびがりまする。</li><l< td=""><td></td></l<></ul>	
g 5			1131
οy	1523	AGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAA	1576
QQ	1132		1151
ò	1577	TAGCTGCTGCTCGCGCTATTCAGGCCGATGCCATGGCCAATGCCTATGCCATTGAGAAGG	1636
QQ	1151	GlnTyrThrLeuSerThrA	1158
ογ	1637	GCAAGCGTCTTTTCTTTGCGGTTTGCGTGAGATGTACCCC	1677
qq	1158	laThrThrThrIleSerGlyLeuLysThrValTyrThrThrTrpCysProLeuThrS	1177
οy	1678		1723
Dp	1177	erLysSerThrLeuGlyAlaThrThrGlnThrSerSerThrAlaLysValArgIleThr-	1196
Qy	1724	ACGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAG	1783
Dp	1197	SerAlaSerSerAlaThrSerThrSerIleSerLeuSerThrSerThrGluSerGluSer	1216
Οy	1784	GCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA	1843
QQ	1217	SerSerGlyTyrLeuSerLysGlyValCysSerGlyThrGluCysThrGlnAspValPro	1236
δλ	1844	TCCTGGACTCTTCCGCACCAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCATA	190
Op	1237	ThrGlnSerSerSerProAlaSerThrLeuAlaTyrSerProSerValSerThrSerSer	1256
Qy	1904	TCGCTTTCCTATCGAACAACGACATCACGGGGGGGTAACT	1945
Dp	1257	SerSerSerPheSerThrThrAlaSerThrLeuThrSerThrHisThrSerValPro	1276
Qy	1946	cgataagaacggccgtctga 	200
QQ	1277	LeuLeuProSerSerSerSerIleSerAlaSerSerProSerSer	129
δy	2006	AAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCGCAATCAGCGTGGACA :::	7
QΩ	1292	ThrSerLeuLeuSerThrSerLeuProSerProAlaPheThrSerSerThrLeuProThr	131
Qy	2066	TCCGCTACGTT	2125

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Alignment Scores:
Pred. No.:
                                                                                                                            Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
"Similar short elements in the 5' regions of the STA2 and SGA genes
from Saccharomyces cerevisiae.";
FEBS Lett. 239:179-184(1989).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.
-!- SIMILARITY: TO S.POMBE SPEC15.13.
-!- SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
SEQUENCE FROM N.A.

STRAIN=S288C / AB972;

Barrell B.G., Badocock K., Bankier A.T., Bowman S., Brown D.,

Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,

Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,

Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

Walsh S.V., Whitehead S.,

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                 ANYH_YEAST STANDARD; PRT; 1367 AA.

D08640; P08068.

D1-40G-1988 (Rel. 08, Created)

O1-FEB-1995 (Rel. 31, Last sequence update)

O1-FEB-1995 (Rel. 31, Last sequence update)

O1-FEB-1995 (Rel. 40, Last annotation update)

G1ucoamylase S1/S2 precursor (EC 3.2.1.3) (G1ucan 1,4-alpha-g1ucan g1ucohydrolase).

STAI OR STA2 OR MAL5 OR YIRO19C.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Pungi; Ascomycota; Saccharomycetina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamashita I., Nakamura M., Fukui S.; "Gene fusion is a possible mechanism underlying the evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLOCOANYLASE S1/S2.
SER/THR-RICH.
N-LINKED (GLCNAC. .) (POTENTIAL).
W-LINKED (GLCNAC. .) (POTENTIAL).
W, 91C00E2DBD61AA9D CRC64;
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EMBL; M16164; AAA35014.1; --
EMBL; M16165, AAA35014.1; --
EMBL; M16165, AAA35015.1; --
EMBL; X13857; CAA32069.1; --
PIR; B26877; B26877.
PIR; A54878; S48478.
SGD; S0001458; MuC1.
Hydrolase; Glycosidase; Polysaccharide degradation; Gly Signal; Multigene family.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-242 AND 762-1331 FROM N.A. MEDLINE-87194600; Pubmed=3106330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-31 FROM N.A.
STRAIN-SPX101-1C;
MEDLINE-89031230; PubMed-3141213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 169:2142-2149(1987)
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210 136
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874 87
1367 AA;
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SEQUENCE
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AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

AMYH_YEAST

BD 10-AMYH

BD 10-AMYH

BD 10-BD

BD 6 Glucoal

BD 6 Glucoal

BD 7 10-BD

BD 6 Glucoal

BD 10-BD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596 TGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGT 655
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355 ProvalProThrProSerSerThrThrGluSerSerAlaProvalThrSerSer 374
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                                                                                                                                                                                                                                                                                                                                                                                                    CGATTCCGGGTC - - TTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 ThrGluSerSerSerAlaProValThrSerSerThrThrGluSerSerAlaProVal
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                                                         Conservative:
Mismatches:
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0y	Oy 995 ATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	TCGCTCGTCTTGACGTGATAGGTCGTA 1054
QQ	647 GluSerSerAlaProvalProThrProSerS	SerSerThrThrGluSerSerSerAla 666
Oy Db	QY 1055 ACCTGCCGAGGAAGAGATTCGCAGACTGGATCCGTAAGAACGCCA	TCCGTAAGAACGCCA 1102 
Oy Db	Qy 1103 AGAGTGCTGTCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	TCGAAAAGGCTTATAAGGAAGGAGCCA 1162     
oy D	1163	
o o	1223	STATCCTCA 
Oy Db	OY 1283 AATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCGCTCG	CCTCGCTCGACCGTAAGGTGCTGCCCG 1342 :::
Oy Dp	Oy 1343CCATGCTCGATATTGTACGCCGGCGTATCCTGCCGACAAGCTCCCGATA	GTATCCCTGCCGACAGCTCCCCGATA 1393
Oy Dp	1394 TATTCAGGAATGTAATGG	ACAAGAAATTCAAAGGCGACACA 1435     ::         ProThrProSerSerSerThrThrGlu 803
oy Dp	1436 AGAAGTATG    ::: 804 SerSerValAlaProVal	CAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCG 1483         :: :: :: 818 ProThrProSerSerSerSerAsnIle 818
9 9	Qy     1484     ACAAGTTCCATGCCATGCTCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGA       D	AGGAAAAGTTTGCCAAGGCTATCGAGA 1543 ::: SerSerThr 832
70 4	1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAG	
9 % Q	1604 ATGCGATGGCCAATGCCTATGCCATTGAGAAGGCCA	GCAAGCGTCTTTTCTTTGCCGGTTTGC 1663
Oy Dp	Oy 1664 GTGAGATGTACCCGGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGC	ATGCCAACTTCACCATGC 1714 :::
Qy Dp	1715 GTATGAGCTACGGCTCCATCAAGGATATGAAC :: :::::             875 IleThrSerSerAlaProSer	CGCAGGACGGTGCCT 1762 :::::    SerIleProPheSerSerThr 888
Oy Dp	1763	-GGTACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGC 1804            :: 
Oy Dp	Oy 1805 AGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA :: ::      :: ::      :: ::      Db 909 GlnThrGluThrSerValSerSerThrThrGluThrThrIleValProThrLysThrThr	TTGCCGTACAGAGAATA 1843 
Oy Dp	Oy 1844 TCCTCGACCTCTTCCGCACCAAAAACTATGGTC	ThrThrThrValCysSerThrGlyThr 948
Oy Dp	1877	-GCTATGCCGAGAACGGTCAGCTCCATATCGCTT 1909    :::      ::::: YCysSerProLysThrValThrThr 965

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                                                                                                                                                                       1970 GCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGT 2029
                                                                                             ----ATCTGCAGGGCACAATCAGCGTGGACATCC 2068
1910 TCCTATCGAACAACGACATCACGGGGGGTAACTCCGGTAGCCCCGTATTCGATAAGAACG 1.969
                    Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfleld J., Button J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Lalsster N.,
Latrellle P., Lighthing J., Lloyd C., Mortimore B., O'Callagha M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sluss M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                     2069 GCTACGTTCTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCC 2119
                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
1-FEB-1994 (Rel. 28, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Hypothetical 86.9 kDa protein C30C11.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; ATP-binding; Multigene family. SEQUENCE 776 AA; 86896 MW; 20FA975FB649FA9C CRC64;
                                                                                                                                                                                                                                                                                                                               776 AA.
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PROSITE; PS000297; HSP70_1; FALSE_NEG.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=94150718; PubMed=7906398;
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InterPro; IPR001023; Hsp70.
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                                                                                                                                              2030 TCGAACCCG-----
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SEQUENCE FROM N.A.
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Q05036;
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### Similarity: 37.48%   Gonservative: 87   193	· 4	Db 505 alGluGluValProAlaGluAlaMetGluV	Qy 1073 CATTCGCAGACTGGATCCGTAAGAACG	Qy 1130 CTTCTCGAAAAGGCTTAT	Qy 1150	Qy 1199 TCTTCGTGGTACCGAGGTGGTTC :::    : Db 584 alTyrGluMetArgAspLysValSerAspG	Qy 1253 CAAATCCTGATGCTCATGCCGGTATCCTCA	Oy 1313 TCCCTCGCTCGACCGTAAGGTGCTGCCGG	Oy 1373 CTGCCGACAAGCTCCCCGATATATTCAAGA :::    Db 635SerGluLeuLysalaValGlyThrP	1433 CGAAGAAGTATGCACACTT   :::        653 hrargLysProAlaPheAs	.Qy 1481 GCGACAAGTTCCATG	Qy 1526 TTGCCAAGGCTATCGAG 1542 	30L	DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence DT 01-OCT-1996 (Rel. 34, Last annotati DE Hansenula MRAKII killer toxin-resis		OX NCBL_TaxID=4932; R (1) RP SEQUENCE FROM N.A. RC STRAIN=YNN 295;		RT overcomes the effects of HM-1 kille RT beta-glucan synthesis."; RL J. Bacteriol. 176:1488-1499(1994). CC -!- FUNCTION: COULD REGULATE BETA-G	CC PROVIDES RESISTANCE TO HM-1 KII CC -!- SUBCELLULAR LOCATION: Type I me CC -!- PTM: COULD BE O-GLYCOSYLATED IN
Pèrestra de la company de la c	rcent Similarity: 37.48% Conservative: 87 st Local Similarity: 21.57% Mismatches: 18 ery Match: 3.76% Indels: 15	: -10-008-355-1 (1-2139) x YLA4_CAEEL (1-776)	113 ATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCGGTTGGATTCGCTCTACAGTTTCG 17	173 ACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGAT	218 GTACCGGTATCACAGGCTCTGATCTTTACCAACCACCACTGCGGATACG	272 CysGluArgValLysLysGlnMetSerAlaAsnGlnThrProlle-ProLeuAsnIleGl 278 GTGCTATCCAGAGCCAAAGCACGGTGGATCACGATATCTGCGGATGGTTTCTTC	338 GCACGATGGGTGAGGAGCTTCCGATTCCG	355	413 AGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGG 5::::	473 AGGTATGCCAAGAACTGGCCAAAAAGAAAATGGACGACGAG	514AACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAAT	557 ACTTCCTCATCGTCTACGATGTATTCAAGGAC	602 TTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGC :::!      ::	662 GTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACAAGCGGC	716 CGGCCGAATACAGACAAGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCTAT	773 CCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGG :::                ::	833 ATCGCTACCTCACTTCTTGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTA ::::: 475LysV	893 TCGAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTA ::::	Qy 953 CCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCG 1012

CAAATCGCTTGACGACAAGTACAAAGACTACC 1312 GCCATGCTCAAGTCCATGGACAAGGAAAGT 1525 AACCGTGAGATGACTTATTTGAGCGAGACGC 1198 CGTTTTGCACAGTTTGCCAACGCATTGGCTA 1252 GCCATGCTCGATATTGTACGCCGCGTATCC 1372 SAATGTAATCGACAAGAAATTCAAAGGCGACA 1432 GTGATAGGTCGTAAGCGTGCCGAGGAAAGAG 1072 ----- 1149 CAAGAGTGTGTT------CCTTATA 1480 GGCAAGAGTGCTGTCTATGGCGATGTATTGT 1129 | | | | | :::||| uThrSerThrGluAspTrpLeuTyrAspGluG 622 ::::::|||:::||| oGlnTyrAlaGluPheIleThrProAlaAlaA 604 |||::::::::: rProvalvalGluArgTyrArgGluSerGluT 653 |:::|||::::| pGlnSerIleMetArgValArgLysAlaTyrG 673 ---SerAlaThrMetTyrGluProArgileV 505 LysPheHisAsnLeuGluLeuGlnMetGlnG 565 :||| ||| ||| ||| ::: |||||||| ralaHisLeuAspSerLysGluMetGluLysV 693 hiratori Y., Miyamoto C.,
.., Furuichi Y.;
evisiae gene whose overexpression
ler toxin, which inhibits -GLUCAN SYNTHESIS. OVEREXPRESSION ILLER TOXIN. membrane protein (Probable). IN SERINE/THREONINE RICH DOMAIN. yeast). charomycotina; Saccharomycetes; ceae; Saccharomyces. ce update) tion update) istant protein 1 precursor. 1802 AA.

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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                            SER/THR-RICH.

12 X 28 AA TANDEM REPEATS OF S-[AV]-[P]-
V-A-V-S-S-T-Y-T-S-S-P-S-A-P-A-A-I-S-S-T-
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SIMILARITY: SOME, TO YEAST MSB2
                                                                                           EMBL; S69101; AAB30051.1; -.
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Glycoprotein; Transmembrane;
SIGNAL 1 21
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TCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGC 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170 CCGTGAGATGACTTATTTGAGC-----GAGACGCTCTTCGGTGGTACCGAGGTGGTTCG 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ThrSerAspThrMetSerSerValLysLysSerThr 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: ::: ||||::: ||||| rvalileileSerThrSerAspSerSerAlavalProArgGluileSerThrOileileTh 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATC 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rThrAspSerGlnIleSerLysGluGluGlyThrLeuAlaGlnThr-----SerSe 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::|||
| rileSerGluThrThrArgIleAlaGlnMetValThrArgValSerGlnIleSerSerIl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eThrAlaAlaSerThrIleAspGlyPheSerSerGluSerThrGlnThrAspPheSerAs 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 olleThrSerPheSerSerSerTyrSerGlnThrThrSerThrGluThrSerGluSerSe 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rPheSerMetSerGluValGluLeuSerThrTyrTyrAspLeuSerAlaGlyAsnTyrPr 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGAC 411
                                                                                                                                           112 AAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGGGTCTGCGCAAAGCTCAG 471
                                                                                                                                                                                                                                                                                           -----AAAGAAATGCAGACGAG 513
                                                                                                                                                                                                                                                                                                                                                                  GluIleAlaThrProSerSerSerIleValProThrProLeuGlnSerTyrSerAspGlu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAAGGAATACTTCCTCATCGTCTAC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerAspThr-Thr------SerSerGluSerSerSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAAACCCTATAAGCCC 753
                                                                GluGlnGlu---ThrGlyThrSerSerGlnTyr------IleSerValThrThr 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rGluSerTyrSerSerSerThrValTyrSerGly-------Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::||| :::||| :::||| :::||| :::
rArgValAlaValGlyValSerArgProSerSerIleThrGlnThrThrSerIleAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGln-----1leSerGlnThrLeuSerHisAsn----
                                                                                                                                                                                                                                                                                           GAGGTATGCCAAGAACTGGCCAAA-----
                                                                                                                                                                                                                   ThrThrGln-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 luAlaSer--
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DOMAIN
  ------CCAAGGCTATCGAGAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGC 1580
                                                                                                                                                                                  TGCTGCTCGCGCTATTCAGGCCGATGCGATGCCCAATGCCATTGCCATTGAGAAGGGCAA 1640
                                                                                                                                                                                                                                                                             1701 CAACTICACCATGCGTAIGAGCIACGGCTCCATCAAGGGATAIGAACCGCAGGACGGIGC 1760
                                                                                                                                                                                                                                                                                                                                                                       1821 TGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTA 1880
                                                                                                                                                                                                                                                                                                                                                                                                                     ---ATATCGCTTTCCTATCGAA 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1920 CAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGAT 1979
1380 CAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAAT-----TCAAAGGCGA 1430
                                            1641 GCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGC 1700
                                                                                                                                                                                                                                                                                                                          1761 CTGGTACAACTATCATACGACAGGCAAGGGGGTATTGGAGAAGCAGGATCCTAAGAGCGA 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2040 TCTGCAGCGCACAATCAGCGTGGACATCC---------GCTACGTTCTTCAT 2084
                                                                                                                                                              442
                                                                                                                                                                                                         463
                                                                                                                                                                                                                                                                                                                                                                                     463 hrSerSerProSerAlaSerValValValProSerAlaTyrAlaSerSerProSerValP 483
                     371 erAsnThrPheAlaValSerSerIle---SerThrThrAsnPheIleValSerSerAlas 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roValAlaValSerSerThrTyrThrSerSerProSerAlaProAlaAlaIleSerSerT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Low-density lipportein receptor-related protein 1 precursor (LRP)
(Alpha-2-macroglobulin receptor) (AZMR).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                        || ::: :: ::
| ro------ValAlaValSerSerThrTyrThrSerSer------P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1980 CGGTCTTGCTTTCGATGCCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 ----ThrSerSerProSerAlaProValAlaValSerSerThrTyrThrSerSerProS
                                                         :: |||||| ::: ||||||| exaspThrValProTyrSerSerValHisSerT
                                                                                                                                                                                                                                                        TIVI---
                                                                                                                410 hrPheValHisAlaThrSer-----SerSerThrTyrlleSerSerSerLeuT
                                                                                                                                                           426 yrSerSerProSerLeuSerAlaSerValSerSer---HisPheGlyValAla----
                                                                                         1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2085 GATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGC 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 erPheSerSerValProValAlaValSerSerThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSUE=Liver, and Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    1881 TGCCGAGAACGGTCAGCTCC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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ID LRP1_CHICK
AC P98157;
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MEDLINE=94103212; PubMed=7506255; Nimpf J., Stifani S., Bilous P.T., Schneider W.J.; "The somatic cell-specific low density lipoprotein receptor-related protein of the chicken. Close kinship to mammalian low density lipoprotein receptor gene family members."; J. Biol. Chem. 269:212-219(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                              AND ACTIVATED ALPHA 2-MACROGLOBULIN, AS WELL AS THE LOCAL METABOLISM OF COMPLEXES BETWEEN PLASMINOGEN ACTIVATORS AND THEIR
                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- ALTERNATUS PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-:- TISSUE SPECIFICITY: SOMATIC.
-:- PIM: CLEAVED INTO A 85 KDA MEMBRANE-SPANNING SUBUNIT (LRP-85) AN A 515 KDA LARGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-COVALENTLY ASSOCIATED.
                                                                                                                                                                                                                                                       ENDOGENOUS INHIBITORS. BINDS VITELLOGENIN, CALCIUM AND ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
EGF-LIKE 2,
EGF-LIKE 3.
EGF-LIKE 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Endocytosis; Glycoprotein;
EGF-like domain; Coated pits;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 22 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IRR001881; EGF_CI.
Interpro; IRR001438; EGF_II.
Interpro; IRR001372; LDL_recept_A.
Interpro; IRR000031; Ldl_recept_A.
Interpro; IRR000031; Ldl_recept_A.
Pfam; PF00008; EGF; 14.
Pfam; PF00058; 1dl_recept_a; 31.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL; 3. PROSITE; PS00022; EGF_1; 5. PROSITE; PS01186; EGF_2; 7. PROSITE; PS01187; EGF_CA; 2. PROSITE; PS01209; LDLRA_1; 27. PROSITE; PS50068; LDLRA_2; 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000152; Asx_hydroxyl
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X74904; CAA52870.1; -. HSSP; Q07954; 1CR8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMARY; SMO0179; EGF_CA; 3.
SMARY; SMO0001; EGF_like; 18.
SMARY; SMO0192; LDLa; 31.
SMARY; SMO0135; LY; 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4543
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SIGNAL
                                                                                                                                                                                                                                                                             MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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TRANSMEM
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Qy	1315	CCCTCGCTCGACC         ProSer-GlvPro	CCCTCGCTCGACCGTAAGGTGCTGCCCATGCTCGATATTGTACGCCGGC	CCATGCTCGATATTGT      SDG]VLVSATGLEUA	13 ThrCvsVa 41	66
Qy	36	GTATCCCTG	CCGACAAGCTCCCCG	ATATATTCAAGAATGT	14	22
qq	4182	::: lLeulleProSer	  ProThrAlaSerAla	::: ::: Val-ValProThrThr	:::        ::    ::::  LeulleproSerProThrAlaSerAlaVal-ValProThrThrAspThrCysAspLeuV 420	02
Qy	1423	AAAGGCGACACGA	AGAAGTATGCAGACTT	rcgtattcgacaagag 	AAAGGCGACACGAAGAAGTATGCACAACAAGAGTGTGGGTTCCTTATAGC 148: :::	82
QQ	4202	alCysLeuAsnGl	alCysLeuAsnGlyGlySerCysPheLeuAsnAlaArg	AsnAlaArg	421	15
ΟŸ	1483	GACAAGTTCCATG	CCATGCTCAAGTCCA!	IGGACAAGGAAAAGTT    :::	GACAAGTICCATGCCATGCTCAAGTCCATGGACAAGGAAAGTTTGCCAA 15: ::	32
QQ	4215	ysGlnAlaLysCy	sArgCysGlnProArc	gTyrAsnGlyGluArg	42	35
οy	1533	GGCTATCG	-GGCTATCGAGAAGATCCGGC	AGTAGA	-AGTAGAGCTTTCCAAGAGCGTA 157	7.5
QQ	4235	ysSerAspTyrCy	sGlnAsnGlyGlyLe	uCysThrAlaSerPro	rGlyMetProThrC 42	55
Qy	1576		GCGCTATTCAGGC	-CGATGCGATGGCCAA	TGCCTAT 162	23
QQ	4255	ysArgCysProTh	: rGlyPheThrGlySe	rArgCysAspGlnGln	ysArgCysProThrGlyPheThrGlySerArgCysAspGlnGlnValCysThrAsnTyrC 427	75
Qy	1624	GCCATTGAGAAGG	GCCATTGAGAAGGCCAAGCGTCTTTT		crrrecceerrrecer 166	65
qq	4275	ysHisAsnAsnGl		nGlnGlyAsnGlnPro	AsnCysArg 429:	92
Qy	1666	GAGATGTACCCCG	GACGTGCTCTGCCGA	SCGATGCCAACTTCAC	17	25
qq	4293	  CysProPr	:: oThrPheIleGlyAsp	:            pArgCysGlnTyrGln		11
Qy	1726		GGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAAGTATCATACGAC	ACGGTGCCTGGTACAA	CTATCATACGAC 1781	
QQ	4311	<pre> ysGluAsnAsnGlyVal</pre>		  CysGln	:::     SGlnMetSerArgAsp 4322	
RESULT YM96_YI	JLT 6					
ID A	YM96.	YEAST STA	) YM96_YEAST STANDARD; PRT; 1140 AA.	; 1140 AA.		
. TO	01-N	OV-1997 (Rel.	35, Created)			
<u> </u>	01-N 01-N	OV-1997 (Rel. OV-1997 (Rel.	35, Last sequents, 35, Last annota	ce update) tion update)		
DE N	Hypo	thetical 113.1	. kDa protein in	PRE5-FET4 inter	genic region.	
so	Sacci	haromyces cere	visiae (Baker's	yeast).		
88	Euka	ryota; Fungi;	Ascomycota; Sac	charomycotina; S	accharomycetes;	
38	NCBI,	TaxID=4932;	Saccinatoniyeeta	ceae; saccinatomy	ر دراه	
R R D	[1]	[1] SFOUENCE FROM N.A.				
. K		IN-S288C / ABS	172;			
RA L		cher C.M., Lou itted (NOV-199	is E.J., Barrel	l B.G., Rajandre GenBank/DDBJ dat	Walsh S.V.	••
8		DOMAIN: CONTAI	-!- DOMAIN: CONTAINS MANY SER/THR-RICH DOMAIN AND REPEATS.	-RICH DOMAIN AND		
88		SWISS-PROT en	try is copyright	t. It is produce	d through a collabor	ration
8		een the Swiss	Institute of B	ioinformatics a	nd the EMBL outstat	tion -
88		European Bioir by non-profi	itormatics Insti t institutions	tute. There are as long as its	no restrictions or content is in no	n its o way
ပ္ပ		fied and this	statement is no	t removed. Usag	e by and for comme	ercial
ខម		ties requires end an email t	a license agreem to license@isb-s.	ment (See http:/ ib.ch).	/www.isb-sib.ch/anno	/eouno
2 2 2 2 3		; Z54141; CAAS	10835.1;	, , , , , , , ,		1 1 1 1 1 1
KW		S0004936; YMF thetical prote	8317W. ein; Repeat.		SGD; S0004936; YMR317W. Hypothetical protein; Repeat.	
ÖS		ENCE 1140 A	A; 113070 MW;	0153EBCA24FE5427	CRC64;	•
re c	NO.	Scores:	0.195	Length:	1140 131	
Per	sent S	Similarity:	36.738	Matches: Conservative:	181 96	

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	592 252 652	269	700	739 309	793 324	850 344	880 364	931 384	991 404	1051 . 424	1111 444	1171 464	1231 478	1279 488	1339 505	1399 518	1453 538
Best Local Similarity: 21.20% Mismatches: 246  Query Match: 3.60% Indels: 145  DB: 3.60% Caps: 21  US-10-008-355-1 (1-2139) x YM96_YEAST (1-1140)	AGCCTTTCTATTCCAACAACGAATA 	LeuSerlleThrSerSerProValSerSerGluAlaProSerAlaTh	TGTGGCCGCGTCTAGCGTATTCCGCGTGTATG	. GTGCCGACAACCGGCCGGCCGAATACAGCAAGAAAAA :::     ::: :::     ::: :::     ::: :::     :::: :::     ::::  :::   :::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   ::::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   :::  :::   ::   :::  :::   ::   ::   ::  :::   :   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   :   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   :   ::   ::   ::   ::   ::   ::   ::   :   ::   ::   ::   ::   ::   :   ::   :	AACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTG	ACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCT::::::::::::::::::::::::	SerSerGlualaproSerSerThrSerSerValSerSerGluIleSerSerThrThr	ACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAGCATCTGGAAGGAAG:::	CCATGAGCCCAGATCAGGCTACCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTA	ACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCG	GTAAGCGTGCCGAGGAAAGAGCATTCGCAGATCCGTAAGAACGGCAAGAGTGCTG	TCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG	GTGAGATGACTTATTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCAC	AGTITGCCAACGCAITGGCTACAAAICCTGATGCTCATGCGGTATCC	TCAAATCGCTTGACGACAAGTACAAA         :::  SerAsnSerIleIleGluSerSerLe	CCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCA	AGAATGTAATCGACAAGAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCG
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1766 ACAACTATCATACGACAG-----GCAAGGGCGTATTGGAGAAGCAGGATCCTAAGA 1816
                                                                                                                                                                                                            1475 CTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGG*****ACAAGGAAAAGT 1525
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--TATTCGACAAGAGTGTGGTTC 1474
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539 LeuSerLysSerSerValIlePheGlyAsnSerSerThrValThrThrSerProSerAla
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
17-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1817 GCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCT----
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SEQUENCE FROM N.A.
STRAIN=D/UW-3/Cx;
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                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                               1516
                                                                                                                                                                                  SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. BNZYME I TRANSFERS THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE (PEP) TO THE PHOSPHORYL CARRIER PROTEIN (HPR).
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                   Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                 ENZYME I IS COMMON TO ALL PTS (BY SIMILARITY).

CATALYTIC ACTIVITY: Phosphoenolpyruvate + protein L-histidine
pyruvate + protein N(pl)-phospho:L-histidine.
SUBCELLULAR LOCATION: Cytoplasmic (By:similarity).
SIMILARITY: BELONGS TO THE PEP-UTILIZING ENZYMES FAMILY.
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PROSITE; PS00370; PEP_ENZYMES_PHOS_SITE; FALSE_NEG.
PROSITE; PS00742; PEP_ENZYMES_2; FALSE_NEG.
Phosphotransferase system; Transferase; Kinase; Sugar transport;
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InterPro; IPR000121; PEP_utilizers.
Pfam: PF00391; PEP-utilizers; 1.
Pfam: PF02896; PEP-utilizers; 1.
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  MEDLINE-99000809; PubMed-9784136;
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eSerLeuGlyArgLeuProCysValGlu-GluGlnAlaAspGlnTyrAlaGlnLeuValG 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       18 X APPROXIMATE TANDEM REPEATS, SER/THR;
                                                      319
                                                                           484
         GATACCCTTGAGCTGTCCTTCTACCTTGTCCGTTACCTTCACGATCTTGCGCAGATACTT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A CORE SUBUNIT.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
AND/OR BY CARBOHYDRATE-MEDIATED COVALENT CROSS-LINKS (POSSIBLE).
PTM: EXTENSIVELY O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                      Roy A., Lu C.F., Marykwas D.L., Lipke P.N., Kurjan J.;
Trha AGAH product is involved in cell surface attachment of the
Saccharomyces cerevisiae cell adhesion glycoprotein a-agglutinin.";
Mol. Cell. Biol. 11:4196-4206(1991).
                                                                          LeuGlyThrSerArgGluArgSerLeuLeuGlyGluArgSerArgValProHisProSer
                                                                                                  CAGATAGTCGTGATCCACCGTGCTTTG-----GCTCTGGATAGCACCGTATCCGCAGTG
                                                                                                                      485 ValileArgMetileHisHisValValGluGlnAlaLysGlnLysAsnValProValSer
                             445 GluIleLeuGlnGluSerSerPheValAlaLeuGlyThrAsnAspLeuAlaGlnTyrThr
                                                      CACGGAAAGACCCCGGAATCGGAAGCTCCTCACCCATCGTGCGAGAAACGAAACCATCGCG
                                                                                                                                                                                                                                                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A-AGGLUTININ ATTACHMENT SUBUNIT.
2 X APPROXIMATE REPEATS.
1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; GPI-anchor; Repeat;
                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Agglutinin attachment subunit precursor.
AGAI OR YNRO44W OR N3431.
                                                                                                                                                          ||| ||||:::
|ValCysGlyGluMetAlaGlyAspProAlaLeuLeu 516
                                                                                                                                             GTGGTTGGTAAA-----GATCAGGCCCTGATC 238
                                                                                                                                                                                                                725 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91304412; Pubmed-2072914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M60590; AAA34382.1; -. EBML, Z71659; CAA96325.1; -. PIR: S17031; S17031. PIR: A41258; A41258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD; S0005327; AGA1.
Glycoprotein; Cell adhesion;
                                                                                                                                                                                                                STANDARD;
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725
493
149
307
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                             AGA1_YEAST
P32323;
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REPEAT
DOMAIN
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                                                                                                                                                                   505
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1031 CTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAAGAGCATTCGCAGACTGGATCC 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 AGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCG---GTATGAACCGCGGTCTCG 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||| ::: |||::: |||::: SerSerThrSerThrSerThrSerThr 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ser---SerIleAlaSerSerShrser----ValSerLeuTyrSerProSerThr 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             914 AAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrSerSerAsnValAlaThrProSerMetThrSerSerThrValGluThrThrValSer 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGCGTATTCC---GCGTGTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGG 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTG 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          794 ACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGG 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SerIleSerSerThrPheThrAspSerThrSerSerLeuGly 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....provalTyrSerValProSer 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGAGAACCAACTCTGCATCGTAGAGCCTTTCTÁTTCCAACAACGAATACTTCCTCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerThrSerThrSerProSer-----SerThrSerThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thr------SerProSerSerThr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854 GIGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||
-----SerGlnSerSerGluTyrIleThrLysSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGAGGCGATACGGACAACTGGATGTGCCCGCGTCACACGGGCG------ACT
                                                                                                                                                                                                                                                                                                                                                                                                       70420C853B0B01F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     725
130
83
200
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22
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-008-355-1 (1-2139) x AGA1_YEAST (1-725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                   22-1.
22-2.
22-3.
22-4.
22-5.
22-9.
2-11.
2-11.
RICH.
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38.738
23.648
3.34%
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Q09625; Q969D4;

	DT 15-JUN-2 DT 15-JUN-2 DE HYPOCHEC	GN ZK945.9/ OS Caenorha OC Eukaryot OC Rhabditi	•		יימם	This betwe the E		EMBL; EMBL; EMBL;		Interi Interi Pfam; Pfam;	DR Ptam; PF DR SMART; S DR SMART; S KW Hypothet		FT TRANSMEN FT TRANSMEN FT TRANSMEN FT TRANSMEN		FT TRANSMEN FT TRANSMEN FT TRANSMEN SQ SEQUENCE	Alignment Scc Pred. No.: Score:	Percent Simil Best Local Si Query Match: DB:	US-10-008-355	Qy 346 GG1
	-							<u></u>								•			_
Glyval 405	-ATGACT 1182 :::    rLeuThr 425	GCCAAC 1242 MetPro 445	GACGAC 1296 :       181aTh 465	ATGCTC 1350     UThrSe 485	GTAATC 1410    hrThrSe 505	NGGCGAC 1431         salaTh 525	AAGTTC 1491 SerGlu 544	CGAGAAAGATCCG 1551 ::::: -GlnGluGlnSer 559	rGCGATG 1611 :LeuSer 578	1660 InSerPr 598	GATGCCAACTTC 1707          -GlnProThrSe 615	TTGGTAC 1767 :: Se 616	::     eSerTh 636	CGCTATGCCGAG 1887 ::::: -SerLeuThrPr 652	TAACTCCGGT 1947 ::: SerSerSe 663	CTGGGAA 2007 :: erileSe 683			
<pre>11eSerThrThr11eProSerPheSerMetSerThrTyrPheThrThrValSerGlyVal</pre>	erGluThrSerTh	TATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAAC :::               :::	GCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGCCT.::	AAGTACAAAGACTACCTCCCTCGCTCGAAGGTGCTGCCCGCCATGCTC	GATATIGIACGCGGCGIAICCCIGCGGCAAGCICCCCGATAIATICAAGAATGTAATC	GACAAGAAATTCAAAGGCGAC     :::      rThrLysSerTrpValSerSerMetThrThrSerAspGluAspPheAsnLysHisAlaTh	ACGAAGAAGTATGCAGACTTCGATATTCGACAAGATGTGGTTCCTTATAGCGACAAGTTC	TGCCAAGGCTAT	GCAGTAGAGCTTTCCAAGAGGGTAATAGCTGCTGCTGCGCGCTATTCAGGCCGATGCGATG :::	GCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCTTGC	CGAGC	ACCATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTAC :: r	AACTATCATACGACAGCCAAGGGCGTATTGGAGAGCAGGATCCTAAGAGCGATGAGTTT :	ACTATGGT	AACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGT 	AGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGCCAACTGGGAA			3178 AA.
serÞheSerMetSei	GAGCCAAGGCCAAC ::: rpCysProTyrSe	TCGGTGGTACCGA( hrThrAspAlaTh)	ATGCTCAT	CCTCGCTCGACCG7    :::  ValGluSerSerTy	ATCCCTGCCGACAA( :::   .GlnThrAlaSerSe	SerMetThrThrSe	TCGTATTCGACAAC	ATGGACAAGGAAAA( ::         leAspSerGluSe	GCGTAATAGCTGC7       :::::::::::::::::::::::::::::::	AGAAGGCCAAGCG:::	AGATGTACCCGG	GCTCCATCAAGGG	AGGGCGTATTGGA(      SerAlaSerThrSe	CTCGACCTCTTCCG          SerThrIleGluSe	SCTTTCCTATCGAA( 	AACGCCGTCTGAT(     :::     ThrSerValThrT	3AGT 2029        Ser 690		PRT;
erThrThrIlePro5	GAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAG- 	rGAGCGAGACGCTC1 ::       ::: etHisGluThrVal1	rGGCTACAAATCCTG    :::     nThrThrSer-Leu	AAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGC 	rTGTACGCCGGCGTA     :::     SerTyrSerSerVal	AGA ::: LysSerTrpValSe	AGAAGTATGCAGACT ::: LySTyrH1SValTh1	CATGCCATGCTCAAGTCCATGGACAAGGTT" 	ragagctttccaaga            sLeuLeuSerThr	ATGCCTATGCCATT( ::::: SpSerThrIle-Leu		TGCGTATGAGCTACC	ATCATACGACAGGC/     AlaileAlaThrile	GCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAA     ::       :: rProSerThrSerValGluSerThrIleGluSerSer	AACGGTCAGCTCCATATCGCTTTCCT 	CCGTATTCGATAAGA            :::: ProSerSerLeuGl	GCTATGAGTGGTGACATCGAGT::: 		L STANDARD;
386 IleSe	1138 GAAAA 406 ThrT	1183 TATT7 :: 426 SerMe	1243 GCAT7 ::: 446 SerG]	1297 AAGT/       465 rSer	1351 GATAT   485 rHis	1411 GACAAGA-     ::: 505 rThrLysS	1432 ACGAZ 1 525 rGlyI	1492 CATGC 545 AlaT	1552 GCAG7 ::: 560 SerH	1612 GCCA/ :::: 579 SerA	1661 598 oval	1708 ACCAS	1768 AACTI :    616 rThri	1828 GCCG         636 rPro	1888 AACG       652 oThr	1948 AGCCO         663 rAla	2008 GCTA' ::: 683 rile	RESULT 9 YS89_CAEEL	ID YS89_CAEEL
qq	Qy Dp	Oy Dp	Qy	Qy Db	Qy	Qy	Qy Db	oy D	Oy Dp	Qy Db.	Oy Dp	Qy Dp	Qy Db	Qy	Qy Dp	. yo	Qy	RES!	Ð

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-1995 (Rel. 32, Created)
-2002 (Rel. 41, Last sequence update)
-2002 (Rel. 41, Last annotation update)
etical protein ZK945.9 in chromosome II.
9/ZK945.10.
habditis elegans.
ota: Metazoa: Nematoda: Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                              R.;
ed (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BCELLULAR LOCATION: Integral membrane protein (Potential).
MILARITY: CONTAINS 1 GPS DOMAIN.
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Beristol N2;
son-Sproat J.;
ted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
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GLY/SER-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 24854; CAB70192.1; -. 248582; CAB70192.1; -. 248582; CAB70102.1; JOINED. 248582; CAB70201.1; -. 248544; CAB70201.1; -. 248544; CAB70201.1; -. Pep; ZK945.9; CE25697.

PPP: JPR001024; Lipoxygenase_LH2.

PPP: JPR001024; Lipoxygenase_LH2.

PPP: JPR001024; M+channel_nlg.

PPF: JPR00203; PRD_cys_fich.

PPF01477; PLAT; 1.

PPF01477; PLAT; 1.

** SM00303; GPS; 1.

T; SM00308; LH2; 1.
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Similarity:
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q		Db 446 rSerThrVal	hrval
2	A STARTON CARACTER AND A START	Qy 1381 AAGCT	AAGCTCCCCGATATATTCAAG
. d		454	rThrSerProValThrSerTh
Οy	409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGGT 453	Qy 1441 TATGC ::: Db 472 -valT	TATGCAGACTTCGTATTCGACA::::
qq	226 AspSerGlnGlyValTyrAspGlyGlnValLeuLySGlyValArgAlaLysGlnPhe 245	1501	CTCAAGTCCATGGACAAGGAAA
ογ d	454 CGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGGCCAAAAAAAGAAAATGCAGACGAG 513 246 Sermet Argill	486	::: rSerThrValThrThrSerTh
ò	AACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATAC	Qy 1543A	AAAGATCCGGCAGTAGA(
e q		206	rSerSerThrProSerSerTh
δý	559 TICCICATCGICTACGATGIATICAAGGACGITCGIATGGIATITGCICCICCCAGCICT 618	1599	GGCCGATGCGATGGCC
qq	285 rValThrSerThr 289	526	nSerSerThrSerThrGlnGl
ογ	GTAGGTAAGTTCGGAGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGGGAGTTC	Db 546 rAspG	old
q	290ValThrSerThrThrValProThrSerThrSerThrValThrThrAlaMetSe.308	QV 1659 TITGO	1659 TTTGCGTGAGATGTACCCCGG
δŏ	TCCGCGTGTATGCCGGTGCCGACAACCGGCCGGAGAATACAGCAAGGACAAT		
a à		QY 1719 GAGCT	1719 GAGCTACGGCTCCATCAAGGG
, d	320 eGluSerThrSerThrPhetDirSer329	Db 575 rGlyL	rGlyLeuGlyIleIleGly
ò	CATGACCATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGT	Oy 1747	C. CCGCAC
q		Db 594 rAsnT	594 rAsnTyrValSerThrThrLys
ογ	856 GTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAA 915	1770	
qq	335ThrSerSerThrSerThrThrGlnGlnSerSerTerThrIleThrSerSe 351	614	gLeuGlyGlyThrTyrProAla
ογ	916 GGCATCTGGAAGGAAGCCATGAGGGCAGATCAGGCTACCGGTATCAAATATGCCA 970	1771	
đQ		634	aThrMetThrThrAspAspLys
ολ	971 -GCAAGTATGCTCAGAGTCCTAACTATTGGAAGAATTCGATCGGTATGAACCGC 1023	1796	TGGAGAAGCAGGATCCTAAC
qq		654	SerSerThrThrIleG
٥y	1024 GGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGAC 1083		CTTCCGCACCAAAACTATGG
qq	389 rThrSerThrThrPheThrThrMetLeuThrSerThrThrGluGluProSerTh 409	4 0	Infrioserinfrios
Oy	1084 IGGATCCGTAAGAACGCCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAG 1143	UY 1899 CCATA 11 Db 694 erThr	ccararcectriccrarceaa 
QQ	409 rSerThrThrThrThrGluValThrSerThrSerSerTh 422	1959	CGATAAGAACGCCCGTCTGATC
ογ	GCTTATAAGGAAGCCAAGGCCAACGGTGAGATGACTTATTTGAGCGAGACGCTCTTC :::.	714	
QQ .	nrThrGluProThrThrThrLeu		TGACATCGAGTTCGAACCCGA1
oy.	GGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGAT	734	erThrThrSerSerSerPro-
å í		QY 2079 CT 2080	80
à é	1264 GCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAGACTACCTCCCCTCG 1320 433	   Db 752 er 752	
6 V	CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGAC	RESULT 10 COLA_CLOPE	
		ID COLA_CLOPE	STANDARD;

qq	446 rSerThrValTh	rThrSerProSe 454
οy	1381 AAGCTCCCCGATATAT	ACGAAGAAG 1440
qa	454 rThrSerProvalThrSerThrValThrSerSerSerSerSerSerSe	r 471
Qy	1441 TATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTT	CATGCCATG 1500
qq	472 -valThrThrProThrSerThrGlu	rSerProse 486
٥y	y 1501 CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGy	1542
qq	486	oserserse 506
Oy	1543	CGCTATTCA 1598
qq	506	rserThrGl 526
٥y	y 1599 GGCGATGCGATGGCC	1614
q o	526 nSe	uThrThrSerSe 546
Qy	Y 1615AATGCCTATGCCATTGAGAGGGCAAGCGTCTTTCTTTGCCGG	CTTTGCCGG 1658
qq	546 rAS	eTyrAspSe 566
Qy	1659 TIT	CATGCGTAT 1718
qo	566	riteuAsnSe 575
Οŷ	1719	1746
qq	575	roThrSerSe 594.
Qy	1747CCGCAGGACGCTGCTACAAC	1770
QQ	594 rAsnTyrValSerThrThrLysAspGlyAlaCysPheThrLysSe	rMetP
Οý	1770	1770
qq	614	Ar
Οy	1771	AT 1795
QQ	634	yrileging 654
Qy	1796	CCTCGACCT 1853
QQ		erSerThrs 674
0y	1854	GTCAGCT 1898
qq	674	luProSerS 694
Qy	y 1899 CCATATCGCTTTCCTATCGAACACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATT	CCCCGTATT 1958
qq	694	euGlnGlus 714
Qy	1959	TATGAGTGG 2018
qq	714	erAspThrS 734
Qy	2019	CTACGTTCT 2078
qq	0 734 erThrThrSerSerProSerSerThrThrAlaAspSerThrSerThrLeuS	erThrLeus 752
Qy	2079 C	
οp	b 752 er 752 ·	
RESUL COLA_ ID	ESULT 10 DLA_CLOPE D COLA_CLOPE STANDARD; PRT; 1104 AA.	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50093; PKD; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Zymogen; Signal; Complete proteome.
SIGNAL 1 39 POTENIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                        Matsushita 0.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Digestion of native collagen in the triple helical region at Xaa -| Gly bonds. With synthetic peptides, a preference is shown for Gly at P3 and P1'; Pro and Ala at P2 and P2'; and hydroxyproline, Ala or Arg at P3'.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M9.
        01-NOV-1995 (Rel. 32, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
16-UNN-2002 (Rel. 41, Last annotation update)
16-UNN-2002 (Rel. 41, Last annotation update)
16-UNN-2002 (Rel. 41, Last annotation update)
                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 87-113.
STRAIN-NCIB 10662;
MEDLINE-94110220; PubMed-8282691;
MATSUSHITA O., Yoshihara K., Katayama S.-I., Minami J., Okabe A.;
"Purification and characterization of Clostridium perfringens 120-kilodalton collagenase and nucleotide sequence of the corresponding
                                                                                                                                                                                                                                                                                                              Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                            Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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ZINC (CATALYTIC) (BY SIMILARITY).
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ZINC (CATALYTIC) (BY S
L -> F (IN REF. 1).
I -> M (IN REF. 1).
G -> E (IN REF. 1).
V -> E (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002)
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InterPro; IPR000169; PkD_domain.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00801; PKD; 1.
Pfam; PF01752; Peptidase_M9; 1.
PRINTS; PR00931; MICOLLPTASE.
                                                                                                                                                                                                                                             Bacteriol. 176:149-156(1994).
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EMBL; D50309; BAA08848'1; -.
MEROPS; M09.002; -.
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                                                                                                                                                                                                                                                                                      STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                         flesh-eater.
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METAL
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349 GAGGAGCTTCCGATTCCGGGTCTT-----TCCGTGAAGTATCTGCGCAAGATCGTG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 GAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCC 189
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141
105
278
258
36
    T -> A (IN REF. 1).
A -> E (IN REF. 1).
I -> T (IN REF. 1 AND 3)
WW; F4B7377194ED021C CRC
                                                                                                                                            Length:
Matches: Conservative:
Mismatches:
Indels:
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1104 AA;
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629	969 675	1026		1143	1176	749	1236° 763	1281	1341	1401	794	1443	1479	829 1518		1551	869	1593 889	1644	606	1659	929	9 .	4 t	696 8c/T
	cancecairiosanesaneccaisanecai	AGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGT				   SerTrpAsnGlyTyrLysThrValThrAlaTyrPheValAsnHisLysValAspGlyAsn	/ ATGACTTATTTGAGGGGGGGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTT		AAATCGCTTGA	GCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATTCAA		? AATGTAATGGACAAGAAATTCAAAGGGGACAAGAAGTAT	GCAGACTTCGTATTCGACAAGAGTGTGCTTAT		::: ::::::::::::::::::::::::::::::::::	GAAAAGTTTGCCAAGGCTATCGAGAAGATCCG		:		LeuSerGluGluAspTyrSerAspLysTyrTyrPheAspValAlaLysLysGlyAsnVal		LysIleThrLeuAsnAsnLeuAsnSerValGlyIleThrTrpThrLeuTyrLysGluGly			occare.icaccaroccaroccaroccarcaroccaroccaroccar
642	099	970	1027	1087	1144	730	1177	1237	1282	1342	786	1402	1444	1480	088.	1519	820	1552	1594	890	1645	910	1660	1699	950
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hyaluronace.
-!- SUBCELLULAR LOCATION: Secreted.
-!- CAUTION: The partially purified protein from strain CPN50 is approximately 70 kDa smaller than the sequence indicated here.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1759 GCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGC 1818
                                                                                                                                                                                                                                                                     1879 TATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGGCGGT 1938
                                                                                                                                                                                                                                                                                                                                                                                                      1939 AACTCCGGTAGCCCCGTATTCGATAAG-------AACGGCCGTCTGATC 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCTGCAGGGCACAATC-----AGCGTGGACATCGGCTACGTTCTCATG 2085
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                                      970 -----ThrTyrThrValAsnValLysGlyAsnLeuLysAsnGluValLysGluThr 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canard B., Garnier T., Saint-Joanis B., Cole S.T.; "Molecular genetic analysis of the nagH gene encoding a hyaluronidase of Clostridium perfringens."; Mol. Gen. Genet. 243:215-224(1994).
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-!- FUNCTION: Putative virulence factor which is likely to act on connective tissue during gas gangene.
-!- CATALYTIC ATTIVITY: Random hydrolysis of 1,4-linkages between Nacetyl-beta-D-glucosamine and D-glucuronate residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1819 GATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAACTATGGTCGC
                                                                                                                                                                                                                                                                                                                                   GGT----CTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCC
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15-JUN-2002 (Rel. 41, Last annotation update)
Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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MEDLINE-94232189; PubMed-8177218;
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SEQUENCE FROM N.A.
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STRAIN=13 / Type A
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P26831;
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ID NAGH_CLOPE

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Ffam; PP00404; Dockerin_1; 2...
Pfam; PP00754; F5_F8_LYPE_C; 1...
SMART; SM00231; FA38C; 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEDLINE-1 TOY N16961 / Serotype 01;
MEDLINE-20406833; PubMed=10952301;
Heldelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                 1875
                                                                                                                                                                                                                                                                                                               1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1906 GCTTTCCTATCGAAC---AACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCGAT 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                      -TATGAACCGCAGGACGGTGCCTGG 1764
                                                                                                                 TACAACȚATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAG 1824
                                                                                                                                                                                                                                                                                                                                                               646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHOLLEGE., Nature 406:477-483(2000).
-I- FUNCTION: This protein promotes the GTP-dependent translocation the nascent protein chain from the A-site to the P-site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-G/EF-2 SUBFAMILY.
                                                  ::: ||| :::||
587 AlaileGlyTyrLeuLysSerAlaileAlaileGluGlyAspAspGluAlaAlaTrp
                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. NCBI_TaxID=666;
                                                                                                                                                                                                               1825 TTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGT------
                                                                                                                                                                                                                                                               -----SerLysThrTyrGlyPheHisTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                            647 MetGlyGlnAsnLeuSerValValIleGlySerIleValAspProAsnArqIleIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                               ------CGCTATGCCGAGAACGGTCAGCTCCATATC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elongation factor G (EF-G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 AA
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TIGR; VC0361; -.
                 1720 AGCTACGCCTCCATCAAGGGA--
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1963 AAGAAC 1968
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125 ThrValTrpArgGlnAlaAspLysTyrGlyValProArgMetValPheValAsnLysMet 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::|||
216 GlnGluTrpArgAsnHisLeuValGluAlaAlaAlaGluAlaSerGluGluLeuMetGlu 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::||| ||||||| ::::::
105 ValLeuAspGlyAlaValValValValPheCysGlyThrSerGlyValGluProGlnSerGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GlnIleLysHisArgLeuGlyAlaAsnProValProIleGlnLeuAsnIleGlyAla 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 GluGluGluPheLysGlyValIleAspLeuIleLysMetLysAlaIleAsnTrpAsnGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 ACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ArgGluAsn 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ATTCTTCTCGGAGCAGCCCTGCTGTTG----GGTGCTTCAGGGGTAGCCAAAGCCGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 GlnAlaValLeuAspAlaValIleGluPheLeuProSerProThrAspValProAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 TACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATC------
                                                                                                                                                                                                                                                                      GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
F44FDA4DB8FC4ECC CRC64;
                                                                             Pfam; PF00679; EFG_C: 1.
Pfam; PF00009; GTP_EFTU, 1.
Pfam; PF01144; GTP_EFTU, 1.
TIGRAMS; TIGR00415; ELONGATNECT.
TIGREAMS; TIGR00231; EF-G; 1.
PROSTIE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                   698
1120
83
202
246
26
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 GACTATCTGCGCGATGGTTTCGTTTCT-------
                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 GGCATGTGG---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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InterPro; IPR000640; EFG_C.
InterPro; IPR0004161; EFTU_D.C.
InterPro; IPR000795; EF GTPbind.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                         24 GT
92 GT
145 GT
76927 MW;
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31.18%
18.43%
3.09%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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NP_BIND
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Qy	490	GCCAAAAAAGAAAATGCAGACGAAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAAC 549 ::: ::: :::        :::     SerValGluArqHisAlaAspAspAspAsh	
δχ	550	AACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT	
QQ	317	.:: SerLeuAlaPheLys1leAlaThrAspProPhe	
οy	610	CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACG 669	
qq	328	val 328	
Qy	670	GGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACAACCGGCCGG	
QQ	329		
δy	730		
Q D	349	AsnSerValLysGlnLysLysGluArgPheGlyArgIleValGlnMetHisAlaAsnLys 368	
οy	790		
qq	369	ArgAspGluIleLysGluIleArgAlaGlyAspIleAlaAlaAlaAlaIleGlyLeuLysAsp 388	
٥y	816	916	
QQ	389	ValThrThrGlyAspThrLeuCysAspProAsnHisValValIleLeuGluArgMetGlu 408	
λο λ	817	TTCCCGGCCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAAC	
Q T	409		
Qy	877	GAGAACAATCCTCGTATCGAAGTTCGCGGTATCAGCAAGGCATCTGGAAGGAA	
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g q	457	SerglwmetglwglufenHisTenBardTle7] 	
3 8			
Š Š	5101	ATGAACCGCGGTCTCGCTCGTCGTCGTCGTAAGCGTGCCGAGGAA	
Q C	4/		
ΟŊ	1069	AGAGCATTCGCAGACTCCCTAAGAACGCCAAGAGTGCTCTATGGC 1119	
Ор	497		
δ	1119	1119	
Db	517	LeuLys1leGluProAlaGluProGlyGlnGlyPheValPheValAspAlaIleAlaGly 536	
οy	1120		
QQ	537		
δy	1153		
QQ	557		
οy	1213		
QQ	577		
ΟŽ	1270	GCCGGTATC	
QQ	597	:::::: LysGlyAlaLeuGluAlaGlnProValLeuLeuGluProLeuMetLysValGluIleThr 616	
ΟŊ	1291	GACGACAAGTACAAAGACTACCTCCCTCGCTCGACGTAAGGTGCTG 1338	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                        1339 ------CCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGAC 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A. Hess J., Wels M., Goebel W.; Hess J., Wels W., Vogel M., Goebel W.; Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparison with a corresponding chromosomal hemolysin sequence."; FEMS *Microbiol. Lett. 34:1-11(1986).
||| ::::::|||
| 655 ---LeuSerGluMetPheGlyTyralaThrAspLeuArgSerAlaThrGlnGlyArgAla 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: SECRETED.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 178:5422-5430(1996).
FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
-!- PIM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
                                                                             637 GluGlyMetAspGluGlyProAlaGlyLeuLysileIleHisAlaLysValPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanley P., Packman L.C., Koronakis V., Hughes C.,
Fatty adylation of two internal lysine residues reguired for the
toxic activity of Escherichia coli hemolysin.";
Science 266:1992-1996(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF URINARY TRACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid IncI2 pHLY152.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The state of the in vivo activation of hemolysin (HlyA) from menhanishia coli ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                   1381 AAGCTCCCGATATATTCAAGAATGTAATCGACAAGAAA----
                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            PRT; 1024 AA.
                                                                                                                                                                                                                   1420 --- TTCAAAGGCGACACGAAGAAGTATGCAGAC 1449
                                                                                                                                                                                                                                          ::: ::: ::: 674 SerTyrSerMetGluPheAlaGluTyrAlaAsp 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE-96404790; PubMed=8808931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE=95099325; PubMed-7801126;
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemolysin, plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
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HLYA_ECOLI
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GTGAAGGTAACGGACAAGGTAGAAGGACAGCTC---AAGGGTATCACTGACGAGATGGAG 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AlaValThrLeuAlaIleSerProLeu-------SerPheLeuSerIleAla 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 TyrAspGlyAspSerLeuLeuAlaAlaPheHis-LysGluThrGlyAlaIleAspAlaSe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ThrThrSerLeuValGlyAlaProValSerAl 397
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                                                                                                                                                                                                                                                                                                                                                                          PALMITATE.
W; 83944917F76C945B CRC64;
                                                                                                               Calcium;
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16 X REPEATS, GLY-RICH
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                          PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTCXINA.
PROSITE; PS00330, HEMOLYSIN_CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat;
Transmembrane; Lipoprotein; Palmitate; Plasmid.
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                  InterPro; IPR001343; Hemiysn_Ca_bind
InterPro; IPR003355; RTXtoxin_N.
InterPro; IPR003995; RtxA.
                                                     Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                       477 GInGinHisTrpAspThrLeuIleGlyGluLeuAlaGlyValThrArg------Asn 493
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                                                                                                                         tPheGluHisValAlaSerLysMetAlaAspValIle-AlaGluTrpGluLysLysHisG 437
                                          397 aLeuvalGlyAlaValThrGlyIleIleSerGlyIleLeuGluAlaSerLysGlnAlaMe 417
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                                                                                           -----CGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAAC
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NEDLINE=2184401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Rod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Rod V., Gwilliam R., Harber S., Basham D., Bowman S.,

Rocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Rochies S., Goble A., Hamlin N., Harris D., Hidaldro J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Nonchy P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Nonchy P., Noule S., Mangall K., Murphy L., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Tutver R., Squares S., Stevens K.,

Rection J., Yolckaert G., Ark R., Robben J., Grymonprez B.,

Noodward J., Volckaert G., Ark R., Robben J., Grymonprez B.,

Weltjens I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

Ralibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
1750 CAGGACGCTGCCTGGTACAACTAT-----CATACGACAGGCCAAGGGCGTATTGGAG 1800
                                                                                    -------CCTAAGAGCGATGAGTTTGCC 1830
                                                                                                                                                                                                                                                                                                                                            1918 AACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTC-----GATAAGAACGGC 1971
                                                                                                                                                                                                                                                      1858 CGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCG 1917
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                                                                                                                                                                                                                751
                                                                                                                          713 ThrAspAsnLeuTyrSerValGluGluLeuIleGlyThrThrArgAlaAspLysPhe--- 731
                                                                                                                                                                                                                                                                                                                                                                Mata J., Nurse P.; "teal and the microtubular cytoskeleton are important for generating global spatial order within the fission yeast cell."; Cell 89:939-949(1997).
                                       693 GluLysThrGlnTyrArgSerTyrGluPheThrHisIleAsnGlyLysAsnLeuThrGlu
                                                                                                                                                                                                            732 PheGlySerLysPheThrAspIlePheHisGlyAlaAspGlyAspAspLeuIleGluGly
                                                                                                                                                                                                                                                                                                752 AsnAspGlyAsnAspArgLeuTyrGlyAspLysGly-------
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41 Last annotation update)
Tip elongation aberrant protein 1 (Cell polarity protein teal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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MEDLINE=97344085; PubMed=9200612;
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                                                                                  1801 AAGCAGGAT------
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473 AGGTATGCCAAGAACTGGCCAAAAAAAAATGCAGACGAGAACCAACTCTGCATCGTAG 532

Qy Db

US-10-008-355-1 (1-2139) x TEAL\_SCHPO (1-1147)

1147 92 70 168 109

Length:
Matches:
Conservative:
Mismatches:

4.53 117.00 36.99% 21.00% 3.06%

> Percent Similarity: Best Local Similarity:

Query Match: DB:

Indels:

Gaps:

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533 AGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACG---

575 -----ADGTATCAAGGACGTTCGTATGGTAT 198 AspAspAspGInSerSerLeuAsnSerGInGlncuSerAsnGInAlaLysAlaGInGly 602 TIGCTCCTCCCAGCTCTG---TAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGC 658

Qy Db Db

518 GluValSerProThrLeuSerPheValProSerSerHisSerMetGluGlnGlyAsnGly

719 CCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGC 778

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                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                     INFLUENCE MICROTUBULER ORGANIZATION, AFFECTING THE MAINTENANCE OF A SINGLE CENTRAL AXIS.
SUBCELLULAR LOCATION: PRESENT AT BOTH POLES OF THE CELL THOUGHOUT THE CELL CYCLE WHETHER THEY ARE GROWING OR NOT. LOCATED AT THE ENDS OF MICROTUBULES GROWING TOWARDS THE CELL POLES. AN INTACT MICROTUBULAR SKELETON IS REQUIRED TO MAINTAIN THE LOCATION AT THE CELL TIPS; ON THE OTHER HAND, A NORMALLY ORGANIZED ACTIN STATOSKELETON IS NOT REQUIRED.
SIMILARITY: CONTAINS 5 KELCH REPEATS.
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del. Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                      -!- FUNCTION: CELL POLARITY PROTEIN. MAY ACT AS AN END MARKER, DIRECTING THE GROWTH MACHINERY TO THE CELL POLES. MAY ALSO
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COLLED COLL (POTENTIAL).
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TyrSerGluLeuSerLysGlnGlnIleValGluTrpPheLysSerLysLeuTyrGluIle 615
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TTCGCGGTATCAAGCCAAGGCATC-----TGGAAGGAAGCC-----ATG 936
                                                                                                                                                                                                                                                                 937 AGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAACTAT 996
                                                                                                                                                                                                                                                                                       CGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     ......IleValGlnThrSerPheGlnLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       811 ValGlnThrGluAsnSerGluLeuValThrGlu------MetAlaLeuLeuLys
                                                                                      Gln-----SerSerValLysThrValAspGluArg
                                                                                                                         ACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAG
                                                                                                                                                                                                                                                                                                                                                                        GluLysAsnAlaAlaLeuCysGluAlaAlaLeuGluLysValProLeuAlaLysHisAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1510 ATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAG
                                                   AAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerAspLeuAspLysGlnLeuLysAspAlaThrAlaSerGlnLysGluLeu----
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(Rel. 29, Last sequence update)
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01-JUN-1994
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ID YK82_YEAST
AC P36170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||| :::|||| :::
|SerSerPheSerSerSerGluValCysThrGluCysThrGluThr------- 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GluSerThrSerThrSerThrProTyrValThrSerSerTrpSer 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----Thr 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ThrSerSerPheSerSerSerGluVa 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTTACCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCG
                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Repeat; Cell wall; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN YKR102W.
SER/THR-RICH.
N-LINKED (GLCNAC...) (POTENTIN N-LINKED (GLCNAC...)) (POTENTIN N-LINKED (GLCNAC...)) (POTENTIN N-LINKED (GLCNAC...)) (POTENTIN N-LINKED (GLCNAC...)) (POTENTIN N-LINKED (GLCNAC...))
              Hypothetical 122.2 kDa protein in SIR1 3'region precursor
                                                                                                                                                        LINKED (GLCNAC. . .) (POT 940C6DFB3569C669 CRC64;
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161
87
287
204
31
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Mismatches:
Indels:
 Last annotation update)
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Matches:
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SGD; S0001810; YKR102W.
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 01-JUN-1994 (Rel.
                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452
515
515
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Qy Db	383	ATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTACAAGGACAGCTCAAGGGTATCACTG 4 	442
yo da	443	AGATGGAGCGTCTCGCCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAA :::   :::   :::	502
oy .	503		520
qq	499	:: erThrSerTyrValThrProTyrValSerSerThrAlaAlaAlaAsn-TyrThrSer 5	518
ΟŊ	521	TCTGCATGGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTAT 5	580
QQ	519		538
λο δ	581		₹ 1
3 8	641		200
g G	559	GluThrGluSerThrSerTyrValThrProTyrValSerSerThrAla	575
٥y	701	TTTACT	160
Dp	576		587
ΟŊ	761		820
qq	588	GluValCysThrGluCysThrGluThrGluSerThrSerThrSerThrProTyrAlaThr	209
οy	821	CGGGCAGTACGGATCGCTACCTCACTTCTGGGGTGTGGAAGATCGTATCGAAAACGAGA E	880
Dp	608		624
ογ	881	ď	925
QQ	625		643
δλ	926	AGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGA 9	985
Op	644		629
ογ	986	TATTGGAAGAATTCGATCGGTATGAACCGCGGTC	1027
q	099	AsnLysGlySerValLysSerTyrValThrSerSerIleHisSerIle	619
δy	1028	TCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCAGG	1066
qq	680		669
ΟŸ	1067	AAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTAT	1126
QQ	700		715
οy	1127	TGTCTCTCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACGGTGAGATGACTTATT 1	1186
QQ	716		724
δy	1187	AGGTGGTTCGTTTTGCACAGTTTGCCAACGCAT	1246
g	725	ThimetLysThrLysValValSerIleSerSerBroThrAsn	739
ģ.	1247.	TGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAG	1306
QQ	740		745
οy	1307	ACTACCTCCCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGC 1111111111111111111111111111111	1366
qq	746	ThrThrSerLysAspSerThrValGlySerSerThrSerSerValSerLeuIleSerSer	765

Search completed: May 16, 2003, 12:29:53 Job time: 88.5 secs

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Sun May 25 15:40:19 2003

2 206 5.4 1349 4 QBWWQ4 QBKEG4 COLORERS	126.5 3.3 666 17 027798 126.5 3.3 3178 5 006904 126.5 3.3 3178 5 006904 126.5 3.3 3178 5 006904 127 3.3 1440 5 027706 128 3.3 1440 5 027706 128 3.3 1440 5 027706 128 3.3 12055 5 0286V7 124 3.2 1325 5 0286V7 124 3.2 1325 5 0286V7 123 3.2 1289 10 09L0J8 123 3.2 1289 16 029087 124 3.2 1289 16 029087 125 3.3 773 2 085051 123 3.2 1289 16 020087 124 3.2 1289 16 020087 124 3.2 1289 16 020087 124 3.2 1289 16 020087 124 3.2 1289 16 020087 124 3.2 1289 16 020087 125 5 0286V7 127 2000 (TrEMBLEL 1.5, Created) 1-0CT-2000 (TrEMBLEL 1.5, Last sequence update) 1-0CT-2
GenCore version 5.1.4_p5_4578  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 12:21:16; Search time 164.5 Seconds  (without alignments) 5358.478 Million cell updates/sec Title: US-10-008-355-1 Sequence: US-10-008-355-1 Sequence: Agapop 10.0, Yappext 0.5 Sequence: Agapop 10.0, Yappext 0.5 Fyapop 10.0, Yappext 0.5 Fyapop 0.0, Papext 0.5 Fyapop 6.0, Papext 7.0 Delop 6.0, Delext 7.0 Searched: 671580 seqs, 206047115 residues Total number of hits satisfying chosen parameters: 1343160 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 10% Listing first 45 summaries	**OVER_FERME_ADD_ADD_ADD_ADD_ADD_ADD_ADD_ADD_ADD_AD

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	esult Query No. Score Match Length DB ID Description
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Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
R. Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Krieger J.E., Kramae E.E., Laigref F., Lambais M.R., Leite L.C.C.,
Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nani A. Jr., Nobrega F.G., Nunce L.R., Oliveira M.A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Ouggio O. R.B., Roberto P.G., Rodrigues V.C., Gargen A.J.M.,
da Silva A.C.R., da Silva A.M., da Silva W.J. Gassa A.J.M.,
da Silva A.C.R., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., Jr., Silva W.A. Jr.,
Ad Silva A.C.R., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., Jr., Silva W.A. Jr.,
Nalada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Nallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
L. Sayo M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sattios A.P., Trenent M.F., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
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L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Maldanis J., Setubal J.C.;
L. Sayon M.A., Zatz M., Waldanis J., Setu
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994 TATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGCTCTTGTTGACGTGATAGGTCGT 1053 ---GCCGGTATCCTCAAATCGCTTGAC 1293 1486 AAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAA 1545 933 891 175 PheSerPheAlaGlyGlyAsnThrTyrArgValPheLysAsnLeuGluIleLysAspVal 194 SerAspGlnProLeuGlyAspGlyAspPheValMetValAlaGlyTyrProGlyArgThr 289 TrpThrTyrProValI1eGlyGlnHisPheLysAsnLeu11eAlaLeuI1eGluAlaAla 934 ATGAGCGCAGATCAGGCTACCGGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCTAAC :::::: 369 GluAlaLeuAlaAlaHisGlnThrLeuValAspLeuThrGluGlnTyr------1162 AAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTT 385 LysalaasnGlnaspargaspPheValLeuGlyGln---PheasnGlySerGlyValIle 1222 CGTTTTGCACAGTTTGCCAACGCATTGGCT-----ACAAATCCTGATGCTCAT---|||| | 104 GlyValAlaValAsnLeuTyrArgLeuAlaIleGluArgThrLysSerAspAlaGlnArg ::: |||||||||| :::|||||||::::: ------ArgArgTyrLeuProGluMetAspArgGlnMetGlnGlnTyrTrpLeuThr 461 GluTyrAsnLysLeuPro------ValLysGlnArgValAlaAlaIleAsp -------GACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAATTCAAA 476 ValTrpLeuGlyAspGlyIleProAlaThrLeuLysArgLeuGlyAspThrLysLeuSer GGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGAC CGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGG ATGTGGCCGCGTCACACGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACAAC CGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTA 772 TCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACG 832 GATCGCTACCTCACTTCTTGGGGTGTGGGAAGATCGTATCGAAAACGAGAACAATCCTCGT ---GGCATCTGGAAGGAAGCC 424 GluAlaGlyTyrGlnGluArgAspLeuProThrIleGluGlyAsnLeuLysGlnMetGlu 1054 AAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGC-----------CTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCC---1294. GACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTG-----SerSerGluGluArg------892 ATCGAAGTTCGCGGTATCAAGCAA-----349 1102 592 195 215 255 1270 712 1336 1378 501 g ò g ò q ð 9 ò g à g à g ò g οy q δ q δý Op ò g ò Q ò g ò g Ş. g ò g ò a

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1546 GATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGAT 1605
                                                                                            1606 GCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTTGCCGGTTTGCGT 1665
                                                                                                                                                                                        1666 GAGATGTACCCC-----GGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATG 1719
                                                                                                                                                                                                                                                                                    1720 AGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACG 1779
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                                                                                                                                                                                                                      ::: |||:::::|||::: 556 AspTyrAsnLysSerHisGlyLysPheValTyrProAspAlaAsnSerSerLeuArgIle 575
                                                                                                                                        536 AsnLysIleArgThrGlyGluLeuLeuLysAlaArgProIleTyrLeuGlnAlaLeuAla.555
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596 ThrLeuGlnGlyValMetAlaLys---AsnThrGlyValGluProPheAspSerProLys 614
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MEDLINE-21426417; Pubwed=11535137;
Escande F., Aubert J.P., Porchet N., Buisine M.P.;
Escande F., Aubert J.P., Porchet N., Buisine M.P.;
Human mucin gene MUC3AC: organization of its 5'-region and central repetitive region.";
Biochem. J. 358:763-772(2001).
Biochem. J. 358:763-772(2001).
                                                                                                                                                                                                                                                                                                               516 AspProAlaIleArgTyrAlaValAlaIleMetProAlaLeuLeuGluIleGluArgGln
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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811 ProThrThrSerThrThrSerAlaPro-----ThrThrSerThrThrSerThr 826
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                                                                                                                                                                                                                                                                                                                                                                                  122 GAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGC--- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        757 ThrSerThrThrSer-------AlaProlleThrSerThrIleSerAla 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              771 ProThrThrSerThrThrSerThrProGlnThrSerThrIleSerSerProThrThrSer 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 TGTATGCCGGTGCCG-----ACAACCGGCCGGCCGAATACAGCAAGGACAATAAAC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791 ThrThrProThrProGlnThrSerThrThrSerSerProThrThrSerThrThrSerAla 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743 CCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATG 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 ACGCTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCGATGGTTTCGTTT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685 ThrThr---SerThrThrSerThrProGlnThrThrSerSerAlaProThrSerSer 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 CTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGA 394
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                                                                                                                                                                                                                                  ----TCCTCAACGAACTCAATCAGGAGAATCTGGATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCG 214
                                                                                                                                               593 CysCysGluThrProLysGlyCysProValThrSerThrSerValThrAlaProSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 TCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 GTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAATGCAGACGAGA
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                                                                                                                                                                                                                                                                                                          613 LeuValGlyGluProProAlaGlnThrGlnSerThrSerSer----
JS-10-008-355-1 (1-2139) x Q8WWQ4 (1-1349)
                                                                           41 TGCTGTTGGGTGCTTCAGGGGTAGCCA---
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-----CCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTG 2089
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85 rProlleIleThrGluSerThrSerSerThrSerRalaSerThrThrGlySerSerSe 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 rSerProLeuProSerThrSerTyserThrSerThrSerIle-Pro---ProT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 ACCACGGTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 hrGlyGlySerSerSerLeuSerThrProIleThrProThrValProProThrSerThrS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 AAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 rSerIleAsnTyrAlaAspLeuLeuLysArgAsnGluAspLeuAsnAlaSerLeuSerTh 66
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
putative glucoamylase, similar to S. cerevisiae STA1, similar to S. SPAPB189-04C.
SPAPB189-04C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharom
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STRAIN=972H-;
O'Neil S., Harris D., Wood V., Rajandream M.A., Barrell is Submitted MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL691402; CAD27470.1; -.
SEQUENCE 800 AA; 79351 MW; F65488E43FE7089A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             800
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Conservative:
Mismatches:
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                                                                                                                                                                        2090 ACAAATGGGGTCAGTGCCCCGTCTCATCC 2119
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uery Match:
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2036
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Sun May 25 15:40:19 2003

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474 177 512 197 572 217 628	230 670 250 706 270	713 290 754 310 800 860 860	350 920 369 980 386 1100 413	11145 433 11187 449 1247 457 1307
GTAGAAGGACACTCAAGGGTATCACTGACGAGA                              GTATGCCAAGAACTGGCCA-AAAAGAAATGCA	hrasnserserpro			CAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAAAAGGC alproprothrSerSerSerThrProLeuThrThrAsnCysThrThrSerThrSerV TTATAAGGAAGGAGCCAAGGCCAACGGTGAGATGATTTT: :: alprofyrThrSerThrProvalThrSerThrProLeuAlaThrThrAsn GAGCGAGACGCTCTTCGGTGGTACCGAGGTCGTTTTGCACATTGCAACGCATT [  ::       CysThrThrSerThrSerValPro
415 164 475 177 513 573 573	217 629 230 671 250	707 270 270 290 755 310 801	330 861 350 921 369 981 1041	1101 413 1146 433 1188 450 1248
	DP Oy Oy	0	00 00 00 00 00 00 00 00 00 00 00 00 00	0

Oy Op	1308 CTACCTCC	roTyrThrSerThrProValThrSerThrProLeuThrThrT	1328
Qy	1329 TAAGGTGCTGCCCGCCAT	GGCGTATCCCTGCCGACAAGC	1388
QQ	ThrThrS	ThrSerThrProValThrS	512
0y	၁ ၂	AATCGACAAGAAATTC	14
QQ .	2 erA	srSerThrProValThrSerThrProValThrT	529
y d	1449 CTTCGTATTCGACAGAG    :::          529 hrThrAsnCysThrThrS	GGTATTCGACAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCCATGCTCAAGTC ::::::::::::::::::::::::::::::::::::	1508 549
Qy	1509 CA	TGGACAAGGAAAAGTTTGCCAAGGGTATCGAGAAAGATCC	1550
đ	   549 roLeuAlaThrThrAsnC		569
Οy	1551 GGCAGTAGAGCTTTCCAA	GGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGAT	1610
QQ	569 hrSerSerAsnTyrThrIleSer	1eSer	576
. Qy	·1611 GGCCAATGCCTATGCCAT	GGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGA	1667
QQ	577	SerSerThrProValThrSerThrProValThrThrA	290
· 0y	-	ACGTGCTCTGCCGAGCGATGCCAACTTCACCA	1711
QQ		ThrSerValLeuTyrThrSerThrProlleThrSerProAsnSerT	019
Qy	1712	TGCGTATGAGCTACGGCTC	1730
ΩD	610 hrserserserThrG	SerSerSerThrGlnValSerTrpAsnSerThrThrProIleThrGlyThrSerT	630
QY	1731 CATCAAGGGATATGAACC	CATCAAGGGATATGAACCGCAGGACGTGCTGGTACAACTATCATACGACAGGCAAGGG	1790
ΩD	630 hrSerLysValThrSerS	erThrSerIleProLeuThrSerThrAsnArgThrSerThrT	650
QY	1791 CGTATTGGAGAAGCAGGA	CGTATTGGAGAACAGGATCCTAAGAGCGATGAGTTTGCCG	1831
Db	650 hrPheThrSerSerThrS	erileSerThrSerSerSerThrAlaThrSerSerThrS	029
Qy	1832	TCTCGACAATATCTCGACCTCTT	1856
qq	670 erPheAlaSerGluSerS	erSerPheTyrSerAsnValThrThrSerSerThrValS	069
QY	1857 CCGCACCAAAAACTATGG	CCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCCTATC	1916
QΩ	690 erThrProProProThrT	hrSerPheProSerThrPheThrThrSerPheI	707
Qy	1917 GAACAACGACATCACGGG	GAACAACGACATCACGGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGCCGTCT	1976
Dp	707 leThrSerSerSerLeus	erSerIleProAsnAsnSerThrGluValLysThrAla	725
Qy	1977 GATCGGTCTTGCTTTCGA	GATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGGACATCGAGTTCGAACC	2036
qa	726SerT	hrserserglyThrGluIleLysThrAlaSerThrSers	740
Qy	2037 CGATCTGCAGCGCACAAT	CGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGACAAATG	2096
QQ	740 erGlySerSerSerS	erSerTyrThrProAlaSerSerThrSerThrThrThrSerS	160
Qy	2097 GGGTCAGTGCCCCGGTCTCATCCAAGAGC	21	
QQ	_	erserser 769	
RES 014 ID AC DT	RESULT 4 014651 ID 014651 PRELIMINARY AC 014651; 014650; DT 01-JAN-1998 (TrEMBLrell.	; PRT; 957 AA. 05, Created)	

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	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)	QY	650 GGATGTG
E E E	-JUN-2001 cin (Intes	, d	
	HOMO Sapiens (Human). Homo Sapiens (Human).	0y	710 ACCGGC
	Longijota, metazoa, choraca, cranizata, vertebrata, butereostomi; Mammalia; Euthberia; Primates; Catarrhini; Hominidae; Homo. NCRT TaxID=9606;	qq	305 SerSerI
	STOTISTICS FEBOR N B	Qy	770 TATCCAT
	DECLINE -974675; PubMed-9334251; GIM T B	qq	323SerI
	. 4	Qy	830 CGGATCG
	mocs number intestinat macin. Analysis of gene stincture, the carboxyl terminus, and a novel upstream repetitive region.";	qq	342
	. BIOI. CHEM. 2/2:200/0-20000(1997).	Qy	890 GTATCGA
	EMBL; ARUO7120; AAB64302.1; EMBL; AF007125; AAB4302.1;	qq	354 ThrSerH
	THEFTO, IFROUDES, EGF-ILKE. SACTOR DECORDS: DEFT INVENTED S	Qy	950 CTACCCG
	FROSITE, FSOURS, ESF_1; UNANUMEZ. PROSITE; PSOURS, ESF_2; I.	qa	374 Leuser-
	OCT 13 DORGER MIL DETTOREOURNER	QY	1010 TCGGTAT
		qq	390 ServalG
Pred. No.	: 0.0267 Length:	QY	1061
Percen	3.00% Conservative:	QQ	410 IleSerT
Best Local S Query Match:	4.118	Qy	1103 AGAGTGC
	UDD: 32	qq	430 GluThrS
2 :	(T-4155) A O14031 (T-557)	. Oy	1163 AGGCCAA
Š 6	155 ATTCGTC/ACAGTT/CGACAACCGTCCATTGCCAATGCCGTGGTTATCTTCGTGGCG Z14 15. Tlantarhantacharhantacharlandannahantacharhantacharhantacharlandannahantacharlandahantacharlandannahantacharlandannahantacharlandannahantacharlandahantacharlandannahantacharlandannahantacharlandannahantacharlandahantacharlandannahantacharland	qq	 450 ArgileT
3 8	CARGENIA THE COLOR AND ACCOUNT TO THE COLOR AND ACCOUNT THE COLOR AND ACCOUNT THE COLOR ACCOUNT THE CO	Qy	1223 GTTTGC
;		qq	466 ValileP
3 ,	201 116 117 201 201 201 201 202 201 201 202 201 201	Qy	1283 AATCGCT
ò á	ACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTATCTGCGCG	qq	::: 480 SerAlaT
a a	InrinilysinrinrserhisserinrproserPhethrserserilethr	Qy	1313 TCCCCTC
δοί	ATGGTTTCGTTTCTCGCACGATGGCTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAAGT	ΩD	   500 SerSerT
a (	InfinfGluinfinfSerHisSerAlaArgSerPhe	Qy	1373
<u> </u>		qa	520 ThrSerG
2 3	The second secon	Qy	1379
5 6		QQ	540 ProSerL
3 :	THE CLUST HE SHE SHE SHE SHE SHE SHE SHE SHE SHE	δy	1418 AATTCAA
5 6		QQ	560 GlySerT
3 8	17 THT THE THE COLUMN	ογ	1475C
5 A	260 GluthrithreeriisSerithree	QQ	579 ThrProT
ò	O TOTAL DE LA COMPANION DE LA	QY	1529 CCAAGGC
; a	octoring the state of the state	qq	598 erThrTh
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TGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTG------ 1060
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|SerSerLeuValGlyThrThrSerProThrMetSerThrValArgMetThrLeu 449
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                                          IleThrThrThrGluThrThrSerHisSerThrProGlyPheThrSer---- 322
                                                                                                                                                                                                                                                                                                 GCTACCTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTC 889
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GGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACA 709
                                                                                                                         CGGCCGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCG 769
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|ThrGluAsnThrProIleSerSerPheSerThrSerIleVal-------
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                                       CCGGTTTGCGTGAGATGTACCCCGGACGTG------CTCTGCCGAGCGATGCCAACT 1705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||| ||| sergerAsnSerSerVallleProLeuProGeuProGlyValSerThr 782
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||||
|ProSerThrThrProCysProGlyThr1leThr1leThr1leValProAlaSerProThr
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|IleProLeuThrMetLysProSerSerSer-----------LeuProThrlle
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                                                                                                                                                                              678 AspProCysValGluMetAspProSerThrGluAlaThrSerProProThrThrProLeu
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                                                                                                                                                                                                                                                                                            718 ThrLeuThrThrTyrMetAspThrSerSerMetMetProGluSerGluSerSerIleSer
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Subaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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MUC3.
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215 GATGTACCGGTATCACAGTGTCCGATCAGG-------GCCTGATCTTTACCAACC 262
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SerIleThrThrSerGluThrProSerHisSerThrProSerSerThrSerLeuIleThr 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCACTG 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 ACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAA 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 ATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCG 214
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SerSerIleThrThrThrGluThrThrSerHisSerThrProGlyPheThrSer-----
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170
93
289
245
32
Biochem. Biophys. Res. Commun. 263:728-736(1999).
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                      PROSITE; PS00022; EGF_1; UNKNOWN_2
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50024; SEA; 1.
EGF-like domain; Glycoprotein.
                  EMBL, AF113616; AAF13032.1; -.
InterPro; IPR000561; EGF-like.
InterPro; IPR000682; SEA_domain.
Pfam; PF01390; SEA; 1.
SWART; SW00181: EGF; 2.
SWART; SW00200; SEA; 1.
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157.00
33.00%
21.33%
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Db 678 AspProCysValGluMet Qy 1732	Qy         1784 GCAAGGGCGTATTGGAGA           bb         758 ThrArg	Oy 1961 ATAAGAACGCCGTCTGA :::      ::: Db 797 LeuArgThrSerSerLys Qy 2021 ACATCGAGTTCGAACCCC Qy 2021 ACATCGAGTTGAACCCC Qy 2081 TCATGATTGACAAATGGC Db 829 SerArgArgThrThrArg	RESULT 6   RESULT 16   Q8TDH7   D Q8TDH7	NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=21845432; FGUM J.R. Jr., Crawl, "MCL17, a novel men Blochem. Blophys. FEMBL, AF430017; AAI NON_TER SEQUENCE 1029 AA; ignment Scores:	Pred. No.:
342	1061	1223 GTTTGCACAGTTTGCCAACGCATTGCTACAAATCCTGATGCTGATGCTGCTGTA	y 1373	1475	## 1595 TTCAGGCCGATGCCAATGCCATTGAGAAGGGCAAGGGTTTTTTTT
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CACCAAAAACTATGGTCGCTATGCCGAGAACG---GTCAGCTCC 1900
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ysProSerSerSer------LeuProThrIle 796
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S.C., Hicks J.W., Szymkowski D.E., Kim Y.S.;
ane=tethered mucin.";
ane: Commun. 291:466-475(2002).
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rimates; Catarrhini; Hominidae; Homo.
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EMBL/GenBank/DDBJ dat  Mw; 45C2B2F85E98A6F6	Length: Matches: Conservative Mismatches: Indels:		TCTCGGAGCAGCCCTGCTGTGGTGCTTCAGGGGTAGCCAAAGCCGAAAGGCATGTG	GCTCCTCAACGAACTCAAGAAAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT :::   :::   :::	CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT         Pro	CGGTGGCGGATGTACCGGTATCACAGTCCGATCAGGGCCTGATCTTTACCAACCA	-ArgAlaGlnSerGlySerAsp	CHGCGGATGCATGCTATCAGAGCAGGGTGGATGCAGCAGTATCTGGGGCGTGGTGG 	TTTCGTTTCTCGCACGACGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAA 	GTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCAC		TGACGAGATGGACGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGCCCAAAAA 	AGAAAATGCAGACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAA	-CGAATACTTCCT-	  SerAlaSerSerProGluThrArgSerArgThrProProArgHisArg		-ArgserProserValserSerProGluProAlaGluLysSerArgSerSer	GGGGGGGGGGATACGGGATGTGGATGTGGCCGCGTCACAGGGGGGCGACTTCAGCGTATTCG 	CGTGTATGCCGGTGCCGAAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAA 	rg	GCCCGTTTACTTCGCTGTGCCGTGTGCAAGGCTACAAGGCTGACGACTATGCCATGAC 	
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Qa	327	rargSerarg-SerargValThrargargargargGlyGlySerGly1
Oy	975	TAT
qq	346	gSerProAlaArgGlnGluSerSerArgThrSerSerArgArgArgArgGlyArgSerAr 366
οy	1035	TCTTGACGTGATAGGTCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCG 1091
QQ	366	gThrProProThrSerArgLysArgSerArgSerArgThrSerProAlaProTrpLysAr 386
οy	1092	TAAGAACGGCAAGAGTG
QQ	386	gSerArg-SerArgAlaSerProAlaThrHisArgArgSerArgSerArgThrProLeuI 406
Qy	1134	TCTCGAAAAGGCTTATAAGGAAGGAGCCAAGCCGAGCGGAGATGACTTATTTGAGGA 1193
qq	406	leSerArgArgArgSerArgSerArgThrSerProValSerArgArgArgSerArgSerA 426
٥y	1194	GA
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Qy	1224	ACGCATTGGCTACAAATCCTGATGCTCATG
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οy	1284	ATGCTTGACGACAAGTACAAAAGACTACCTCCCTCGACCGTAAGGTGCTGCCCGC 1343
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δλ	1379	ACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
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ογ	1437	GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAGTT 1490
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Οy	1590	CGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTT 1649
QQ	563	:::
οy	1650	CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCGGAGCGATGCCAACTTCAC 1709
Op	580	rgThrProArgThrAlaArgGlyLysrargSerLeuThrArgSerP 595
Οy	1710	CATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGACGGTGCCTGGTACAA 1769
QQ	595	ro
δy	1770	ATCATACGACAGGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGGGGAGGTTTGC 18
QO	607	erSerAspArgSerArgSerAlaThrProP 617

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0y 18	ATATCGCTTTCCTATCGAACAACGACATCACGGCGGTA	, <sup></sup>
qq	631 laLeuAsnSerSerArgMetSerCysPheSerArgProSerMetSerProThrProLeuA 651	qq
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qq	651 sp	qa
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qq	679 MetMetaspGlyProArgIleProAspHisGlnArgThrSerValProGluAsn 698	qq
Qy 2:	2115 CATCCAAGAGCTGAATCTA 2138	٥٧
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RA TE	O.; Unidentified human general	qa
	clones from brain which ca	Qy
	COUGE TO I RAISE PIOCEARS IN VILLO. ;  DNA RES. 4:141-150(1997).	qq
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Οÿ	27 TCTCGGAGCAGCCCTGCTTGGGTGCTTCAGGGGTAGCCCAAAGCCGACAAAGGCATGTG 86	QY
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Qy	87 GCTCCTCAACGAACTCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT 146	Qy
Dp	::    :::    : 623 SerProArgArgSerArgSerGlySerSerProGluValLysAspLysProArgAlaAla 642	qa (
Οy	147 CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT 206	δ d
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1134 TCTCGAAAAGGCTTATAAGGAAGGAGCCAAGGCCAACGTGAGATGACTTATTTGAGGGA 1193
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                                                                                                                                        651 ------SerSerProGluProLysAlaProAlaProArgAlaLeuProArgArg 666
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441 TGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACT---GGCCAAAAA 497
                                800 ---GlyLeuGlnArgSerArgSerArgSerArgGluLys------
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RESULT 9

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87 GCTCCTCAACGAACTCAATCAGGAGAATCTGGATGGAATGCGTGAGCTCGGCTTTACGCT 146
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702 ---ArgGlySerArgSerSerProGluProLysThrLysSerArgThrProProArgArg 720
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                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.

icke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,

obinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,

oodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,

eng S., Tatum O., Campbell C., Fawcett J., Deaven L.;

Sequencing of Human Chromosome 16p13.3.";

ubmitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 TCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGGGTAGCCAAAGCCGACAAAGGCATGTG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Jammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Large Scale Sequence Analysis and Annotation with the Sequence omparison Analysis (SCAN) System."; ubmitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
MBL: AC004493; AAC08453.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUENCE 1791 AA; 191306 MW; 3A7B5530AEE95F3E CRC64;
                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
PRT; 1791 AA.
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156.00
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  PRELIMINARY;
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ocal Similarity:
Match:
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SerProValThrArgA	Db · 1038 erArgSerArgThrSerProValThrArgArgArgSerArgSerArgThrProProAla1 1058 Ov 1536 #A#FGRGARA#GRGGGGGGGGGGGGGGGGGGGGGGGGGGG	1058 leArgArgSerArgThrProLeuLeuProArg	OY 1590 CGCTATTCAGGCCGATGCCTATGCCATTCAGANGGCCAAGCGTTTT 1649 1::	OY 1650 CTTTGCCGGTTGGGTGAGATGTACCCCGGACGTGCTGCCGAGCGATGCCAACTTCAC 1709	QY 1710 CATGCCTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAA 1769	Qy 1770 CTATCATACGACAGGCAAGGCCTATTGGAGAAGCAGCATCAAAGAGCGATGAGTTTGC 1829 ::	Qy. 1830 CGTACAGGAGAATATCCTCGACCTCTTCCGCACAAAACTATGGTCGCTATGCCGAGAA 1889	QY 1890 CGGTCAGCTCCATATCCCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAG 1949 :::::    :::        ::: Db 1140 laLeuAsnSerSerArgMetSerCysPheSerArgProSerMetSerProThrProLeuA 1160	QY 1950 CCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTCGATGGCAACTGGGAAGC 2009  1:	Qy 2010 TATGAGTGGACATCGAACCCGATCTGCAGCGCACAATCAGCGTGGA 2063	Oy 2064CATCCGCTACGTTCTCTTCATGATTGACAAATGGGGTCAGTGCCCCGGTCT 2114	Qy 2115 CATCCAAGAGCTGAAGTTGATCTA 2138          ::::::          Db · 1208 HisAlaGInSerArgilealaLeu 1215	000		OS Homo Sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI TaxID=5606;		Submitted (JUL-1998) to the EMBL/GenBank/DDBJ data EMBL; AB016092; BAA83718.1; InterPro; IPR002965; P. rich.extensn. PRINTS; PR01217; PRICHEXTENSN.	SQ SEQUENCE 2752 AA; 299672 MW; 109C64F181097123 CRC64;
	SerAlaSerSerProGluThrArgSerArgThrProProArgHisArg	579 ATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTT 629	630 CGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCG 689	CGTGTATGCCGGTGCCGACAACCGGCCGCCGAATACAGCAAGGACAATAAACCTATAA	GCCGTTTACTTCGCTGCCGTATCCATGCAGGCTACAAGGCTGACGACTATGCCATGAC	CATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTAT	ATCGAAGTTCGCGGTATCAAGCCAAGCCATCTGGAAGGA  [	AGCCATGAGCGCAGATCAGCTACCCGTATCAAATATGCCAGCAA 97	GTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGGGGTCTCGCTCG	855 gSerProAlaArgGlnGluSerSerArgThrSerSerArgArgArgArgArgGlyArgSerAr 875 1035 TCTTGACGTGATGGCGTGCCGAGGAAGAGATTCGCAGACTGGATCC 1091	gimiriorioinisselargussargsselargsselargimisselruoalaaruoiipbyssal os TAAGAACGGCAAGAGTG	SPEIRIG SPEIRIGAGNEIFICAIGIII FINI GALGNEIALGNEIALGNEIALGNEITEN COLOCA TOTOCAGAGAGGCTAATAGGGAGGGGGGGT	GTTCG	TTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAA 12	ATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCGCTCG	1344 CATGCTCGATATTGTACGCCGCGTATCCCTGCCG	1379ACAAGCTCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436 	

Sun May 25 15:40:19 2003

Pred. No Score: Percent Best Lo Query Mo	No Loc Ma	.: Similarity: al Similarity: tch:	0.0535 156.00 34.428 23.908 4.088	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2752 184 81 276 229 35	
US-10	0-008-	355-1 (1-2139	) x Q9UQ35 (1-2	2752)		
O O	27	TCTCGGAGCAGCC(1111 111 111 111 111 111 111 111 SerGlySerSerP)	GCAGCCCTGTTGGGTGCT' 	TCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGGGTAGCCAAAGCCGACAAGGGATGT 	CCGACAAAGGCATGTG	86 1591
ογ	87	GCTCCTCAACGAAC	CTCAATCAGGAGAAT	CTGGATCGAATGCGTG	GCTCCTCAACGAACTCAAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCT	146
qq	1592	SerProArgArgSerArgSerGlyS	er	ııı SerProGluValLysAspLysProArgAl	  pLysProArgAlaAla	1611
οy	147	CCCGTTGGATTCG	CTCTACAGTTTCGAC	AAGCCGTCCATTGCCA	CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT	206
qq	1612	1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1612
٥y	207	CGGTGGCGGATGT	<b>ACCGGTATCACAGTG</b>	GGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTTTACCAACCA	TCTTTACCAACCACCA	266
qq	1613		ArgA	SerA	ds	1619
0y	26	CTGCGGATACGGT	SCTATCCAGAGCCAA	CTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGATATCTGCGCGATG	ACTATCTGCGCGATGG	326
g	1620	88	erSerProGluProL	erSerProGluProLysAlaProAlaProArgAlaLeuProArgAr	gAlaLeuProArgArg	1635
δ d	32	TTCGT	rcrcgcacgargggr	GAGGAGCTTCCGATTC	-TTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGGGTCTTTCCGTGAA	0
â	1030	serargsererys	эг эег эег ьузы уу.	seralyserserberlysalyargalyrroserrroglualyserser	uGlyserserrnr	1655
QY Dp	381	GTATCTGCGCAAG	GTATCTGCGCAAGATCGTGAAGGTAACGGA     :::  SuSerProGluHisProProLysSer	GACAAGGTAGAAGGAC        ArgTh	GTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAAGGGTATCAC	440
ò	441	TGACGAGATGGAG	GTCTGCGCAAAGCT	CAGGAGGTATGCCAAG	AACTGGCCAAAAA	_
. a	7	  ArgGlySerA	:::      ::: 	ArgGlySerArgSerSerProGluProLysThrLysSerArgThrProProArgAr	Pr	1688
0y	498	AGAAAATGCAGAC	SAGAACCAACTCTGC	AGAGC	ATTCCAACAA	551
qq	1689		  srSerProGluLeuT		::::: uSerArgArgSerArg	1708
οy	552			CGAATACTTCCT	-CATCGTCTACGATGT	578
Op	1709	SerAlaSerSerS	er ProGluThrArgS	aSerSerFroGluThrArgSerArgThrProProArgHisArg	9HisArg	1725
ογ	579	ATTCAAGGACGTTCG	ATTCAAGGACGTTCGTATGGTATTTGCTCC-		⋖-	629
QQ	1726	ArgSe	erProSerValSerS		: uLysSerArgSerSer	1742
ογ	630	CGGAGGCGATACGC	SACAACTGGATGTGG	CCGCGTCACACGGGCG	GGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCG	689
q	1743	ArgArgArgArg-		erAlaSerSerProAr	gThrLysThrThrSer	1757
ογ	069	CGTGTATGCCGGT	SCCGACAACCGGCCG	GCCGAATACAGCAAGG	CGTGTATGCCGGTGCCGACAACCGGCCGGCCGAATACAGCAAGGACAATAAACCCTATAA	749
Q	1758	ArgArgGlyArgSe	ArgargGlyArgSerProSerProLysProArg	roArg		1768
οy	750	GCCCGTTTACTTCC	SCTGCCGTATCCATGO	CAAGGCTACAAGGCTG	GCCGGTTTACTTGGCTGCATGCAAGGCTACAAGGCTGACGACTATGCCATGAC	608
q	1769	GlyLeuGlnAı	GlyLeuGlnArgSerArgSerArgSerArgArgGluLy	erArgArgGluLys		1781
δ	810	CATCGGTTTCCCGG	SGCAGTACGGATCGC	TACCTCACTTCTTGGG	CATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTAT	869
qa	1782				.ਜੂ ਜੂ	1785
oy Op	870	CGAAAACGAGAACAATCCTCG     :::   : ArgArgArgAspArgSerGly	TATCGA	GTTCGCGGTATCAAGC	GAAAACGAGAACATCCTCGTATCGAAGTTCGCGTATCAAGCAAG	929
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	٥٧ و	930 A	AGCCATGAGCGCAGATCAGCCGTATCAAATATGCCAGCAA :	974
	ίδ			03
	q	m		1843
	Qy Db	1035 TC   1843 g'	TCTTGACGTGATAGGTCGTACCGAGGAAAGAGATTCGCAGACTGGATCCG	1091 1863
	Qy	1092 T		1133 1883
	δδ	1134 TO	TCTCGAAAAGGCTTATAAGGAAGGACCCAAGGCCAACGGTGAGATGACTTATTTGAGCGA ::	1193
	QY	1194 G		1223 1923
	Qy Dp	1224 T		1283 1933
	oy Db	1284 A'	ATCGCTTGACGACAAGTACAAAGACTACCTCCCTCGCTCG	1343
	Qy	1344 CA 1952 FC		1378
	Qy	1379 - 1972 e		1436 1992
	Qy	1437 G	GAAGTATGCAGACTTCGTATTCGACAGAGTGTGGTTCCTTATAGCGACAAGTT :	1490
	Qy	1491 CC   2006 e	CCATGCCATGCTCAAGGACAAGGAAAAGTTTGCCAAGGC :	1535 2026
•	Qy Db	1536 TV : 2026 1e	TATCGAGAAAGATCCGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGG ::	1589 2039
	oy Op	1590 CC		1649 2057
	Qy	1650 CC 2057 FG	CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCAC :	1709 2072
	Qy Db	1710 CV 1 2072 FC	CATGCGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAA ::	1769 2084
	Qy	1770 CT : 2084 e	CTATCATACGACAGGCAAGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTGC ::	1829 2094
•	Qy	1830 CC 1 2094 rc	CGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAA CONTACTATGGTCGCTATGCCGAGAA CONTACTATGGTCGCTATGCGGAGAAAAAAAAAAAAAAAAAA	1889 2108
	Qy	1890 CC	CGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACGGCGGGTAACTCCGGTAG	1949

2009 2009 2136 2063 2015 2114 2115 2115 21175 21175 21175 21175 21175 21175 21176 21176 21176 21176 21176 21176 21176 21176 21176 21176 21176 21176 21176 21177 2117 21177 211		:::       ::: roSerMetSerProThrProLeuA 2128		:::     :::  SerAsnGlvPheTleS
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### Control of the Co	TTCGATAAGAACGGCCGTCTGATCGGTC		QV Db	358
	TGGTGACATCGAGTTCGAACCCGATCTGC. :::        roLeuGlySerSerArgThrProMetSer'	Glyser	Oy Dp	376376 309 AsnSerSerGluThrP
PRELIMINARY   PRT; 1236 AA.   CTEMBRICAL   183   PRELIMINARY   PRT; 1236 AA.   DB 348	CATCCGCTACGTTCTCTTCATGATTG. 		. Qy	418 GAAGGACAGCTCAAGG     328 HisSerSerSerLysS
PRELIMINANY;   PRT; 1236 AA.			QQ .	478 TGCCAAGAACTGGCCA                 348 -AlaLeuAsnPro
(TTEMBLEEL 17, Created) (TEMBLEEL 17, Last sequence update) dding enzyme, by similarity to 5. cerevisiae STA1, contains  maily signature.  The sequence sequence update)  The signature of the sequence update of the sequence	PRT;	AA.	Qy	538 TTCTATTCCAACAACG :::        366 rAlalleSerThrlle
Company   Comp		update)	Qy	598 GTATTIGCTCCTCCCA
######################################	ucoamylase I (alpha-1,4-gluca ading enzyme, by similarity t		g ko	658 CCGCGTCACACGGGCG
Fingli, Ascomycotal Schizosaccharomycetes;  ### Schizosaccharomycetes;  ### Schizosaccharomycetes;  ### Schizosaccharomycetecee;  #### Schizosaccharomycetecee;  ##### Schizosaccharomycetecee;  ##### Schizosaccharomycetecee;  ######## Schizosaccharomycetecee;  #################################	.amily signature. IC. paromyces nombe (Fission yeast		qa	   393 yAlaThrSerVal
### A PARTIES D.;  DAY 757  DAY N.A.  DAY 2001) to the EMBL/GenBank/DDBJ databases.  ARY 2001) to the EMBL/GenBank/DDBJ databases.  SES):  CAGAGASTA CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL.  BRO01223; Glyco_hydro_18.  PRO01223; Glyco_hydro_18.  PRO0123; Glyco_hydro_18.  PRO01223; Glyco_hydro_19.  PRO01223; Glyco_hy	Fungi; Ascomycota; Schizosaccharom aromycetales; Schizosaccharom aromyces.	aromycetes; retaceae;	O. O.	718 GCCGAATACAGCAAGG :::   :: 412 eValSerThrSerThr
### Parrell B.G., Seeger K., Harris D.; ### Parrell B.G., Carlina B.G., D.	-4896; OM N.A.		δλ	
TITY: BELÖNGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL 565).  SES).  PRO01213: GLYCO_HYDTO_L18.  PRO01217: NHITLANSE_L2.  PRO01221: NHITLANSE_	"; jandream M.A., Barrell B.G., APR-2001) to the EMBL/GenBank	K., Harris	ପ୍ର ଓ	432 rValSerThrValThr
5; CACGGATACATCACCATCATCACCATCATCACCATCATCACCATCAT	ITY: BELONGS TO CHITINASE CLASES).	FAMILY 18 OF	90	
045 G1yco_hydro_18; 1. 04. G1yco_hydro_18; 1. 0599; AA_TRANSFER_CLASS_2; UNKNOWN_1. 060599; AA_TRANSFER_CLASS_2; UNKNOWN_1. 1236 AA; 123387 MW; 5A2D33A3OB87CDD8 CRC64;  0 0.0455	605; CAC36921.1; PR001223; Glyco_hydro_18. DP001917: NH+rangf 2		Qy	877 GAGAACAATCCTCGTA
Hydrolase.  36 AA; 123387 MW; 5A2D33A30B87CDD8 CRC64;  16 0.0455 Length: 1236 154.50 Matches: 145 154.50 Matches: 258 154.04 Mismatches: 258 16 AD: 20.424 Mismatches: 258 17 Gaps: 24 18 Gaps: 24 19 A Gaps: 24 11	04; Glyco_hydro_18; 1. 00599: AA TRANSFER CLASS 2: U	L NWONX	QQ	460 rAlaSerValAlaSe
0.0455   Length:   1236   Db   478	Hydrolase. 1236 Aa; 123387 MW; 5A2D33A		OY	937 AGCGCAGATCAGGCTA
1236			qa	478 478
: 20.42% Mismatches: 258 4.04% Indels: 198 Gaps: 24  3	: 0.0455 154.50 ty: 35.92%		Oy Db	997 TGGAAGAATTCGATCG
225 234 234 258 258 254 254 254 318 268 268 27 1117 29 1177 20 2137 218 26	: 20.42% 4.04% 3		Qy	1057 CGTGCCGAGGAAGAG
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234	GACAAGCCGTCCATTGCCAATGCCGTGGT		Qy dr	1117 GGCGATGTATTGTCTT
254 Db 514 254 Qy 1237 318 Db 519 268	AspPheLeuSerIleHisThrPheAsnSe		λŏ	
254 QY 1237 318 Db 519 268	acnSormhrphoAcnalamrnValClumv		QC	514
218 Db 519			Qy	1237 GCCAACGCATTGGCTA
	CACIGOGAIACGGIGCIAICCAGAGCCA        SerLeuPheTvrGly		QQ	519
	GTTTCGTTTCTCGCACGATGGGTGA		Oy	1297 AAGTACAAAGACTACC

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CCTCCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATT 1356
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                                                                                                                                                                                                                                                                                SerSerHisAspSerSerGlnGlyLeuGluSerThrSerSerIle 347
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eSerGlnAspHisThrLysThrValThrSer------ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTCTGTAGGTAGGTTCGGAGGCGATACGGACAACTGGATGTGG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACAACCGGCCG 717
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|ThrThrThrThrLysThrAspPheAspThrValThrThrThrIl 412
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|||| ::: ::: ::: SerProLysAsnLeuThrArgAspLeuLeuAsnTyrLysAlaAsn 288
                                                                                                                                                        ---GTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTA 417
                                                                                                                                                                                  |||::: ::: ||||||:::
|PheValGluAlaIleHisLySIleLeuAspThrLysSerLys--- 327
                                                                                                                                                                                                                                                                                                                                       AAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCT 537
                                                                                                                                                                                                                                                                                                                                                                                                                              GAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATG 597
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----GlySerSerAlaIlePro----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1815 GAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAACTATGG 1874
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                                                                                                AAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT 1473
                                                                                                                                                                                                                             1515 CAAGGAAAAGTTTGCCAÁGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGT 1574
                                                                                                                                                                                                                                                                                              1575 AATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAA 1634
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                                                  1474 CCTTATAGCGACAAGTTCCATGCCATGCTCAAG-----TCCATGGA
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                                GTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATA---TATTCAAGAATGTAATCGAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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SEQUENCE FROM N.A.
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             MEDLINE-21426417; PubMed-11535137;
Escande F., Aubert J.P., Porchet N., Buisine M.P.;
"Human mucin gene MUC5AC: organization of its 5'-region and central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rThrLeuValThrArgAsnCysHisProArgCysThrTrpThrLysTrpPheAspValAs
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Indels:
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Matches:
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NON_TER 2448
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                                                         repetitive region.";
Biochem. J. 358:763-772(2001).
EMBL. AJ298317; CAC83674.1; -
InterPro: IPR001209; Ribosomal.514.
InterPro: IPR001209; TIL. Cysrich.
InterPro: IPR001907; VWF_C.
InterPro: IPR001846; VWF_D.
Pfam; PF001826; TIL; 2.
Pfam; PF001846; VWC, 3.
SWART; SW00214; VWC, 3.
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35.64%
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Query Match:
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QQ	1932			7
δy	954			-
οp	1946			7 .
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qq	1981	:::   LeuArgAspGluGlyTyrThrPheCysGluSerProArgSerValGlnCysArgAlaGlu 2000		7
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οy	1122		à É	4 (
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οy	1239		RESULT Q29071	57
qq	2059		AC D	$\alpha \alpha$
٥y	1298			000
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QΫ	1334	4TGCTGCC 1340		v ы
Dp	2098	8 roThrAlaThrSerValThrGlnGlyThrHisThrProValThrArgAsnCySHisP 2118		ΣZ.
٥y	1341		X X G G	- S 0
qq	2118	8 roargCysThrTrpThrTrpPheAspValAspPheProSerProGlyProHisGlyG 2138		ο Σ E
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QQ	2138	8 lyAspLysGluThrTyrAsnAsnIle-IleArgSerGlyGluLysIleCysArgArgPro 2157		: E :
δλ	1434	GAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCA        :::       ::	R R R	3 — S
QQ	2158			ΩΣ
δλ	1494	4 TGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGC 1535		₽

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2202 ysMetCysLeuAsnIleGluValArgValLeuCysCysGluThrProLysGlyCysProV 2222
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2319 laAlaThrThrSerThrIleSerAlaProThrThrSerThrThrSerValProGlyThrT 2339
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STRAIN-YORKSHIRE/CHESTER WHITE/HAMPSHIRE CROSS; TISSUE-GASTRIC MUCOSA;
MEDLINE-952775264; PubMed=7755593;
Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras M., Specian R.D.,
LaMont J.T.;
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STRAIN-FORKSHIRE/CHESTER WHITE/HAMPSHIRE CROSS; TISSUE-GASTRIC MUCOSA;
MEDLINE-94102478; PubMed-7506218;
Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras M., Specian R.D.,
||| |||::: ||| :: ||| 2165 CysArgAlaLysSerHisProGluValSerIleGluHisLeuGlyGlnValValGln--- 2183
                                                                                           1536 TATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCTCGCGCTAT 1595
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                                                                                                                                                     -----CysSerArgGlu 2187
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                                                                                                                                                                                                                                                                        2188 GluGly-------LeuValCysArgAsnGlnAspGlnGly--ProPheL
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Sus scrofa (Pig).
Sus scrofa (Pig).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                            1656 CGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCA----
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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			127	187	247	307	367	52	427	487	65	547	607	667	700	4	138	805	865
LaMont J.T.; "Pig gastric mucin: isolation and characterization of a cDNA clone with a novel tandem repeat."; Gastroenterology 106:200-200(1994). EMBL; U10281; AAC48256.1; NON_TER 528 528 SEQUENCE 528 AA; 49907 MW; OBF0F6879203B2EA CRC64;	Alignment Scores:  Pred. No.:  Score:  149.00  Matches:  154  Percent Similarity:  34.23  Conservative:  Mismatches:  21.51  Mismatches:  3.90  Gaps:  Gaps:	-355-1 (1-2139) x Q29071 (1-528)	AAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGC :::   :::	GTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTG	CCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCC	TGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATC	ACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGATTCCGG		GTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGC	TCAAGGGTATCACTGACGAGGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAAC	ProProlleSerSerThr	TGGCCAAAAAAAATGCAGAGAGCAAACTCTGCATCGTAGAGCCTTTCTATTCCA :::	ACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTGCTC :::             :::       :::           ThrThrSerThrThrSer	CTCCCAGCTCTGTAGGTAAGGTTCGGAGCGATACGGACAACTGGATGTGGCCGCGTCACA	CGGGCGACTTCAGCGTATTCCGCGTGTATGCCG	GTGCCGACCGGCCGGCCGAATACAGCAAGGACAATAAACCT	SerSerGlySerValProThrThrSerAlaThrSerValGlnSerSerSerSerSer	ATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCA :::	TGACCATCGGTTTCCCGGGCAGTACGGTACCTCACTTCTTGGGGTGTGGAAGATC
Lamont J "Pig gas with a n Gastroen EMBL; Ul NON_TER	nment Sc . No.: e: ent Simi Local S y Match:	-008	68	128	188	248	308	52	368	428	9	488	548	608 85	999	701	119	746	806
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qq	155	SerProProlleSerSerThrValSerValGlnProSer 167
Qy	866	HTCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAAGCAAG
д Д	168	rerserSerAlaProThrThrSerAlaThrSerValGlnProSerSerSer 18
٥y	926	STATCAAATATGCCAG
q	187	SerProPro1leSerSerThrValSerValGlnThrSerSerSerSer 203
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QQ	_	rSerSerValProThrThrSerAlaThrSerValArgSerSerSer 232
oy Ob	1106	GTGCTGTCTATGGCGATGTATTGTCTTCTCGAAAAGGCTTATAAGGAAGG
οy	99	FTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTT 12
QQ	253	 ProthrThrSerAlaThrSerValGlnProSerSerSer 266
Qy	1226	TTGCACAGTTTGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAAT 1285
Dp	267	SerThrProIleProSerThrThrSerValGlnProSerSerSer 282
οy	œ.	GCTTGACGACAAGTACAAAGACTACCTCCCTCGACGTCGTAAGGTGCTGCCGCCA 13
qq	283	SerAlaProThrThrSerAlaThrSerValGlnProSerSerSerSerProPro 301
Qy	1346	3CCGCGTATCCTGCCGACAAGCTCCCCGATA1
qq	302	
Qy	1406	ATCGACAAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGT
qq	313	SerSerSerProThrThrSerThrThrSerValGlnProSerSerSerGlySer 331
οy	1466	GTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGT 1525
Db	332	AlaProThrThrSerAlaThrSerValGlnProSerSerSerSer 346
QY,	1526	YTCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCT
qq	347	SerProProIleSerSerThrIle 354
Qy	1586	CTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTC 1645
ΩD	355	ServalGinProSerSer 361
Oy	1646	TTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACT 1705
QQ	362	Glyser 3
Oy	1706	GAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTG 1
qq	380	6
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Qy	1820	TGCCGTACAGGAGAATATCCTCGACCTCTTCCGCACCAAAAACT 18
qq	412	hrserValGlnProSerSerSerSerValF
Qy	1871	ATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGTTTCCTATCGAACAACGACATCA 1930
Dp	432	SerAlaThrSerValGlnThrSerSerSerSerThrProlleProSerThrThrSer 451

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valGlnProSerSerSerSerAlaProThrThrSerAlaThrSerValGlnProSer TCGATAAGAACGCCGTCTGATCGTTTCGATGGAACGGAAGCTATGAGTG	7 dd	ThrValGlnA
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		241 CAGGGCCTGATCITTACCAACCACCAC :::       :::    308 GluGlyLeuArgValPheVal
2018 GTGACATCGAGTTCGAACCCGATCTGCAGCGCACATCAGCGTGGACATCCGCTACGTTC 2077  1::	Qy 48	ACGGTGGATCACGACTATC
TCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAGAGC 2125	δ δ	31/ IntrheaspripelutyrArgintaly 352 GAGCTTCCGATTCCGGGTCTTTCCGTGAAG
	qa °	
RESULT 14 Q8WZX1 IID Q8WZX1 PRELIMINARY; PRT; 1037 AA.	Oy Db	412 AAGGTAGAAGGACAGCTCAAGGGTATCACT :::         345 ArgSerGluGlyAsp
QBWAZH. 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)	Qy	GAGGTATGCCAAGAACTGGCCAA
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B/N14.040. Neurospora crassa. Eukaryota; Fungota; Pezizomycotina; Sordariomycetes;	da .	532 GAGCCTTTCTATTCCAACAACGAATACTTC ::: 367 LysalalleLysSerArgArgThrHisPhe
SOLUGITATES, SOLUGITACERE, NEGLOSPOIA. NCBL_TAXID=5141;	QY	592 CGTATGGTATTTGCTCCTCCCAGCTCTGTA
4 4 5 5	qa	385 ArgileSerTyrValPro
·, nottalld	Qy	652 ATGTGGCCGCGTCACGGGGGGACTTCAGO
2) EBOUENCE FROM N.A.	qa	391
erman Neurospora genome project; submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.	Qy	ACA
	QQ	401 GluProGluGluGluAspAsnGlu
InterPro, IPR002950; Josephin. InterPro; IPR003903; UIM.	δδ í	772 TCCATGCAAGGCTACAAGGCTGACGACTAT
InterPro; IPMOUISSZ; APGC_KAO. Ffam; PF02809; UIM; 2. Ffam; PF00867; XPG II. 1.	gg ào	419 SerAspAspGluPheAspAlaGluAspGL
Pfam; PF00752; XPG_N; 1. SMART; SM00484; XPGI; 1.	<u>.</u> අ	
	ζŎ	835 CGCTACCTCACTTCTTGGGGTGTGGAAGAT
SQ SECUENCE 103/ AA; 114115 MW; C39//8//D9444239 CKC64; Alianment Gords.	qa	::: 454 GluThrValAlaLysLeuGlyValProLeu
0.139 Length: 147.00 Matches:	ζŎ	895 GAAGTTCGCGGTATCAAGCAAGGCATCTGG
ocal Similarity: 31.96%	qa	467IleTrp
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	ζŎ	1135 CTCGAAAAGGCTTATAAGGAAGGAGCCAAG
GlyPheProSerLeuGluValLeuArgTyrTyrThrHisProValValSerLysSerGlu	qa —	521 -ThrSerAspTyrLeuSerLeuAspSerSe
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QY		-cgcacgargggrgag 3
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Dp	335	
οy	412	AAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAG 471
Op	345	ArgSerGluGlyAspAspAspThrAspAspLeuArgArgLysGlu 359
QY	472	GACGAGAACCAACTC
QQ	360	
δλ	532	GTCTAC
qq	367	::: LysAlaIleLysSerArgArgThrHisPheSerThrAspAlaThrProGluLeu 384
QY	592	CGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAGGTTCGGAGGCGATACGGACAACTGG 651
qq	385	:::
QY	652	ATGTGGCCGCGTCACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACAAC 711
qq	391	IleLysValValThri,euAspLeuAspAla 400
Qy	712	CGGCCGGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTA 771
Db	401	GluproGluGluGluAspAsnGluGlyPheGlyArgValGlyLeuAlaLeuAsn 418
QY	772	TCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACC 831
QQ	419	uThrproGlys
Qy	832	GAT
Ωp	434	GlnGlyGlySerSerAlaLysProPheAspProPheLysProAspLeuAlaTrpllePro 453
δy	835	CGCTACCTCACTTCTTGGGGTGTGGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATC 894
QQ	454	GluThrvalAlaLysLeuGlyValProLeuThrValGlu
δy	895	GAAGTTCGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACC 954
qq	467	Lillissilli silli
Qy	955	CTATTGGAA
QQ	476	GluLeuLysAlaAlaAsnLysGlyThrArgLysAlaGlnThrThr[ysGlnThrGlyGly 495
Qy	1015	ATGAACCGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCA 1074
QQ	496	Metbroaladlyala 500
δλ	1075	TTCCCAGACTGCATCCTAAGAACGCCAAGAGTCCTGTCTATGCCGATGTATTGTCT 1134
QQ	501	LeuGluLysTyrValLysValThrLysGlySerAlaThrAlaGlyThrValThrLysSer 520
Qy	1135	CTCGAAAAGGCTTATAAGGAAGCCAAGGCCAACCGTCAGATGACTTATTTGAGCGAG 1194
QQ	521	ThrSerAspTyrLeuSerLeuAspSerSerProProArqSerSerHisIleAlaProPr 540

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ογ	ACGCTCTTCGGTGGTACCGA	
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ò	1255 AATCCTGATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTAC 1302	
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9 6	1303 AAAGACTACCTCCCTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGC 1362           :: :::       :: 568 uLysthtthrthrserLysGlythrthrLysAlaSer	
ò	CGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTC 14	
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oy	1534 GCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCT 1593	
qq	610 slleThrLysAsnIleAlaSer	
Qy	1594 ATTCAGGCCGATGCGATGCCCAATGCCTATGAGAAGGGCAAGCGTCTTTCT 1651	
qq	618SerGlnProAlaAlaLySThrSerLeuPheAspHi 629	_
ογ	1652 -TIGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGGGATGCCAACTTCACC 1710	
qq	629 sGluProlleLeulleSerSerProSerValProGlyLysArgLeuProAsnSerPr 649	
δ	1711 ATGGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCT 1762	
QQ	√sn.	
δ	1763 -GGTACAACTATCATACGACGGCGAATGGGGGAAGCAGGATCCTAAG 1815	ο΄ —
qq	661 eGlySerSerProProArgIleAlaProTrpLysGluArgLeuProAlaThrAr 679	
ò	1816 AGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTTTCCGCACCAAAACTATGGT 1875	
QQ	aspProThrArgHisProSerGlnArg	
ô	1876 CGCTATGCCGAGAACGGTCAGCTCCTTTCCTATCGAACAACGACATC 1929	_
Dp	699 lArgTrpArgSerGlnSerSerAlaLeuAlaSerSerProArgLysGlyProAlaPheGl 719	
0y	1930 ACGGCGGTAACTCCGGTAGCCCCGTATTCGATA	
qq	719 yLysaspLysThrProThrLysGlnArgSerIleLeuAspPheGlyTyrProSerThrTh 739	
ô	sccercre	
qq	739 rLysGluGlnAlaGlySerArgLeuPheGlyArgThrGlnSerAlaValLeuPr 757	
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STRAILVE-ST30. AAUCC.700294 / SEROTYPE M1;
STRAILVE-ST30. AAUCC.700294 / SEROTYPE M1;
MEDLINE-ST30. AAUCC.700294 / SEROTYPE M1;
MEDLINE-ST30. AGShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Frimeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Oian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Youn X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, AR006549; AAK33036.1;
Hypothetical protein: Complete proteome.
SEQUENCE 1368 AA; 158440 MW; 07004F0B5965762F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:::|||||| || || ::: ::::: ||||||| ||| |||| AsnGluGluAsnGluAspIleELeuGluAspIleValLeuThrLeuThrLeuPheGlu--- 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 TACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 GGTATCACAGTGTCCGATCAGGGCCTG----ATCTTTACCAACCACCACTGCGGATAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LeuPheAspAspLysValMetLysGlnLeuLysArgArgArgTyrThrGlyTrp 659
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699 AspAspSerLeuThrPheLysGluAspIleGlnLysAlaGlnValSerGlyGlnGlyAsp 718
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Streptococcus pyogenes.
Bacteria, Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcacaes; Streptococcacaes; Streptococcus.
NGBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AspArgGluMetIleGluGluArgLeuLysThrTyrAlaHis-----
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167
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228
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⋩	604	GCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGT 663	
ą	830	830	
<u>~</u>	664	CACACGGGCGACTTCAGCGTATTCCGCGTGTGTGCCGGTGCCGACAACGGCCGGC	
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ž q	724	TACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCTATCCATGCAAGGC 783 	
<b>≿</b> €	784	TACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGGCAGTACGGATCGCTACCTC ::: Dhelonive and some and some actions are some actions and some actions and some actions are some actions and some actions and some actions are some actions and some actions and some actions are some actions and some actions and some actions are some actions and some actions and some actions are some actions and some actions and some actions are some actions and some actions and actions are some actions and some actions are some actions and some actions and some actions are some actions and actions are some actions and actions are some actions are some actions and actions are some a	
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ъ д	857	ALIULIOGGIGIOGGAMARIOCIALIOGAMARIOCAMARALATICATICATICATICATICATORIOCAGATITACO 903	
γ	904	GGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGGGCAGATCAGGCTACCGGTATCAAA 963	
ą	877		
λ	964	CCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGC	
ð	897		
۸.	1024	GGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGACCA 1074	
ð	907		
λ	1075	TTCGCAGACTGGATC 1104	
ą	927	IleThrLysHisValalaGlnIleLeuAspSerArgMetAsnThrLysTyrAspGluAsn 946	
<u>۲</u>	1104	1104	
ą	947	AspLysLeulleArgGluValLysValIleThrLeuLysSerLysLeuValSerAspPhe 966	
λ.	1104	1104	
ą	196	ArgLysAspPheGlnPheTyrLysValArgGluIleAsnAsnTyrHisHisAlaHisAsp 986	
λ	1105	AGTGCTGTCTATGGCGATGTATTGTCTTCTCTCTGGAAAAG 1143	
ą	987	ValGiyThrAlaLeuIleLysLysTyrProLys	
<u>~</u>	1144	GCTTATAAGGAAGGA	
ဍ	1007	GluPheValTyrGlyAspTyrLysValTyrAspValArgLysMetIleAlaLysSerGlu 1026	
λ	1171	CGTGAGATGACTTATTTGAGGGAGGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCA 1230	
ą	1027	GlnGluIleGlyLysAlaThrAlaLysTyrPhePheTyrSerAsnIleMetAsnPhePhe 1046	
λ	1231	CAGTITGCCAACGCATTGGCTACAAATCCTGATGCTCATGCCGGTATCCTCAAATCG 1287	
q	1047	LysThrGluIleThrLeuAlaAsnGlyGluIleArgLysArgProLeuIleGluThrAsn 1066	
λ	1288		
q	1067	GlyGluThrGlyGluIleValTrpAspLysGlyArgAspPheAlaThrValArg 1084	
<u>ک</u> دو	1330	AAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGT	
3 )		njavarbeacerracerracerracerracerracerracerra	
λ	1369		

qq	1105	PheSerLysGluSerIleLeuProLysArgAsnSerAspLysLeu 1119
Οy	1402	AATG
QQ	1120	11eAlaArgLysAspTrpAspProLysLysTyrGlyGlyPheAsp 1135
Qy	1462	AAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCC
QQ	1136	SerProThrValAlaTyrSerValLeuValValAlaLysValGluLysGlyLysSerLys 1155
Qy	1498	ATGCTCAAGTCCATGGACAAGGAAAAGTTTGCC 1530
qq	1156	LysLeuLysSerValLysGluLeuLeuGlylleThr1leMetGluArgSerSerPheGlu 1175
Óγ	1531	
qq	1176	LysAsnProlleAspPheLeuGluAlaLysGlyTyrLysGluValLysLysAspLeuIle 1195
Qy	1555	GTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCC 1614
Dp	1196	IleLysLeuProLysTyr 1201
δy	1615	AATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTT
Op	1202	SerLeuPheGluLeuGluAsnGlyArgLysArgMetLeuAlaSerAlaGlyGluLeuGln 1221
δÿ	1675	CCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGC 1722
Ωp	1222	LysGlyAsnGluLeuAlaLeuProSerLysTyrValAsnPheLeuTyrLeuAlaSerHis 1241
ογ	1723	TACGCCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAAC 1770
QQ	1242	
δy	1771	ACGACAGG
qq	1261	GlnHisLysHisTyrLeuAspGluIleIleGluGlnIleSerGluPheSer 1277
Qy	1831	GTACAG1836
Dp	1278	.:. LysArgValIleLeuAlaAspAlaAsnLeuAspLysValLeuSerAlaTyrAsnLysHis 1297
δy	1837	GAGAATATCCTCGACCTCTCGCACCAAAAAC 1869
ΩD	1298	ArgAspLysProIleArgGluGlnAlaGluAsnIleIleHisLeuPheThrLeuThrAsn 1317
Qy	1870	TATGGTCGCTATGCC 1884
QΩ	1318	leuGlyalaProAlaAlaPheLysTyrPheAspThrThrIleAspArgLysArgTyrThr 1337
Qy	1885	
οp	1338	SerThrLysGluValLeuAspAlaThrLeuIleHisGlnSerIleThrGly 1354

Search completed: May 16, 2003, 12:35:34 Job time: 221.5 secs

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OM nucleic - nu Run on:	OM nucleic - nucleic search, using sw model Run on: May 23, 2003, 04:53:13 ; Search time 3810 Seconds (without alignments)
	16338.819 Million cell updates/sec
Title: Perfect score:	US-10-008-355-1
Sequence:	
Scoring table: OLIGO_NUC Gapop 60.0	OLIGO_NUC Gapop 60.0 , Gapext 60.0

Total number of hits satisfying chosen parameters: 4109280 Minimum DB seq length: 0 Maximum DB seq length: 2000000000

2054640 seqs, 14551402878 residues

Searched: Word size : Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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		ð			SUMMARIES		
Sul	SC	uery atch	Lengt	В	QI	escri	uo
1		. 0	5898	8	3836	38360	
7			o		5	14	Homo sapi
m			166143		4	344	Homo sapi
			$\circ$		7	AC096541	Homo sapi
S			4309		AC017213	AC017213	Drosophil
			5890T		30	AE004008	xylella r
					AFUU185U 3.0083836	APUOIRO	HOMO Sapi
о <i>о</i>	20	n o	131813	<i>ر</i> د	AC03828 AC011067	00.0	Drosophil
7					AC120223	AC12023	Rattus no
c 11					2	AC095129	Rattus no
1					AL391294	AL391294	Human DNA
г					AC019024	AC019024	Homo sapi
14					AC009253	AC009253	
15					AC098197	AC098197	Rattus
<del></del> 1					AC005552	AC005552	НОШС
c = 17					AC079735	AC079735	Mus mu
-					AC125392	AC125392	Pan
- (					AC104241	AC104241	НОЩ
7 (		•			AC128439		Rattus no
מיני					CN30/EGF	ALCOLOR	Mus mu
10					AC123979	AC123979	Dani
10					AC053525	AC053525	HOMO SAD
1 ~					AC073967	AC073967	Homor
2					AC129152	AC129152	Rattus
27					AC080124	AC080124	Ношо
28					AC016702	AC016702	
29					AC092733	AC092733	Ношо
c 30		-			AC116933	AC116933	Papic
31					AC006443	AC006443	Ношо
35					AC091579	AC091579	Homo
c 33		•			AL512504	20	Human
m					AL844530	33	Mus n
35		•			AE003669	AE003669	Dros
36		•			AC127582	58	
c 37					AC124538	153	Mus muscu
38		•	148		42	145	Oncorh
39		•	218		61	61	
40			237		AF104589	S	-
41		٠	237		AF104590	5	Oncorh
42			237		0460	0460	Salmo
43		•	240		0460	0460	
44		٠	240	ഹ	161	AF104610	Salmo

ALIGNMENTS

RESULT 1 AY038360 LOCUS DEFINITION ACCESSION	AY038360 5898 bp DNA linear PLN 09-AUG-2002 Nectria haematococca mpVI retrotransposon Nht2, complete sequence. AY038360
VERSION KEYWORDS SOURCE	AY038360.1 GI:14700031 Nectria haematococca mpVI.
ORGANISM	Nectria haematococca mpVI Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.
REFERENCE AUTHORS	<pre>1 (bases 1 to 5898) Shiflett, A.M., Enkerli, J. and Covert, S.F.</pre>
TITLE	Nht2, a copia LTR retrotransposon from a conditionally dispensable chromosome in Nectria haematococca

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Location/Qualifiers
                                                                                                                                                                                                                                /clone="RP11-543D5"
                                                                                                                                                                                                                                                                                                                                                                                                                                Db 134330 GCACGATGGTGAGGAGCTTC 134350
                                                                                                                                                                                                                                                                                                                                                         1.00,
100.0%; PET
0;
                                                                                                                                                                                                                                                                                                                                                                                                                 338 GCACGATGGGTGAGGAGCTTC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC013447.4 GI:10334968
                                                                                                                                                                                                                   /chromosome="1
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Matches 21; Conserv
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TITLE
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AUTHORS
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JOURNAL
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AC013447
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SOURCE
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165743)
                                       2 (bases 1 to 5898)
Shiflett, A.M., Enkerli, J. and Covert, S.F.
Direct Submission
Submitted (06-JUN-2001) Forest Resources, University of Georgia,
Brooks Drive, Athens, GA 30602-2152, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                             <3984. .>5537
/note="similar to reverse trancriptase and RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL691459.24 GI:22415898
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                             /note="mpVI"
1. .5898
/note="degenerate copia-like retrotransposon"
/transposon="Nht2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Length 5898;
                                                                                                                                                                                                                                                                                                                                                                                                                1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 15% of reads
Chemistry: Dye-terminator Big Dye; 84% of reads
Consensus quality: 165711 bases at least 040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                         1. 5898
/organism="Nectria haematococca mpVI"
/isolate="156.30-6"
/db_xref="taxon:70791"
/chromosome="MAKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL691459 165743 bp DNA 1
Homo sapiens chromosome 1 clone RP11-543D5,
PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                  5666. .5893
5894. .5898
/note="3' duplicated target site"
/rpt_type=direct
a 1483 c 1265 g 1383 t
                                                                                                                                                                                                                                                                   /note="5' duplicated target site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      core 21; DB 8
pred. No. 12;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 21;
100.0%; Pred. No.
Live 0; Mismatcl
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 09-MAY-2001
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Direct Submission
Submitted (11-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (28-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166143)
Sulston, J.E. and Waterston, R.
Consensus quality: 165743 bases at least Q30 Consensus quality: 165743 bases at least Q20 Insert size: 165743; sum-of-contigs Insert size: 179024; 7.4% error; agarose-fp Quality coverage: 11.08x in Q20 bases; sum-of-contigs Quality coverage: 10.63x in Q20 bases; agarose-fp
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HOMO Sapiens BAC clone RP11-543D5 from 1, complete sequence.
AC013447
                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Joshu,C., Stoneking,T., Gregory,S. and Burkett,M.
The sequence of Homo sapiens BAC clone RP11-543D5
Unpublished
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Pred. No. 12;
0; Mismatches
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39965 c 40507 g 43666
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18565..18980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence fidelity of RP11-543D5 from base position 100749 to 101626 can not be guaranteed. This region is made up of a variable GT run where there are single M13 and PCR only regions. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/jsc
                                                                 63108, USA
                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The clone sequenced to the left is RP11-689122. Actual start of this clone is at base position 1 of RP11-543D5; actual end is at base position 166143 of RP11-543D5.
                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
                                       Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 28, 2000 this sequence version replaced gi:7631057
                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                  Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                 Center project name: H_NH0543D05
                                                                                                                                                                                                              Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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5456. 5581
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    Waterston, R.
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AC096541 200368 bp DNA linear PRI 31-MAY-2002 Homo sapiens chromosome 1 clone RP11-330M19, complete sequence. AC096541 AL359084 AC096541.2 GI:21281550
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Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.

Direct Submission

Submitted (18-SEP-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

J bases 1 to 200368)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
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Center: University of Washington Genome Center
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Web Site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                      DB 9;
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Mismatches
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                                                                                                                                                                                                                                                                                                                      Score 21;
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25694. .25846
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23705. .23875
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                                                                   /rpt_family="MaLR"
24440. .24732
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
of this entry's ASN.1 file. <800 <800 <800 <800 SeqDerMap FngrPrnt 797 5875 5875 6406 7267 4657 problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. 1611 BglII Consensus quality: 200007 bases at least Q30 consensus quality: 200368 bases at least Q20 Insert size: 200368; sum-of-contigs quality coverage: 9.5x in Q20 bases; sum-of-contigs 549 2761 5843 6408 7217 4723 2067 9556 1632 5875 100 108 255 751 <800 <800 SeqDerMap FngrPrnt <800 7749 1365 1129 1199 8787 8399 4005 1129 3782 8027 964 ECORI 470 8696 1389 1144 8353 1209 1150 8058 169 7794 4077 505 3804 5': Mapping in progress 3': RP11-307017 AL451079 Overlapping Sequences: Sequence Validation: SeqDerMap FngrPrnt 862 6512 <800 <800 1888 <800 <800 3413 1502 1776 4136 <800 5304 4924 6382 5425 4932 1519 1788 4138 709 859 449 1893 538 3378 512 567 468

<800

<800

<800

3040     3036     5425     5378     908     934       6507     6512     4189     4224     2599     2589       2751     2807     6624     6730     252     <800       2303     2375     2208     2224     11460     1441       344     <800     11408     11348     135     <800	Ouery Match 1.0%; Score 21; DB 9; Length 200368; Best Local Similarity 100.0%; Pred. No. 12; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 338 GCACGATGGGTGAGGAGCTTC 358 Db 12725 GCACGATGGGTGAGGAGCTTC 12745	RESULT 5 AC017213 CDCUS DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces. ACCESSION AC017213 VERSION AC017213 VERSION AC017213 COURCE Drosophila melanogaster. CRGANISM Drosophila melanogaster. ELMARYOLE BLARYOLE CRGANISM Drosophila melanogaster. CRGANISM Drosophila melanogaster. ELMARYOLE BLARYOLE	REFERENCE 1 (bases 1 to 4309) AUTHORS Adams, M. and Venter, J.C. AUTHORS Adams, M. and Venter, J.C. TITLE Direct Submission JOURNAL Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA COMMENT This sequence was identified as CDM:10209899 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a "Working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.  FEATURES 1. 4309 ACCEPTION 1270 a 846 c 857 a 1326 t	tch al Similari 20; Cons GCAAATGAAAI GCAAATGAAAI	RESULT 6 AE004008/C LOCUS LOCUS LOCUS DEFINITION Xylella fastidiosa 9a5c, section 154 of 229 of the complete genome. ACCESSION AE004008 AE003849 VERSION AE004008 1 G1:9106961 KEYWORDS SOURCE Xylella fastidiosa 9a5c. ORGANISM Xylella fastidiosa 9a5c. SAURCE ORGANISM Xylella fastidiosa 9a5c. ATLEARENCE ORGANISM Sylella. REFERENCE 1 (bases 1 to 10689) AUTHORS SIMPSON,A.J., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
4222 797 6486 4222 <800	9122 1203 4222 797	2589 4033 10286 3595 1611 3401	934 6800 3595 6800 9558 6800	1766 .0965 <800 934 6761	2589 <800 4657 3595 0176 3401
4222 797 16486 4222 <800	91 12 42 7	2589 4033 20286 3595 1611 3401	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1766 10965 . <800 934 6761	2589 <800 4657 3595 10176 3401 <800
4278 4278 840 16573 4181	12127	2549 4070 4070 20135 3615 1653 1653 4250	218 3602 3602 3602 3602 5888 5888	1766	2476
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Alvarenga,R., Alves,L.M., Araya,J.E., Bala,G.S., Baptista,C.S., Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R., Bueno,M.R., Camargo,L.E., Carraro,D.M., Carrer,H., Colauto,N.B., Colombo,C.Costa,F.F., Costa,M.C., Costa-Neto,C.M., Carrer,H., Coutinho,L.L., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H., Farga,J.S., Franca,S.C., Franco,M.C., Forno,J.A., Fraga,J.S., Franca,S.C., Franco,M.C., Frolme,M., Fullan,L.R., Ho,P.L., Hoheisel,J.D., Junquelra,M.H., Gomes,S.L., Gruber,A.,
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1. .10689
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                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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DQQPSSGGASSPPSSGTAMPSFCSWASVVODFIDWWKSDETLKRPLVPDDVPYVDKL
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similarity; putative; ORF located using Glimmer/RBSfinder"
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PHIVMCFLVAWGFHFLFTVVRD"
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Hepatocellular Carcinoma Pathogenesis 1
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens genomic DNA, chromosome 4q22-q24, clone:343A4,
Complete sequence.
AP001860
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Pred. No.
                                                                                                                                                                                                                                                                    complement(4481. .4702)
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/gene="XF1878"
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Homo sapiens
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100.0%; Pre
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                                                                  /transl_table=11
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Best Local Similarity
Matches 20; Gonserva
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ORGANISM
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TITLE
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AUTHORS
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ACUB3826 129240 bp DNA linear PRI 07-NOV-2001
Homo sapiens BAC clone RP11-289C17 from 4, complete sequence.
AC083826
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Submitted (24-APR-2000) Shih-Feng Tsal, National Yang-Ming University, Institute of Genetics: 155 Li-Rong St. Section 2, Peitou, Talipei, Tamain 11221, Republic of China (E-mail: ympetsal@ym.edu.tw, URL:http://genome.ym.edu.tw/, Tel:886-2-28267043, Fax:886-2-28264930) On Feb 22, 2001 this sequence version replaced gi:7649705. Quality: the expected Phred/Phrap calculated error rate (per 10 kb) is 0.0019; Estimated total number of errors is 0.0167.
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Direct Submission
Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Sulston, J. E. and a complete human genome sequence
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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VanBrunt, A. and Meyer.R.
The sequence of Homo sapiens BAC clone RP11-289C17
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Contact: sapiens@watson.wustl.edu
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/db_xref="taxon:9606"
/chromosome="4"
/map="4q22-q24"
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Waterston, R.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                   Mapping information for this clone was provided by Dr. John D. Werberson. Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                        all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="match to EST AI791382 (NID:95339098) oh0lall.y5"
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                                                                                                                                                     This sequence was finished as follows unless otherwise noted:
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"note-"similar to Homo sapiens EST AV650986
NID:99872000)"
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NID:g13050347)"
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NEIGHBORING SEQUENCE INFORMATION:
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25. .309
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(310. .1593
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/rpt_family="L1"
2627. .2900
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t_family="Alu"
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594. .1870
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rpt_family="L1"
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4734. :5275

//note="similar to Homo sapiens EST BG757135

(NID:g14067788)"

4734. :5179

//note="similar to Homo sapiens EST BE018798 (NID:g8278841)
                                                                                                                                                                                                                             i681. .5216
/note="similar to Mus musculus EST AA059627 (NID:g1553413)
                                                                                                                                                                                                                                                                                                                                                                                        EST BE484374 (NID:99603907)"
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/note="imilar to Mus musculus EST BF462055
(NID:911531238)"
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(NID:912297873)"
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//octe="similar to Bos taurus EST BE484374 (N
4697. .5115
//oncte="similar to Homo sapiens EST BG386439
(NID:913279885)"
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/note="similar to Homo sapiens EST BG576912
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(NID:914174653)"
4728. 5272
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/note="similar to Mus musculus EST BG923425
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/note="similar to Homo sapiens EST AW367838
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/note="similar to Homo sapiens EST BE007807
(NID:98268040)"
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(NID:911614610)"
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                               /rpt_family="AT_rich"
3597. .3662
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contig of 714 bp in length gap of unknown length contig of 559 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 605 bp in length gap of unknown length contig of 1077 bp in length gap of unknown length gap of unknown length contig of 1700 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 1700 bp in length gap of unknown length length gap of unknown length length gap of unknown length length gap of unkno
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of 1242 bp in length
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Direct Submission

Direct Submission

Submitted (01-007-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 20, 2000 this sequence version replaced 91:6984326.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdggefruitfly.berkeley.edu. All contrigs in this submission meet
the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence record is
* nork known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

S Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,

Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,

Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,

Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,

Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R.,

Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.,

Richards,S., Sethil,H., Svirskas,R.R., Wan,K.H., Webster,D.,

Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.

Sequencing of Drosophila melanogaster

L Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster chromosome 2 clone BACR09L20 (D1140)
RPCI-98 09.L.20 map 39A-39A strain y; cn bw sp, *** SEQUENCING IN
AC011067
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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Pred. No. 44;
4865. .5343
/note="similar to Homo sapiens EST BE779572
(NID:9102000770)"
4870. .5387
/note="similar to Homo sapiens EST BG283401
(NID:913033252)"
                                                                                                                                                                                     4874. 5379
/note="similar to Homo sapiens EST AW991862
(NID:98251932)"
4875. 5383
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HTG; HTGS_PHASE1.
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Best Local Similarity 100.
Matches 20; Conservative
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AC011067
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RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Alaberooks, S. L., Amaretunge, H. C., Are, J. R., Ayele, M., Banks, T., Barberooks, S. L., Amaretunge, H. C., Are, J. R., Ayele, M., Banks, T., Barberooks, S. L., Amaretunge, H. C., Are, J. R., Ayele, M., Bronnin, D., Burberooks, S. L., Entunge, H. C., Burell, R. Brown, M., Bronnin, D., Bunch, P., Briege, R., Chacko, J. (Abracz, D., Carroo, T. E., Garter, M., Cavazos, S. R., Chacko, J. (Abracz, D., Chen, R., Chen, R., Chen, R., Chen, C., Coyle, M.D., Dathorne, S. R., David, R., David, R., Davis, C., Davy-Carroll, L., Dedarich, D. A., Davis, C., Davy-Carroll, L., Dedarich, D. A., Delaney, K.R., Deland, C.D., Edwards, C. C., Edoti, M., H. H., Davis, C., Davy-Carroll, L., Dedarich, D. A., Delaney, K.R., Delaney, K.R., Delaney, K.R., Delaney, K.R., Dayer, R. Carroll, L., Dedarich, D. A., Barnhart, C., Edgar, D., Edwards, C. C., Edday, C., Edwards, C. C., Eddy, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C. C., Eddy, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C. C., Eddy, C., Henris, R., Gunarathe, P., Hales, S., Hamilton, K., Harris, C., Harris, C., Harris, C., Hollins, B., Hernandez, O., Hodgson, A., House, M., Holloway, C., Hollins, B., Harris, C., Hugeshi, A., Landry, M., Mollows, C., Joudah, S., Karlsson, E., Kally, S., Khan, U., Kind, L., Kovah, J., C., Marting, E., McCard, M., Lucier, R., Lucier, S., Joudah, S., Marting, E., McLody, M., Moyuen, M., More, G., Mitchell, T., Mohabbat, K., Morgan, M., Monse, M., Mitchell, T., Mohabbat, K., Morgan, M., Mitchell, T., Mohabbat, K., Morgan, M., Mitchell, T., Mohabbat, K., Morgan, M., Moser, M., Rab, M., Rojas, A., Rojas, A., Follas, B., Peyton, B., Peyton, B., Solergren, E., Sonaike, T., Sparks, A., Follas, M., Rojas, A., Follas, A., Tabor, P., Tamerisa, K., Wasquez, L., Vera, V., Villalon, D., Villas, M., Will, M., Y., Wallians, A., Wallians, A., Wal ACLIAU223
136241 bp DNA linear HTG 18-JUL-2002
Rattus norvegicus clone CH230-307M22, \*\*\* SEQUENCING IN PROGRESS
\*\*\*, 50 unordered pleces. ö Submitted (05-MAY-2002) Human Genome Sequencing Center, Department Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Gaps ; 0 0.9%; Score 20; DB 2; Length 131813; 0; Indels 93491: gap of unknown length 94063: contig of 572 bp in length 94143: gap of unknown length Pred. No. 44; Mismatches 0; DD 10083 GCAAATGAAATTAAAAGTA 10102 AC120223.2 GI:21746475 Query Match 0.9%; Best Local Similarity 100.0%; Matches 20; Conservative 0 (bases 1 to 136241) 3 GCAAATGAAATTAAAAAGTA 22 Norway rat. Rattus norvegicus HTG; HTGS\_PHASE1. Unpublished 93412 93492 94064 Worley, K.C AC120223 RESULT 10 AC120223/c LOCUS DEFINITION ORGANISM JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE TITLE ò

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COMMENT

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Gaps
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NOTE: This is a "working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                  Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20452765.

Center: Baylor College of Medicine
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 136241)
                                                                                                                                                                                                                              Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-herbebcm.tmc.edu
Contact: hgsc-herbebcm.tmc.edu
Contact: hgsc-herbebcm.tmc.edu
Center project Information
Center project lame: GUNL
Center clone name: CH30-307M22
Consensus yearlity: 91485 bases at least Q30
Consensus quality: 97486 bases at least Q30
Consensus quality: 101277 bases at least Q20
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 73 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
On Jul 9, 2002 this sequence version replaced gi:17942055
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Sequencing vector: Dye-terminator Big Dye: 100% of r.
Assembly program: Phrap; version 0.990329
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Consensus quality: 89611 bases at least Q30
Consensus quality: 94789 bases at least Q20
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                                     Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                          HTG 10-JUL-2002
                                                                                                                                                               *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 150505)
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                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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73 unordered pleces.
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Direct Submission

L Submitted (06-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 8, 2000 this sequence version replaced gi:11064146.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clohe name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL: Sww. SWISSPROT; Tr:, TREMBL: Wp:, WORMPEP: Information on the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the entire insert of clone RP11-19664 The true right end of clone RP13-104H2 is at 71449 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-19664 is from For further details see
        PRI 06-DEC-2001
  AL391294 152120 bp DNA linear PRI 06-DEC-200 Human DNA sequence from clone RP11-19664 on chromosome X Contains part of a novel gene and a CpG island, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="27 copies 2 mer ac 98% conserved"
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/note="75_copies 2 mer tt 58% conserved"
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/note="L1M1 repeat: matches -1186. .-1037 of consensus"

repeat\_region misc\_feature misc\_feature

31654 TGCAGACGAGACCAACTCT 31635

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RESULT 12 AL391294/c

.2714 of consensus"

/note="LiM1 repeat: matches -523. comptement(8868. .9026) /note="match: GSS: Em:AZ392746" 8952. .9312

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/note="Lind" repeat: matches -2. .556 of consensus"
31629 .34385 .
Anote="Lind" repeat: matches 1818 .4658 of consensus"
Anote="12" repeat: matches 1818 .4658 of consensus"
Anote="24" copies 3 mer tat 68% conserved"
Anote="12" copies 6 mer ttatta 68% conserved"
A5500 .34956 //note="Lind" repeat: matches 5724 .5163 of consensus"
Anote="Lind" repeat: matches 7724 .5163 of consensus"
Anote="Lind" repeat: matches 7355 .1833 of consensus"
37383 .37833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC019024 160279 bp DNA linear HTG 14-MAR-2002
Homo sapiens chromosome 11 clone RP11-478E10 map 11, WORKING DRAFT
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#49302. #49911

/note="L1PA5 repeat: matches 5529. .6138 of consensus"

/note="L1PA5 repeat: matches 5135. .5552 of consensus"

/note="L1PA5 repeat: matches 5135. .5552 of consensus"

50392. .31778

51779. .2334 repeat: matches 2176. .3577 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                     30037. .30502
/note="LIPA8 repeat: matches 5696. .6161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="LIMD2 repeat: matches 5575. .6116 of consensus"
31104. .31624
                                                     27655. .28025
/note="THBIC repeat: matches 1. .371 of consensus"
28026. .28120
/note="FLMA repeat: matches 29. .123 of consensus"
28186. .28209
/note="12 copies 2 mer ac 100% conserved"
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'note="THE1C-internal repeat: matches 1524. .1576 of
                                                                                                                                                                                                                                                                                                                       Anote="Alusx repeat: matches 5. .305 of consensus" 29427. .30036
Anote="LiPA8 repeat: matches 10. .602 of consensus"
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                                                                                                                                                                                                                                         "MLT2A repeat: matches 9. .453 of consensus"
.29426
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AC019024.5 GI:19424608
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. Homo saplens.
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Mismatches
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/note="MLT2A re
29122. .29426
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AC019024/c
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//gene="match: CDNAs: Em:AKO24111 Em:AKO01535 Em:AL050030
match: ESTS: Em:AL252657 Em:BE673995 Em:AA947819
Em:BF142469 Em:AW89384 Em:BE073959 Em:AA947819
Em:BF141391 Em:AW892817 Em:BE05185 Em:BB180722
Em:BF107336 Em:AA968512 Em:AA63496 Em:BF139073 Em:F12610
Em:BF107336 Em:AA968512 Em:AA63496 Em:EP139073 Em:F12610
Em:BF107336 Em:AA968512 Em:AA63496 Em:EP139073 Em:BF281553
Em:BF14999 Em:BE016748 Em:H17605 Em:A1094593 Em:AW524670
Em:A7198375 Em:BE005114 Em:A110805 Em:BF140831
Em:AN36780 Em:AW885772 Em:AW885736 Em:BF065380
Em:AN36790 Em:AW885772 Em:AW889619 Em:BF065380
Em:AN3693831 Em:BE171599 Em:BE881116 Em:AA24338
Em:BF170557 Em:AA603412 Em:AA280341 Em:AA262381
Em:AW993831 Em:BE163571 Em:BE170628 Em:AA262381
Em:AW892807 Em:AW865540 Em:AW87711225
Em:AW892807 Em:AW762521 Em:EP170659 Em:AA7711225
Em:AW892807 Em:AW762521 Em:T25165 Em:AA242913 Em:W8779991
Em:BE915168 Em:AW770659 Em:ER827044 Em:R87609 Em:AW877935
Em:BE27475 Em:AN771253 Em:AW60653"
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21236. .21293
// (acta = organism)
21236. .21293
// (acta = organism)
21550. .21678
// (acta = organism)
21550. .21678
// (acta = organism)
21681. .2476
// (acta = organism)
21804. .21855
// (acta = organism)
21804. .25642
// (acta = organism)
25634. .26219
// (acta = organism)
25634. .26219
// (acta = organism)
// (acta = orga
                                                                                                                                                                                                                                /note="AluJb repeat: matches 138. .289 of consensus" 9180. .12619
/note="LIMA2 repeat: matches 2325. .5786 of consensus" 12614. .14951.
/note="LIPA13 repeat: matches 3768 .:6152 of consensus" 14961. .15487
/note="LIMA2 repeat: matches 5769. .6303 of consensus" complement(15532. .17999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6225, .26480
note="LIMD1 repeat: matches 5566, .5825 of consensus"
6518, .27573
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/note="LIMEc repeat: matches 358. .1420 of consensus"
27597. .27650
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// gene="bal9648: Em:A271635"
// note="match: GSS: Em:A271635"
// note="match: GSS: Em:A271635"
// note="match: GSS: Em:A0710263"
// note="match: GSS: Em:A0730707"
                                           /note="match: GSS: Em:AQ552982 Em:AQ568449"
3971. .9159
                                                                                                                /note="match: STS: Em:Af002096"
/note="match: GSS: Em:AQ236903"
complement(8971. .9176)
                                                                                                                                               complement(9021. .9179)
/note="match: STS: Em:G09176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<15532. .17999)
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15801. .16081
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ORGANISM

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Noptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 160282)
S Celniker, S. E., Adams, M. D., Krommiller, B., Tyler, D., Wan, K. H.,
Holt, R. A., Evans, C. A., Gocayne, J. D., Amanatides, P. G., Brandon, R. C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K. Y., Busam, D.A.,
Dodson, K., Dorsett, V., Doup, L. E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R. F., Garg, M. S., George, R. A.,
Inbeyam, C., Jalali, M., Kruse, D., Li, P., Matlei, B., Moshrefi, A.,
McIntosh, T. C., Moy, M., Murphy, B., Nelson, C., Nelson, K. A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfelffer, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster, chromosome 2L, region 39A-39A, BAC clone BACR24F17, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 77856: contig of 77856 bp in length 77857 77956: gap of 100 bp 77957 779539: contig of 1283 bp in length 77957 7939: contig of 1283 bp in length 79340 79339: gap of 100 bp 79340 160279: contig of 80940 bp in length.
                                          Insert size: 163000; agarose-fp
Insert size: 160079; sum-of-contigs
Quality coverage: 19.1 in 020 bases; agarose-fp
Quality coverage: 19.5 in 020.
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
Consensus quality: 159947 bases at least Q20
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1. .77856
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42570 a 40290 c 38390 g 38828 t
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; Pred. No. 45;
0; Mismatches
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77957._.79239
/note="assembly_fragment"
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-478E10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 66837 CTCGAAAAGGCTTATAAGGA 66818
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AC009253.16 GI:16798933
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Matches 20; Conservative
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                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160279)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-478E10 Unpublished
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      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Nov 8, 2001 this sequence version replaced g1:7264755.
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Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Striskas, T., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 2L, region 39A-39A
                                                                                                                                           Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciessiolka,L., Doyle,C.M., Farfani,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Mohrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sequeira,A., Sair,E., Sair,E., Sair,E., Mark,S., Pariskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="BACR24F17 (D1038)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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1. 160282
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/strain="y; cn bw sp"
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HTG; HTGS_PHASE1.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                        Jnpublished
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Dinh, H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Daraper, H., Dagan-Rocha, S., Durbin, K.J., Daraper, H., Dagan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Frantz, P., Gabisi, A., Gao, J., Ford, J., Poster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, M., Ginlar, Harris, F., Harris, C., Harris, C., Harris, Hart, M., Havlak, P., Hawes, A., Hamilton, K., Harris, C., Harris, C., Haber, J., Hulyk, S., Hame, J., Jackson, E., Jacobson, B., Jai, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Lucker, E., Martin, R., Martin, R., Martin, R., Lucker, J., Lut, M., Luus, R., Lut, M., Luus, R., Luus, R., Lut, J., Lut, M., Luuseged, H., Lozado, R.J., Lut, J., Lut, J., Lut, M., Luuse, R., Martin, R., Scherz, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Ruses, M., Rojas, A., Tabor, P., Tameris, R., Tameris, R., Taneris, R., Taneris, R., Taneris, R., Taneris, R., Wartin, R., Waltin, R., Martin, R., Waltin, R., Martin, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 163706)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
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Center clone name: CH230-9714

Center clone name: CH230-9714

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 116803 bases at least Q40
Consensus quality: 121625 bases at least Q30
Consensus quality: 125275 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Worley, K.C.
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Query Match 0.9%; Score 20; DB 2; Length 163706; Best Local Similarity 100.0%; Pred. No. 45; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

OY 1160 CCAAGGCCAACCGTGAGATG 1179
Db 136347 CCAAGGCCAACGTGAGATG 136366

Search completed: May 23, 2003, 08:42:14 Job time : 5892 secs

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Sequence 253, App Sequence 657, App Sequence 657, App Sequence 657, App Sequence 4511, Ap Sequence 1856, App Sequence 126, App Sequence 2414, App Sequence 2414, App Sequence 2414, App Sequence 25073, A Sequence 25073, A Sequence 855, App Sequence 855, App Sequence 857, App Sequence 857, App Sequence 65, App Sequence 29, App1 Sequence 26, App1 Sequence 100, App 2 US-10-044-090-253 US-10-046-915-657 US-09-918-178-657 US-09-923-876-4571 US-09-918-995-18569 US-09-918-995-18569 US-09-918-995-18569 US-09-918-995-3910 US-09-918-995-3910 US-09-918-995-3910 US-09-918-995-3928 US-09-919-590-8450 US-09-919-580-857 US-09-910-580-857 US-09-910-800A-857 US-09-983-152-26 US-09-452-599-166 US-09-974-300-4593 US-09-887-527-12 US-10-001-857-87  $\circ \circ \circ \circ$ 2139

## ALIGNMENTS

	H.	RESULT 1	E L
•	22	T-666-800-0T-SO	1-025
•	••	Sequence	Sequence 1, APPLICATION US/10008355
		Parent N	Patent No. USZUGIO14/39A1 EBNEDAT INFORMATION:
	• •	APPLICA	ADDITORNY: Travis. James
		APPLICANT:	THE POTENTY AND S
		APPLICA	
-	••	TITLE O	TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
	••	FILE RE	FILE REFERENCE: 235.00440101
	••	CURRENT	CURRENT APPLICATION NUMBER: US/10/008,355
	••	CURRENT	CURRENT FILING DATE: 2001-11-08
	••	PRIOR A	PRIOR APPLICATION NUMBER: US 60/246,827
	•	PRIOR F	PRIOR FILING DATE: 2000-11-08
	••	NUMBER	NUMBER OF SEQ ID NOS: 26
	••	SOFTWAR	SOFTWARE: Patentin version 3.0
	••	SEQ ID NO 1	0 1
	••	LENGTH: 2139	: 2139
	••	TYPE: DNA	DNA
	••	ORGANI	ORGANISM: Porphyromonas gingivalis
	30	T-558-800-01-80	355-1
i ,,		Query Match	tch 100.0%; Score 2139; DB 9; Length 2139;
1,1 A		Best Loc	Pred. No. U;
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Ap	Qy	, 61	GTAGCCAAAAGCCACAAAGGCATGTGGCTCCTCAACGAACTCAAGGAGAATCTGGAT 120
, A Ap	qa	61	GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT 120
A A	Å	121	081 30004404000000000000000000000000000000
An An	3		
A	qa	) 121	CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG 180
Ap 11i	Qy	7 181	TCCATTGCCAAIGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT 240
1. 1.	Ĉ		
77	ar T		TCCATTGCCAATGCCG1GG11ATC11CGG1GGCGGA1G1ACCGG1A1CACAG1G1CGGA1

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(without alignments) 14634.553 Million cell updates/sec 1 atgcaaatgaaattaaaaag.....aagagctgaagttgatctaa May 23, 2003, 07:01:32 ; Search time 193 Seconds 5.1.4\_p5\_4578 Compugen Ltd. Total number of hits satisfying chosen parameters: 828747 segs, 660231138 residues version: using sw model OLIGO\_NUC Gapop 60.0 , Gapext 60.0 GenCore Copyright (c) 1993 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-10-008-355-1 2139 nucleic search, 0 Title: Perfect score: Sequence: Scoring table: Word size : OM nucleic Searched: Run on:

Post-processing: Listing first 45 summaries

Published\_Applications\_NN:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NRW\_PUB.seq:\*
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
4: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
5: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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9: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
12: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
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12: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
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13: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
14: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
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17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli	Sequence 37887, A	Sequence 37842, A	Sequence 528, App	Sequence 10103, A	Sequence 7766, Ap	$\overline{}$	Sequence 9104, Ap		Sequence 5137, Ap	Sequence 11256, A	Sequence 12448, A	Sequence 6022, Ap	Seguence 14538, A	Sequence 1375, Ap	Sequence 3, Appli	1,	Sequence 5, Appli	Sequence 9, Appli
SUMMARIES	ID	US-10-008-355-1	US-09-918-995-37887	US-09-918-995-37842	US-09-954-456-528	US-09-960-352-10103	US-09-974-300-7766	US-09-960-352-12702	US-09-960-352-9104	US-09-960-352-10777	US-09-960-352-5137	US-09-960-352-11256	US-09-960-352-12448	US-09-864-761-6022	US-09-960-352-14538	US-09-918-995-1375	US-08-834-666A-3	US-08-834-666A-1	US-08-834-666A-5	US-09-919-497-9
	DB	. 6	σ	6	10	10	10	10	10	10	10	10	10	10	10	σ	8	8	8	10
	Query Match Length DB	2139	490	502	4163	203	252	355	408	410	417	418	427	466	479	499	2699	2798	2915	3995
æ	Query Match	100.0	6.0	6.0	6.0	0.8	0.8	0.8	0.8	0.8	0.8	0.8	9.0	0.8	0.8	0.8	0.8	0.8	0.8	0.8
	Score	2139	19	19	19	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
	Result No.		2	e	4	S	و ن	7	ω	σ	10	11	12	c 13	14	15	16	17	18	19

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AGCCAAAGCACG 300 	AAGGACTTCCG 360 	ACAAGGTAGAA 420 	AGGAGGTATGC 480 	TAGAGCCTTC 540 	STTCGTATGGTA 600 	GGATGTGGCCG 660                GGATGTGGCCG 660	AACCGGCCGGCC 720 		ACGGATCGCTAC 840 	CGTATCGAAGTT 900 	SGCTACCCGTATC 960 	VTCGGTATGAAC 1020 	GAGCATTCGCA 1080 	CTTCTCTCGAA 1140 	TTGAGCGAGACGTC 1200 	TTGGCTACAAATCCT 1260 	ACCTCCCTCG 1320 	ATCCCTGCCGAC 1380
TTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCAC 	GGTTTCGTTTCTCGCACGATGGGTGAG 	CTGGGCAAGATCGTGAAGGTAACGGACAAG 	3AGATGGAGCGTCTGCGCAAAGCTCAGG 	GGCCAAAAAAGAAATGCAGACGAGAACCAACTCTGCATA( 	ATCGTCTACGATGTATTCAAGGACGTTC 	CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATG' 	CACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCGACCAACCGGCCGG	GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCGTATCC 	CTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGC 	GTGGAAGATCGTATCGAAAACGAGAACAATCCTC 	AAGGAAGCCATGAGCGCAGATCAGG 	AAATATGCCAGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCC 	MTAGGTCGTAAGCGTGCCGAGGAAAGAC 	AGTGCTGTCTATGGCGATGTATTGTCTTC 	AAGGAAGGACCAAGCCAACCGTGAGATGACTTATTGA 	TTGCACAGTTTGCCAACGCA: 	CATGCCGGTATCCTCAAATGCTTGACGACAAGTACAAAGACTACCTCCCCTCC 	GCCCGCCATGCTCGATATTGTACGCCGGCGTA
CAGGCCTGATCTTTACCAACCAC 	GTGGATCACGACTATCTGCGCGATGGTTTCC 	ATTCCGGGTCTTTCCGTGAAGTATC 	GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGT( 	CAAGAACTGGCCAAAAAAGAAAT( 	TATTCCAACAACGAATACTTCCTCATCGTCTAGGAT(	TTTGCTCCTCCCAGCTCTGTAGGT)	CGTCACACGGGCGACTTCAGCGTA'	GAATACAGCAAGGACAATAAACCC' 	GGCTACAAGGCTGACGACTATGCC 	CTCACTTCTTGGGGTGTGGAGAT(	CGCGGTATCAAGCAAGCCATCTGGAAGGAAGCCATGAGCGCAGATCAG	AAATATGCCAGCAAGTATGCTCAG	CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAG	GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGG 	AAGGCTTATAAGGAAGGAGCCAAG( 	TTCGGTGGTACCGAGGTGGTTCGTT"	GATGCTCATGCCGGTATCCTCAAN [	CTCGACCGTAAGGTGCTGCCCGCC
Oy 241 Db 241	Qy 301 Db 301	Oy 361 Db 361	Qy 421 Db 421	Oy 481 Db 481	Qy 541 Db 541	Oy 601 Db 601	Oy 661 Db 661	Oy 721 Db 721	Oy 781 Db 781	Oy 841 Db 841	Qy 901 Db 901	Oy 961 Db 961	Oy 1021 Db 1021	Qy 1081 Db 1081	Qy 1141 Db 1141	Oy 1201 Db 1201	Qy 1261 Db 1261	0y 1321

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1321 CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGAC 1380
                                                                        1801 AAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGC 1860
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                                                                                                                                                                                                       1501 CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG 1560
                                                                                                                                                                                                                                                                             1561 CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC 1620
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Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2101 CAGTGCCCCGTCTCATCCAAGAGCTGAAGTTGATCTAA 2139
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                                                       1381
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APPLICANT: Tao, Wingling APPLICANT: Tao, Morbing C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REPERENCE: 16511.066/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10103
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Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka. Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PILICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-06
PRIOR APPLICATION NUMBER: 06/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bos taurus
CTHER INFORMATION: Clone ID: 43-LIB34-066-Q1-E1-C12
US-09-960-352-10103
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red. No. 24;
Mismatches 0;
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7;
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                 PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 19;
                        APPLICATION NUMBER: US/60/235,711
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10103, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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    FILING DATE: 2000-09-26
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 18; Conservative
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US-09-954-456-528
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US-09-960-352-10103
                                                                                                                                                                                                                                                                                                          TYPE: DNA
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TITLE OF INVENTION: Sets
TITLE OF INVENTION NUMBER: US/69/234,456
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
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; Sequence 37842, Application US/09918955
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICART: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 2041-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR RPLING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTESQ for Windows Version 3.0
; SEQ ID NO 37842
; LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 19; DB 9; Length 505; llarity 100.0%; Pred. No. 6.8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                        Length 490;
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                                                                                                                                                                                      Score 19;
Pred. No.
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Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
                                                                                                                                                                  0.9%; Scor.
100.0%; Pre
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37842
                                                                                       CCATION: (1) ... (490)
CTHER INFORMATION: n = A,T,C or US-09-918-995-37887
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                                                                                                                                                                                                                                                                                                        274 CAGGGCCTGATCTTTACCA 292
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Best Local Similarity 100.
Matches 19; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: NAME/KEY: misc_feature
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                                                                      NAME/KEY: misc_feature
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Matches 19; Conserv
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                                                FEATURE:
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## APPLICANT: Tao..., mesity.c.
### APPLICANT: Byat, John C.
### APPLICANT: Byat, John C.
### APPLICANT: Byat, John C.
### APPLICANT: Mathialagan, Nagapan
### TILLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
### TILLE OF INVENTION: MUSCLE AND FAT DEPOSITION
### FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
#### SEQ ID NO 10777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tao, Nengbing APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILE REPRENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5137
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COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: 46-LIB34-016-Q1-E1-D6
US-09-960-352-10777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-030-01-E1-F5
US-09-960-352-5137
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100.0%; Pred. No. 25;
1ve 0; Mismatches 0
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100.0%; Pred. No. 25;
ive 0; Mismatches 0
                                                                                                                                                           ; Sequence 10777, Application US/09960352
patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5137, Application US/09960352; Patent No. US20020137139A1
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100.0%; Pre
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100.0%; Pre
                        1160 CCAAGGCCAACCGTGAGA 1177
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                                                              384 CCAAGGCCAACCGTGAGA 401
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APPLICANT: Warren, Wesley C.
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Best Local Similarity 100.
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                         US-09-960-352-10777
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US-09-960-352-5137
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APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND PAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12702
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND STAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9104
LENGTH: 408
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 54-LIB34-010-Q1-E1-F10
US-09-960-352-12702
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100.0%; Pred. No. 25;
tive 0; Mismatches 0,
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100.0%; Pred. No. 25;
ive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7766
LENGTH: 252
                                                                                                                                                             Score 18;
Pred. No.
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100.0%; Pr.
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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Matches 18; Conservative
                                                                            ; TYPE: DNA
; ORGANISM: Bacillus clausi1
US-09-974-300-7766
                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 18; Conserv.
                                                                                                                                                                              Best Local Similarity
Matches 18; Conserv
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DB 10; Length 466;
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EXPRESSED IN ADULT LIVER, SIGNAL
EXPRESSED IN LUNG, SIGNAL = 1.8
EXPRESSED IN HELA, SIGNAL = 1.9
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FETAL LIVER, SIGNAL
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Pred. No. 25;
0; Mismatches
                                                      PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
   CURRENT APPLICATION NUMBER: US/09/864,761
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Patent No. US20020137139a1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                 GENERAL INCOMMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WOLCELE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB34-016-Q1-E1-D8
US-09-960-352-11256
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12448
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Pred. No.
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100.0%; Pred. No.
                            Sequence 11256, Application US/09960352 Patent No. US20020137139A1
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Matches 18; Conserv
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US-09-864-761-6022/c
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US-09-960-352-11256
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FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT PALICATION NUMBER: US/09/960,352
CURRENT PELLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14538
LENGTH: 479
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100.0%; Pred. No. 25;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1375, Application US/09918995
Publication No. US2003007362341
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR PILLING DATE: 1999-01-20
                                                                                                                                                                                                                            TYPE: DNA POSANISM: BOS LBURUS COTHER INFORMATION: CLONE ID: 62-LIB3058-022-01-K1-H6 US-09-960-352-14538
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SOFTWARE: FastSEQ for Windows Version 3.0
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NAME/KEY: misc_feature

LOCATION: (1)...(499)

OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1375
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Search completed: May 23, 2003, 09:58:00 Job time: 210 secs

327 GACTATGCCATGACCATC 344

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796 GACTATGCCATGACCATC 813

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	.ion 5.1.4_p5_4578 .03 Compugen Ltd.	el	<pre>Search time 328 Seconds (without alignments) 14686.050 Million cell updates/sec</pre>	aagagctgaagttgatctaa 2139		residues		rameters: 4370478		รอ	eneseq_101002:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*	DAT: DAT: DAT: DAT:	97/geneseqn-embl/NA1988.DAT:* 92/geneseqn-embl/NA1988.DAT:* eq/geneseqn-embl/NA1989.DAT:*	eq/yeussqurembl/NR1991.DAT:* eq/geneseqnrembl/NR1991.DAT:* eq/geneseqnrembl/NR1992.DAT:* eq/geneseqnrembl/NR1993.DAT:*	eq/geneseqn-embl/NA1994.DAT:*	eneseqn-embl/NA19 eneseqn-embl/NA19 eneseqn-embl/NA19	genesedn embl/NA19 genesedn-embl/NA29	genesedn embl/NA20 /genesedn-embl/NA20 /genesedn-embl/NA20 /genesedn-embl/NA20	of results predicted by chance to have a qual to the score of the result being printed,	score distributi	IKLES	Description		Drosophila melanog		Drosophila Drosophila	Drosophila
	GenCore version Copyright (c) 1993 - 2003	nucleic search, using sw model	May 23, 2003, 04:44:52 ;	US-10-008-355-1 2139 1 atgcaaatgaaattaaaaag	OLIGO_NUC Gapop 60.0 , Gapext 60.0	2185239 seqs, 1125999159	0	hits satisfying chosen parameters	length: 0 length: 200000000	: Listing first 45 summaries	N_Geneseq_101002:* 1: /SIDS2/gcgdata/genese 2: /SIDS2/gcgdata/genese	3: /SIDSZ/gcgdata/genese 4: /SIDSZ/gcgdata/genese 5: /SIDSZ/gcgdata/genese 6: /SIDSZ/gcgdata/genese 7: /SIDSZ/gcgdata/genese	8: /SIDSZ/gcgdata/genese 9: /SIDSZ/gcgdata/genese 10: /SIDSZ/gcgdata/genese	11: /JIDSZ/gcgdata/genesed/g 13: /SIDSZ/gcgdata/geneseg/g 13: /SIDSZ/gcgdata/geneseg/g 14: /SIDSZ/gcgdata/geneseg/g	15: /SIDS2/gcgdata/gene: 16: /SIDS2/gcgdata/gene:		` ' '	/SIDS2, /SIDS2, /SIDS2,	No. is the number of results greater than or equal to the	by analysis of the	SUMMARIES 8 Onerv	Match Length DB ID	2139 24	9 948 23	2252 23	0.9 2324 23 ABL27552 0.9 2916 23 ABL03838	.9 3006 23
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or periodontitis). The present DNA sequence encodes the Porphyromonas gingivalis (e.g., gingivitis dingivalis dipeptidase-7 (DPP-7) enzyme of the invention. of Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas ginglvalis 4; 65pp; English 2002-490075/52 P-PSDB; AA015205 Claim 11; Fig disease 

544 A; 543 C; 565 G; 487 T; 0 other; Sequence 2139 BP;

ö 180 180 240 300 300 360 360 420 120 120 420 480 480 099 9 9 Gaps 1 ATGCAAATGAAATTAAAAAGTATTCTTCTGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGAT CAGGGCCTGATCTTTACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAA CAAGAACTGGCCAAAAAAAAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTC GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCCAAAGCTCAGGAGGTATGC Length 2139; ö Indels DB 24; ; 0 100.0%; Score 2139; 100.0%; Pred. No. 0; ive 0; Mismatches Local Similarity 100 nes 2139; Conservative Query Match Matches 61 61 121 121 181 181 241 241 301 301 481 361 361 421 421 481 541 541 501 601 à 유 ò ŏ q a 9 9 g QQ g පු οχ à ò ò ò ò 8 ò

780 960 CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATC CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1741 TATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAG CGCGGTCTCGCTCGTCTTGACGTGATAGCTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAA AAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTC TTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCT GATGCTCATGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAAGACTACCTCCCCTCG TATGCAGACTTCGTATTCGACAAGAGTGTGTGCTTCCTTATAGCGAAGTTCCATGCCATG 1441 TATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATG CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG GGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGATCGCTAC CTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT CTTTCCAAGAGCGTAATAGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA CGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGA 1021 1321 1561 1081 1081 1141 1201 1261 1381 1381 1441 1621 661 781 901 196 1021 1141 1201 1261 1321 1501 1561 1681 721 721 781 841 901 196 661 QQ ò g ò g ò g δ q οy g ò Q ò g οy g ò q ò QQ οy g δ Q ò 8 ò g ò a ò g δ Dp à

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1861 ACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAAC 1920
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                                                                                                                                                                                                                                                                                             insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signalling and cell
                                                           AAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCTCTTCCGC
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11-JUL-2000; 2000US-0614150.
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell.signalling and cell-cell
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Mismatches 0; Indels
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                                                                   Length 315
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to nucleic acid sequences useful as probes AB067188 AB071219 from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of spee expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                    genomic sequences from Listeria species, useful for detection, atment and prevention of infection, also related polypeptides,
                                                                                                                Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          and pathogenicity of Listeria (potential therapeutic agents), alk treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1431 BP; 434 A; 278 C; 333 G; 386 T; 0 other;
                                                                                            Listeria monocytogenes 4b contig DNA sequence #279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19;
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                            ABQ70337 standard; DNA; 1431 BP.
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(CNRS ) CNRS CENT NAT RECH SCI
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antibodies and modulators
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                                                                                                                                                Listeria monocytogenes 4b
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                                                                                                                                                                                                                                                                                        Kunst F, Glaser P;
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                                                                                                                                                                    WO200228891-A2
                                                                                                                           infection; ds
                                                                     29-AUG-2002
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ABL27548
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ABQ70337
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA equences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 25;
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100.08; Pre-
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ID ABL27550 standard; DNA; 2315
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11-JUL-2000; 2000US-0614150.
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Drosophila melanogaster.
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Best Local Similarity
Matches 19; Conserv
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
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                                                                                  SEQ ID NO 34123; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                     0; Indels
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100.0%; Pred. No. 25;
iive 0; Mismatches
Myers EW;
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2000US-0614150.
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Best Local Similarity 100.
Matches 19; Conservative
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Adams M,
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                    WPI; 2001-656860/75
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Venter JC,
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                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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insecticides, therapeutics and pharmaceutical drugs. The invention
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Pred. No. 25;
Mismatches 0: ThAsl
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                         discloses genomic DNA sequences (ABL16176-ABL30511), exsequences (ABL01840-ABL16175) and the encoded proteins
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red. No. 25;
Mismatches 0;
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Matches 19; Conservative
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P-PSDB; ABB59735.
                                                   sequences (ABL01840 (ABB57737-ABB72072)
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Matches 19; Conserv
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ID ABL038
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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            Lung cancer related gene sequence SEQ ID NO:3555.
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2000US-234052P
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2000US-235077P.
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Weaver 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-188264/24.
                                                                                                                                                 WO200194629-A2
                                                                                                                      Homo sapiens
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Soppet DR,
                                                                                                                                                                                                                                           05-JUN-2000;
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                                                                                          gene; ds.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w1po.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 5876.
                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
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100.0%; Pred. No. 25;
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                                                                                                                   ABL03798 standard; cDNA; 3006 BP
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tive 0;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
P-PSDB; ABB59695.
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Best Local Similarity
Matches 19; Conserv
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                                                                                     RESULT 9
ABL03798/c
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Horrigan S;

RESULT 10 ABL65218

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agent to be tested for anti-neoplastic activity, determining a change in agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) a signature gone set, where (1) comprises a sequence (5) selected from 847 sequences (given in ABL50610), or is at least 95% identical to (5), where a change in expression is indicative of anti-neoplastic activity. (1) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer.

Coesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancinoma, neuroendocrine infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; growth factor; hematepoisesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; metolideration; metolide cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 19; DB 24; Length 4163;
100.0%; Pred. No. 25;
lve 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                              carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                 0.5c,
100.0%; Pre
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Liu C,
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ABA09031/c
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of faceting the novel polypeptides.

Or polypeptides in a sample, and methods of detecting the nucleotides and polypeptides of the invention at house of detecting the nucleotides of polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby alving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haventoned activities; stem cell growth factor activity; chamunomodulatory activity; tissue growth activity; chrombotic or chemokinetic activities; haemostatic, thrombotic or thrombotic activities; name activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of conditions, e.g., by protein or gene therappy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell activitiens of disorders), chromic in disorders (e.g., myeloid or lymphoid cell activitiens of alsorders) chromic hardens and an arthritis), or only ferst incorders become and an arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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Pred. No. 25;
0; Mismatches 0; Indels (
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                                                 Claim 1; Page 713-715; 1963pp; English.
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100.0%; Pre-
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ches 19; Conserv
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ID AAZ183
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\overset{\mathsf{N}}{\otimes} \overset{\mathsf{N}}{\otimes
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95US-0487429.
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   ASTH1 protein, for e.g. s
or function of ASTH1 prot
predisposition to asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
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21-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 -OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
  ASTH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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   δ
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                                                                                                                                                         The invention identifies a genetic locus ASTH1, associated with asthma, mapped to human chromosome 11p. ASTH11 and ASTH13 are genes present within the locus, located close to each other on human chromosome 11p, and have similar patterns of expression, and common sequence motifs. The ASTH1 genes and fragments, encoded protein, genomic regulatory regions and arti-ASTH1 antibodies are useful in the identification of individuals predshosed to development of asthma, and for the modulation of gene activity in vivo for prophylactic and therapeutic purposes. The ASTH1 protein is useful as an immunogen to raise specific antibodies, in drug screening for compositions that minic or modulate ASTH1 activity or expression, including altered forms of ASTH1 protein, and as a therapeutic. The present sequence represents a human ASTH1 genomic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids other than naturally occurring chromosomes encoding
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                      Sequence 72928 BP; 20042 A; 15100 C; 16036 G; 21750 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                             Length 72928;
                                                                                                     Mammalian asthma related genes, useful for diagnosis of a predisposition to development of asthma
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buckler A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTH1 locus; ASTH1J; human; chromosome 11p; asthma;
                                               Carey AH;
                                                                                                                                                                                                                                                                                                                                            DB 20;
27;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cardon L,
                                              Cardon L,
                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 19;
Best Local Similarity 100.0%; Pred. No.
Matches 19; Conservative 0; Mismatch
                                                                                                                                      Claim 15; Page 75-96; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA80253 standard; DNA; 72928 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ASTHlJ 5' genomic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      North M,
                                              Brooks-Wilson AR, Buckler A,
Galvin M, Miller A, North M;
                                                                                                                                                                                                                                                                                                                                                                                                      Db 42822 CCATTGAGAAGGCCAAGCG 42804
                                                                                                                                                                                                                                                                                                                                                                                         1625 CCATTGAGAAGGGCAAGCG 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brooks-Wilson AR, Carey AH;
 98WO-US01260
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97US-0051432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AXYS-) AXYS PHARM INC.
                      (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller A,
                                                                              WPI; 1999-479058/40.
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21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6087485-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galvin M,
                                                                                                                                                                                                                                                                                                   seduence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA80253;
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The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH1 and ASTH1 genes, which are associated with a genetic predisposition to asthma and bronchial hyperreactivity. The ASTH1 and ASTH11 and ASTH13 genes are oriented in opposite directions with the ASTH1 locus, and have similar patterns of expression and common sequence motifs. They are both expressed in trachea, lung and several other trasues. ASTH11 and ASTH13 are novel members of the ets family of transcription factors, which have been implicated in the activation of a variety of genes including the TCR gene and cytokine genes known to be important in the actiology of asthma. CC gene and cytokine genes known to be important in the actiology of asthma. Splicing of transcripts has no effect on the open reading frame of ASTH13, as the exons involved are all 5 to the start codon in exon b. In contrast, alternative splicing of ASTH1 transcripts results in 3 different ASTH1 isoforms. The invention also encompasses mouse asth13 crocliarly predisposition to asthma, as probes for identifying ASTH1 crelated genes, for identifying expression of the gene in a biological cypectime, and for generating genetically modified non-human animals or site specific gene modifications in cell lines. The encoded ASTH1 confoculation as a mannoses to raise specific antibodies; in drug correction as a mannoses of frame of the expression of ASTH11 and/or ASTH11 and/or ASTH11 and/or asthat main or modilate activity or expression as a theory as a theory or asthat main or modilate activity or expression or ASTH11 and/or ASTH11 and/or asthat main or modilate activity or expression as a theory as a theory or asthat main or modilate activity or expression as a theory or as the asthat and activity or expression as a theory or asthat main or as an an activity or asthat and as a probation as a probation as a mannosition and activity or expression as a theory or asthat as a probation and for general and activity or expression as a theory 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic. The ASTH1 genes or fragments thereof, encoded proteins
for e.g. screening compositions that modulate expression ASTH1 proteins or as diagnostics for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72928 BP; 20041 A; 15101 C; 16036 G; 21750 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae complete genome sequence.
                                                                                                                                                                                                                                               Claim 7; Column 49-112; 131pp; English.
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White 0;

Smith HO, Venter JC,

Fleischmann RD,

Adams MD,

WPI; 1996-485782/48.

(HUMA-) HUMAN GENOME SCI INC.

SNING OLYU ( OLYU)

95US-0476102.

07-JUN-1995;

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This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence in a computer readable form, it is possible to identify genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFs can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                                                                                                                Haemophilus influenzae Rd genome recorded on computer readable medium – useful for identifying commercially important nucleic acid fragments by homology searching
                                                                                                                                                                                                                                                                                          Claim 1; Page 77.2-77.1091; 1291pp; English.
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ö Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other; Gaps 0.9%; Score 19; DB 17; Length 1830121; ilarity 100.0%; Pred. No. 29; Conservative 0; Mismatches 0; Indels 0; Local Similarity es 19; Conserv Query Match Matches

1138 GAAAAGGCTTATAAGGAAG 1156 ò

ABN69869 standard; DNA; 228 (first entry) 01-JUL-2002 ABN69869; RESULT 15 

Streptococcus polynucleotide SEQ ID NO 7651.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

Streptococcus pyogenes

WO200234771-A2

02-MAY-2002.

29-OCT-2001; 2001WO-GB04789.

27-OCT-2000; 2000GB-0026333. 24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001GB-0005640.

(GENO-) INST GENOMIC RES. (CHIR-) CHIRON SPA

Grandi G, Masignani V, Margarit Ros YI, Pettelin H; relford J,

Fraser C;

WPI; 2002-352536/38. P-PSDB; ABP29238.

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5813 sequences (51), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABN6604.ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus mappe. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein
                                                                                                                                                                                                                                                      Claim 7; Page 3903; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus proteins.
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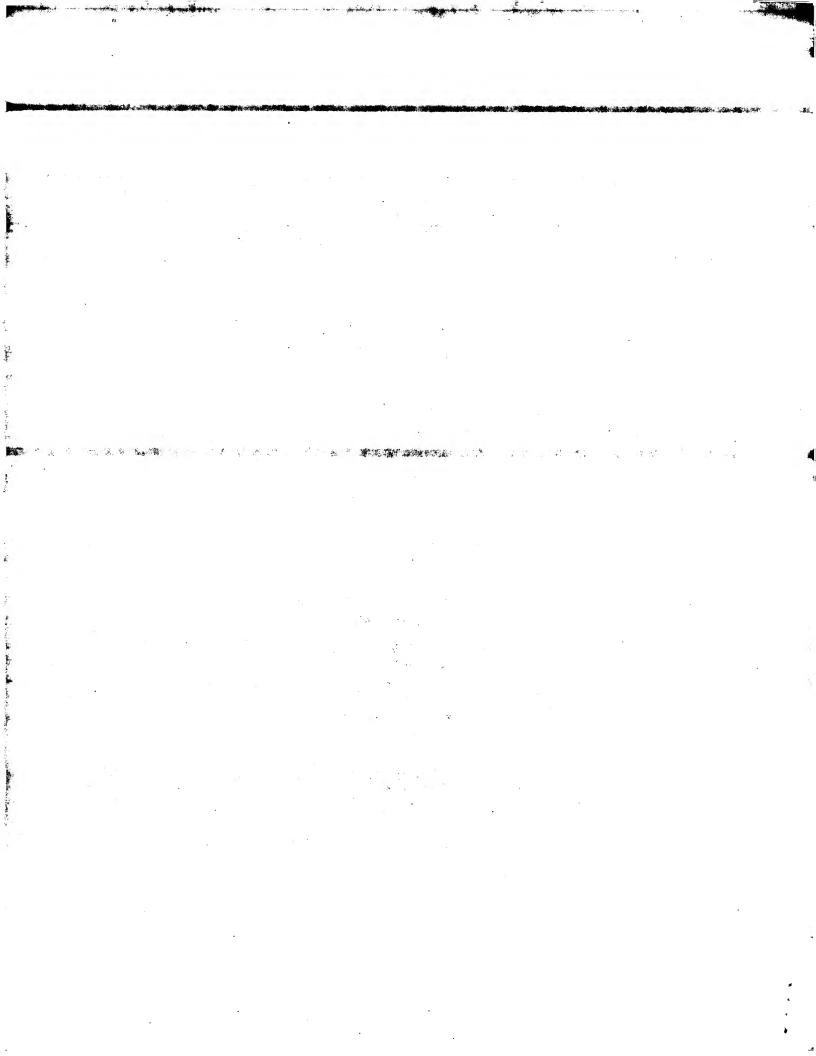
Sequence 228 BP; 85 A; 23 C; 46 G; 74 T; 0 other;

Gaps .. 0 Score 18; DB 24; Length 228; Pred. No. 80; Indels ;; 100.0%; Prec. .... 0.88; Best Local Similarity 100. Matches 18; Conservative Query Match

;; 0

7 ATGAAATTAAAAAGTATT 24 4 ATGAAATTAAAAAGTATT 21 Db ò

completed: May 23, 2003, 07:31:39 ne : 2006 secs Job time Search



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> US-09-134-001C-1336 US-08-480-6048-25 US-08-405-496A-25 US-08-915-136-25 US-08-740-223A-21 US-09-709-188-21 US-08-286-872-5 US-08-328-322-18 US-09-709-188-23 US-08-201-118-8 US-08-238-821B-8 PCT-US95-05744-8 US-08-328-322-9 rrrrrrrrrrrrrrrr 00000000000000000 110 110 110 110 110 110 110 (without alignments) 10580.348 Million cell updates/sec US-10-008<sup>-</sup>355-1 2139 1 atgcaaatgaaattaaaaag......aagagctgaagttgatctaa 2139 May 23, 2003, 05:20:28 ; Search time 62 Seconds GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model OLIGO\_NUC . Gapext 60.0

## ALIGNMENTS

8, Appli 8, Appli 8, Appli 9, Appli

Sequence 5, Apsequence 18, Apsequence 8, Apsequence 8, Apsequence 8, Apsequence 8, Apsequence 9, Aps

Sequence Seq

FENERAL INFORMATION: A TO TOTAL OF THE REPERT OF INVENTION: Bruce C. TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF CORRESPONDENCE ADDRESSE: ADDRESSER. COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA: 27340-20021.00 IMBER: US/09/221,017B 23-DEC-1998 APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION: Sequence 726, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION: ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto 32,430 REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600 TELEX: 706141 INFORMATION FOR SEQ ID NO: 726: SEQUENCE CHARACTERISTICS: PP2911 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP291
FTLING DATE: 09-APR-1998 IBM Compatible LENGTH: 1974 base pairs TYPE: nucleic acid STRANDEDNESS: double NAME: Monroy, Gladys H REGISTRATION NUMBER: 33 COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 650-494-0792 PRIOR APPLICATION DATA: APPLICATION NUMBER: CLASSIFICATION: FILING DATE: US-09-221-017B-726 TELEPHONE: TELEFAX: TELEX: 70

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

0

Word size :

Searched:

441362 segs, 153338381 residues

Perfect score: Sequence:

Run on:

Scoring table:

/cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\* Issued\_Patents\_NA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result	t Soore	Query	1000	9	Ć.	1
	-	Marci		: : B	TT.	pescription
	1 1500	70.1	1974	4	US-09-221-017B-726	Sequence 726, App
	2 92	4.3	561	4	US-09-221-017B-12	
υ	3 19	6.0	72928	m	US-09-009-913-1	٦,
	4 18	0.8	1317	4	US-09-221-017B-382	
	5 18	0.8	4403765	4	US-09-103-840A-2	2, 1
	6 18	0.8	4411529	4	US-09-103-840A-1	٦,
	7 17	0.8	861	~	US-08-743-637B-166	.99
	8 17	0.8	861	m	US-08-526-840B-166	166,
	9 17	9.0	1958	4	US-09-570-454-1	1, 4
c 1	10 17	8.0	2352	4	US-08-997-251-3	m
7	11 17	0.8	2692	<del>, , i</del>	US-07-932-454A-2	7
1	.2 17	8.0	2822	7	US-08-679-405-1	1,
-	3 17	9.0	2822	~	US-08-842-799-1	1,
1	4 17	0.8	2822	ស	PCT-US96-11458-1	1,
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c 1	1	0.7	20	7	US-08-832-468-5	'n
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	18 16	0.7	313	4	US-09-169-119-1	1,
1	-	0.7	360	4	US-09-060-756-211	211
	7	0.7	592	4	US-09-385-982-126	126,
0	7	0.7	615	4	US-08-998-416-1063	1063,
	-	0.7	652	4	US-09-328-111-161	161, 4
	16	. 0.7	705	4	US-08-998-416-1059	1059,
7	4 1	0.7	735	4	US-09-535-008-32	32, Ap
7	5 1	•	1063	4	US-09-077-675A-1	Ţ,
7	6 1	0.7	1322	4	US-09-446-821A-2	2,
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JIY: Palo Alto
STATE: CA
COUNTRY: IICT
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                                                                                  Score 1500;
Pred. No. 0;
                                 GINGIVALIS
DNA (genomic)
NO
                                                                                 70.1%;
99.8%;
                       ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS
                                                NAME/KEY: misc_feature
LOCATION: 1...1974
                                                                                           Best Local Similarity 99.8 Matches 1730; Conservative
                UNKNOWN
MOLECULE TYPE:
HYPOTHETICAL:
                                                                 US-09-221-017B-726
                ANTI-SENSE:
                                                                                   Query Match
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TITLE OF INVENTION: P. GINGIVALIS
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
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APPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
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Best Local Similarity 100.0%; P.
Matches 19; Conservative 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: SI
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-327-3231
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
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                                                                                                                                                                                                                                                                                                           21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGET: INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 72928 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                  ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ZIP: 94304-1018
  Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 561,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.3%; Score 92; DB 4; 99.3%; Pred. No. 1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27340-20021.00
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Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       PARCE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                    UMBER: US/09/221,017B
23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CGAATGCGTGAGCTCGGCTTTAC 143
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TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1...561
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Best Local Similarity 99.3
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN
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TELEFAX: bou
TELEFAX: 706141
                                                                                                                                                                                                FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-221-017B-12
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US-09-009-913-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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Gaps

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SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                            APPLICANT: WHITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION UNDBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 4; Length 4411529;
Pred. No. 13;
Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414),277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 EAST WISCONSIN AVENUE CITY: MILWAUKEE STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11.5EP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 166, Application US/08743637B Patent No. 5994066 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELETTE, MATC
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPEC
TITLE OF INVENTION: DROBES AND A
TITLE OF INVENTION: IDENTIFY COM
TITLE OF INVENTION: ANTIBIOTIC R
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSE: QUARLESS:
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Matches 18; Conservative C
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ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (414)277-5591 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-743-637B-166
RESULT 6
JS-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: HITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DMA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: DMA SEQUENCES.
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PATCHIN VOT: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 18; DB 4; Length 1317; 100.0%; Pred. No. 13;
                FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INPORMATION:
NAME: MONLOY, Gladys 132,430
REGISTRATION NUMBER: 32,430
REFERENCE/POCKET UNBER: 27340-20021.00
TELECOMMUNICATION: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                            TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1325 ACCGTAAGGTGCTGCCCG 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature
; LOCATION: 1...1317
US-09-221-017B-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 18; Conserv
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LENGTH: 4403765
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US-09-103-840A-2
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Gaps
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GENERAL INFORMATION:

APPLICANT: Department of Veterans Affairs

APPLICANT: Department of Veterans Affairs

APPLICANT: Department of Veterans Affairs

TITLE OF INVENTION: factor releted protein

FILE REFERENCE: 107999.00106

CURRENT APPLICATION NUMBER: US/09/570,454

CURRENT APPLICATION NUMBER: 60/134,200

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
AITLE OF INVENTION: PLANT REGULATORY PROTEINS III
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Boulevard
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO AU96/00383
FILING DATE: 21-UNN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN6470/95
FILING DATE: 09-NOV-1995
PRIOR APPLICATION NUMBER: AU PN3779/95
FILING DATE: 23-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17;
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100.0%; Pre
0;
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Patent No. 6271440
                 RESULT 9
US-09-570-454-1/c
Sequence 1, Application US/09570454
; Patent No. 6399743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1255 CCAATGCCTATGCCATT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1613 CCAATGCCTATGCCATT 1629
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA; ORGANISM: Rattus norvegicus US-09-570-454-1
                                                                                                                                                                                                                                                                                                             Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winner, Ellen P.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-997-251-3/c
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1958
                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BERGERON, Michel G.
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: NOY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFFACATION PRIMERS TO RAPPLLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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                                                                                                                                                                                                         Gaps
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                                                                                                                                                               Length 861;
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                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                           Score 17; DB 2;
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 17; DB
100.0%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: BAKER, Jean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                    RESULT 8
8-208-526-840B-166
5 Sequence 166, Application US/08526840B
7 Patent No. 6001564
                                                                                                                                              0.8%; Scc.
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-500
TELEPAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-526-840B-166
                                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-743-637B-166
                                                                                                                                                                                                                                                                      466 GCCCTGCTGTTGGGTGC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 GCCCTGCTGTTGGGTGC 482
          LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                           Query Match 0.8 Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                                                                                                                37 GCCCTGCTGTTGGGTGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
SEQUENCE CHARACTERISTICS
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Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Milwaukee
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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ADDRESSEE: No. 58663930 No. 5866393disk of No. 5866393th America, Inc. STREET: 405 Lexington Avenue, Suite 6400 CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                GEMERAL INFORMATION:
APPLICANT: Fuglsang, Claus
APPLICANT: Halkier, Torben
APPLICANT: Oxenboll, Karen M.
APPLICANT: Oxenboll, Karen M.
APPLICANT: Cherry, Joel
TITLE OF INVENTION: Haloperoxidases from Curvularia
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2822;
                         Length 2692,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER EAAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
COMPUTER: TEW PC - DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/679,405
FILING DATE: Ully 9, 1996
CLASSIFICATION NUMBER: US/08/679,405
FILING DATE: July 14, 1995
PRICK APPLICATION NUMBER: 08/603,534
FILING DATE: July 14, 1995
PRICK APPLICATION NUMBER: 08/603,534
FILING DATE: February 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECOMMUNICATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 17; DB 2;
00.0%; Pred. No. 46;
.ve 0; Mismatches
                                                   Pred. No. 46;
Mismatches
                            Score 17;
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100.0%; Pre-
                            0.8°,
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                            1394 TATTCAAGAATGTAATC 1410
                                                                                                                                                      1809 TATTCAAGAATGTAATC 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                         Query Match 0.8%
Best Local Similarity 100.C
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GCAAATGAAATTAAAAA 19
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New COUNTRY: U. ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-679-405-1
                                                                                                                                                                                                                                                   RESULT 12
US-08-679-405-1
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APPLICANT: GUTHRIE, ELLEN P.

TITLE OF INVENTION:

TITLE OF INVENTION:

THE SAME

NUMBER OF SEQUENCE:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             ö
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OTHER INFORMATION: Anote= "METHYLASE GENE STARTS AT
OTHER INFORMATION: POSITION 703/ENDS AT 1653. RESTRICTION
OTHER INFORMATION: ENDONUCLEASE STARTS AT POSITION 1703/ENDS AT 2410"
                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                            DB 4; Length 2352;
45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHWAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,454A
FILING DATE: 19920820
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLLAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: 42078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-3400
TELEFX: 200291 STRE UR
INFORMATION FOO 2:
SEQUENCE CARRACTERISTICS:
LENGTH: 2692 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
STRANDENESS: Gouble
FATURE:
FATURE:
COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         Ouery Match 0.8%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 45; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07932454A Patent No. 5262318
                    LENGTH: 2352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: OFFER SELVA
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
1703..2410
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396..2054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-932-454A-2/C
                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-997-251-3
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US-07-932-454A-2
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Sequence 1, Application US/08614770A
Fatent No. 5773267
GENERAL INFORMATION:
APPLICATE WILLIAM S. JACOBS AND GRAHAM F. HATFULL,
TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11458 FILING DATE: 9-JUL-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 17; DB 5;
100.0%; Pred. No. 46;
                                       E: Novo Nordisk of North America, 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,194
FILING DATE: 14-JUL-1995
PRIOR APPLICATION NUMBER: 08/603,534
APPLICATION NUMBER: 08/603,534
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4441.204-WO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                   COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2629 GCAAATGAAATTAAAAA 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2822 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GCAAATGAAATTAAAAA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477..2276
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                         STATE: New York COUNTRY: U.S.A. ZIP: 10174
                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
; LOCATION: 477
PCT-US96-11458-1
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                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                           3: No. 59654180 No. 5965418disk of No. 5965418th America, Inc. 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haloperoxidases from Curvularia
Verruculosa and Nucleic Acids Encoding Same
                                                                                                                                                                                                             Haloperoxidases from Curvularia
Verruculosa and Nucleic Acids Encoding Same
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17; DB 2; Length 2822;
Pred. No. 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

SOFTWARE: Patentin RC-DoS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/842,799

FLING DATE: 16-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,405

FLING DATE: July 9, 1996

APPLICATION NUMBER: 60/001,194

FLING DATE: July 14, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/603,534

FLING DATE: FEDITARY 21, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 34,411.210.US

TELEPHONE: (212) 867-0123

TELEPHONE: (212) 867-0123

TELEPRATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORPUSADE: COMPUSADE: COMPUSADE: COMPUSADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9611458 GENERAL INFORMATION:
                                     Sequence 1, Application US/08842799 Patent No. 5965418 GENERAL INFORMATION:
                                                                                               APPLICANT: Fuglsang, Claus
APPLICANT: Halkier, Torben
APPLICANT: Oxenboll, Karen M.
APPLICANT: Cherry, Joel
APPLICANT: Cherry, Joel
TITLE OF INVENTION: Haloperoxid
TITLE OF INVENTION: Verruculosa
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.8%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2629 GCAAATGAAATTAAAAA 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2822 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GCAAATGAAATTAAAAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-842-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-11458-1
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                US-08-842-799-1
                                                                                                                                                                                                                                                                                                                                                                              STATE:
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Length 2822;

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Query Match 0.8%; Score 17; DB 1; Length 49272; Best Local Similarity 100.0%; Pred. No. 47; Matches 17; Conservative 0; Mismatches 0; Indels (
HELING DATE: MARCH 7, 1996
ATTORNEY FAGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REPRENENCE/COCKET NUMBER: 96700/402
TELEPAN: (212) 697-5995
TELEPAN: (212) 697-5995
TELEPAN: (212) 286-082
TELEPAN: (212) 286-081
TELEPAN: (212) 897-595
TELEPAN: (212) 897-59
TELEPAN:
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Search completed: May 23, 2003, 10:27:15 Job time : 6285 secs

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Sun May 25 15:40:22 2003

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20 0.9 260 12 20 0.9 410 10 20 0.9 419 12 20 0.9 463 14 20 0.9 463 14	12 20 0.9 473 12 BF654963 13 20 0.9 509 9 AI718392 14 20 0.9 519 12 BE809994 15 20 0.9 523 13 BI847597 16 20 0.9 531 13 BJ080132	20 0.9 547 10 AW653212 20 0.9 568 17 CNSO7HUQ 20 0.9 570 9 AA582263 20 0.9 668 13 BJ043920	20 0.9 787 13 BM029390 20 0.9 988 13 BM321169 19 0.9 313 14 D68316	24 19 0.9 334 10 AW597013 25 19 0.9 352 17 AQ057720 26 10 0.9 569 11 HE0551	19 0.9 350 14 108301 19 0.9 360 14 088463	28 19 0.9 360 14 D09803 29 19 0.9 368 14 B0301839 30 19 0 368 14 B0317843	19 0.9 369 17 BH807962 19 0.9 376 10 BB809399	19 0.9 402 9 AANDESBUI 19 0.9 414 17 AZS41761 10 0.0 410 14 DEFOND	25 19 0.9 418 14 N.30128 N.30128 V.3104903.17 1	19 0.9 587 19 0.9 599	ALIGNMENTS	z	ACCESSION AQ820052 VERSION AQ820052.1 GI:5782445 KEYWORDS GS:	_	RS Mahairas, G.G., Wallace, J.C., Smith, K., Keller, A., Shaker, R., Furlong, J., Young Hood, L.	TITLE Sequence-tagged connectors: A sequence approach to mapping scanning the human genome JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)		
GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.	using sw model 05:02:37 ; Search time 2048 Seconds (without alignments) 16915.110 Million cell updates/sec	.taaaaagaagagctgaagttgatctaa 2139	Gapext 60.0	8097743376 residues		satisfying chosen parameters: 32308132	00	45 summaries				* * *	< * * * *	*:.**	results predito to the score	Of the total score SUMMARIES	3 ID Description	17     AQ820052       9     AI928924       17     AG084100       13     BM55331       10     AW200173       10     AW200173       10     AW881153       2     AW881153       3     AW881153       4     AW881153
Ger Copyright (c)	OM nucleic - nucleic search, us. Run on: May 23, 2003, 01	Title: US-10-008-355-1 Perfect score: 2139 Sequence: 1 atgcaaatgaaattaaaag	table: OLIGO_NUC Gapop 60.0 , Ga	Searched: 16154066 seqs,	size: 0	number of hits satisfying	DB seq length: 0 DB seq length: 200000000	Post-processing: Listing first	Database : EST:*  1: em_estba:* 2: em_esthum:* 3: em_estlin:* 4: em_estmu:* 5: em_estpu:* 6: em_estpu:* 7: em_estpu:*	υσ 			20: em_9ss_Pin: 3 21: em_gss_vrt:* 22: em_gss_fun:* 23: em_gss_fun:*		, th		Query Score Match Length DB	21 1.0 444 1 21 1.0 591 9 21 1.0 800 1 20 0.9 223 1 20 0.9 257 1

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/note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1928924 Schneider fetal brain 00004 Homo sapiens CDNa clone IMAGE:2518932 5' similar to 9b:X63432_cds1 ACTIN, CYTOPLASMIC 1
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 591)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
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/tissum.cue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/note="Organ: brain: Vector: pBluescript SK (Stratagene);
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 846 row: O column: 19
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 444.
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40RP from Gibco
High quality sequence stop: 329.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 17; Length 444; pred. No. 20; Mismatches 0; Indels
                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="Plate=846 Col=19 Row=0"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:5606"
/clone="InA62:2518932"
/clone_lib="Schneider fetal brain 00004"
                                                                                                                                                                                                                                        /organism="Homo sapiens"
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Best Local 9
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JOURNAL
COMMENT
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AUTHORS
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Eujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totocki,Y., Watanabe,H. and Sakaki,Y.
Totocki,Y., Watanabe,H. and Sakaki,Y.
Totocki,Y., Watanabe,H. and Sakaki,Y.
Totocki,Y., Watanabe,H. and Sakaki,Y.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
I-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                   Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-081L22.R.
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0
                                                                                                                                                  The library was
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                                                                                                   and 3' adaptor sequence:
5'-GAGAGAGACTCGACTTTTTTTTTTTTTTTTT.3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Librar was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy). " lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="mais"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
?14 c 148 q 254 t
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100.0%; Pred. No. 22;
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
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R.Site 1 : SacI
R.Site 2 : SacI.
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Matches 21; Conservative
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AG084100
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ACCESSION

RESULT 4

οy QQ LOCUS

VERSION KEYWORDS

REFERENCE

COMMENT

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wacterbou, K. and wilson, K.
WashU Xenopus EST project, 1999
Unpublished (1999)
Other_ESTs: da12e08.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway. Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library constructed by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
Seq primer: -40RP from Gibco
High quality sequence stop: 125.
Location/Qualifiers
Irree
Location/Qualifiers
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/Lissue_Irpe="Tooyte (stages 5 and 6)"

/Lissue_Irpe="Tooyte (stages 5 and 6)"

/Listue_Irpe="Tooyte 6"

/
                                                                                                Xenopodinae; Xenopus.
1 (bases 1 to 223)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW881153 23-MAY-20
QVO-OT0033-170400-197-c10 OT0033 Homo sapiens cDNA, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collection (XGC) library."
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AW881153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Bukaryota: Metzoos; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1061)

NHF-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs.remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAML2761 row: o column: 11
High quality sequence stop: 682.
Location/Qualifiers
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Pred. No. 24;
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   Mismatches
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/clone_lib="NIH_MGC_119"
/tissue_type="medulia"
/lab_host="DH108"
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                                                                                                575 GAATACTTCCTCATCGTCTAC 595
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                                                             553 GAATACTTCCTCATCGTCTAC 573
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Matches 21; Conservative
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Matches
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FEATURES

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1. 260
//do_xanian="Sorghum bicolor"
//db_xref="taxon:4558"
//clone_lib="Embryo l (EM1)"
//clone_lorgan: Embryos germinated for 24 hr; Vector:
//polescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis
Eukaryota: Metazoa Chordata: Craniata: Vertebrata; Euteleostomi;
Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidea: Pipidae;
Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidea: Pipidae;
Aenopodinae: Xenopus.
1 (bases 1 to 410)
Clifton.S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Thelsing, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Willson, R.
                           Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 27-JUN-2001
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Library constructed by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -40UP from Gibco
High quality sequence stop: 286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dal2e08.xl Xenopus laevis occyte Xenopus laevis cDNA clone
XENOPUS_SOURCE_ID:xlnoc003o15 3' similar to SW:CLN3_CANFA Q29611
CLN3_PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1800
Fax: 314 286 1810
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/db_xref="texorn:8355"
/clone="xeNoPUS_SOURCE_ID:xlnoc003015"
/clone_lib="Xenopus laevis oocyte"
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100.0%; Pred. No.
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High quality sequence stop: 116
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100.0%; Pre
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                                                                                                                                     Seq primer: JEN REV
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  Fax: 706 583 0210
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AW199497/c
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/db_xref="taxon:9606"
/clone_lib="corous3"
/dev_stage="Adult"
/note="Organ: ovary; Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

86 a 30 c 57 g 84 t
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-OT0033-170 Seq primer: puc 18 forward
                         1 (bases 1 to 257)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deolivein,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG158262 260 bp mRNA linear EST 08-NEML_9_F06.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
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Reid.S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
An EST database from Sorghum: developing embryos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                      sequence tags
Proc. Ntl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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100.0%; Pred. No. 61;
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BG158262.1 GI:12691912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +55-11-2707001
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                                                                                                                                                                                     Simpson, A.J.
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Query Match Best Local

Matches

BASE COUNT

ORIGIN

BG158262/c DEFINITION

RESULT

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ACCESSION

VERSION KEYWORDS SOURCE

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EST 22-MAY-2002
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cllivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ed0058F03r"
/clone_lib="GASSypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
       /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                                                                                                                                                                                                            Gaps
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                            Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

1.47 c 118 g 78 t
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta: Magnoliophyta; eudicotyledon;; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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68;
                                                                                                                                                               DB 12; Length 419;
67;
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Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 1; Pred. No. 68; 0; Mismatches
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
Total High Quality bases = 447
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                    Pred. No.
                                                                                                                                                               0.9%; Score 20;
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High quality sequence stop: 464
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Conservative 0;
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144 c 6
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BQ412487.1 GI:21100174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="AKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Sasas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
,G.L., Heaton, M.P., Lagereid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
/tissue_type="oocyte (stages 5 and 6)"
/lab_host="rop-10 F'"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
%hol; cDNA was prepared from 2ug of poly A+ RNA.
BCORI **Ahol cut CDNA was then ligated into Unizap-xR
(Stratagene) with EcoRI at the 5' end and Xhol at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
                                                                                                                                                                             to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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0.9%; Score 20; DB 10; Length 410;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 20; Conservative 0; Mismatches 0; Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                     Collection (XGC) library.
101 c 112 g 76
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/db_xref="taxon:9913"
/clone_lib="MARC_2BOV"
/issue_type="pooled"
/lab_host="DH10B"
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PCR PRimers
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Contact: Smith TPL
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1 (base 1 to 473)

Smith.T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Neckown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                                                          Gossypium arboreum:

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

I (bases 1 to 472)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 25-APR-2001
GA_Ed0058F03f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ed0058F03f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:29729"
/clone="GA_Ed0058F03f"
/clone=lib="GASSPpium arboreum 7-10 dpa fiber library"
/clone_lib="GGSSSpium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. col1"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
80 c 131 g 124 t
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100.0%; Pred. No. 68;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                           Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Clemson University
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Total High Quality bases = 216
Seg primer: TAATACGACTCACTAATAGGG
High quality sequence start: 3
High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="8400"
                                           BQ403470
BQ403470.1 GI:21091157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1489 TTCCATGCCATGCTCAAGTC 1508
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BF654963.1 GI:11920095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="AKA
                                                                                                             Gossypium arboreum
                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100. Matches 20; Conservative
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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KEYWORDS
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ORGANISM
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ORIGIN
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BF654963
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MEDLINE
                                           ACCESSION
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal a 175 c 125 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 50%). Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,M., Wylie,T., Wylie,T., Waterston,R. and Wilson,R. Theising,B., Washi. V. Imman, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 220.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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IMAGE:2333050 3' similar to SW:Y281_HUMAN Q92556 HYPOTHETICAL
PROTEIN KIAA0281 ;, mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 473
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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68;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 bp
                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 74 row: G column: 8
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1. .473
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100.0%;
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 TCTTCTCGGAGCAGCCTGC
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Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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Length 519;

EST 04-0CT-2001

bovine cDNA

us-10-008-355-1.oli.rst

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
vv0.980904 e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 523)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasas, E., Way, J.E., White, J., Cho, J., Pahrenkrung, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized be libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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469747 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BI847597
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Fax: 402 762 4390
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0
                                        DB 12;
70;
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70;
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                                                                              Mismatches
                                        0.9%; Score 20; 00.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
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1..523
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Job time : 2065 secs
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BACKWARD: GTTTTCCCAGTCACGACG
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100.08; Pre-
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                                                                                                                                       95 TCTTCTCGGAGCAGCCCTGC 114
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Best Local Similarity 100.0
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
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                                                                              Conservative
                                                          Best_Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21180013
                                            Query Match
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                                                                                                                                                                                                                RESULT 15
BI847597
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                                                Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Bovinae; Bos.
1 (bases 1 to 519)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                             Length 509;
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 456
Fax: 402 762 4390
/clone_lib="Barstead colon HPLRB7"
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                             Score 20; DB 9;
Pred. No. 69;
                                                                                                                                                                                                                                                      132 t
                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No.
                                      /dev_stage="adult, age 25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Location/Qualifiers
1. .519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 75 row: D column: 10
                                                                                                                                                                                                                                                    140 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 g
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Matches 20; Conservative
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ACCESSION
VERSION
KEYWORDS
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ORIGIN
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/note="Vector: pcMv SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium.

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GenCore version 5.1.4_p5_4578  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - protein search, using frame_plus_n2p model  Run on: May 16, 2003, 13:03:17; Search time 30 Seconds	Title: US-10-008-355-1 Perfect score: 712 Sequence: 1 atgraaatgaaattaaaaagaagagctgaagttgatctaa 2139	ray canter.	Word size: 1  Total number of hits satisfying chosen parameters: 438908  Minimum DB seq length: 0  Maximum DB seq length: 2000000000	Post-processing: Listing first 45 summaries Command line parameters:	-WORDEL=Krame+_ing_p.model_bEvarip -WORDEL=Krame+_ing_p.model_bEvarip -Q=_cgn2_1/USFTO_spool/US10008355/runat_16052003_110427_g763/app_query.fasta_1.2311 -Q=_cgn2_1/USFTO_spool/US10008355/runat_16052003_110427_g763pp_query.fasta_1.2311 -DB=Issued_artents_AA -QFWT=fastan -SUFFIX=Olin2p.rai -MINNATCH=0.1 -LOOPCL=0 -LGPEXT=0 -UNITS=bits -STRAT=1 - END=-1 -MATRIX=Oling - TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTPWT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000 -USFR-USI0008355_GCN_1_33_qcnuat_16052003_110427_g763 -NCPU=6 -ICPU=3 -NO XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7	Database: Issued_Patents_AA:*  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  No. Score Match Length DB ID  Description	1 10 1.4 213 3 US-08-523-373-22 Sequence 22, Appl 2 10 1.4 214 3 US-08-523-373-23 Sequence 23, Appl 3 US-08-523-373-24 Sequence 24, Appl 4 10 1.4 214 3 US-08-523-373-24 Sequence 24, Appl 5 10 1.4 344 1 US-08-523-373-5 Sequence 5, Appl 1 1 1 392 3 US-08-523-373-5 Sequence 5, Appl 1 Sequence 6, Appl 1 1 1 532 1 US-08-557-192-9 Sequence 6, Appl 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: 24
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: Alexandria
                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                 001560-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08523373
Patent No. 6037145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meuth, Donna M. 1607
RECISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                  TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: not relevant
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 TELELY: 704-02 DE NO: 22
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
FNGTH: 213 amino acids
                                                                                                                                                                                                     0.351
10.00
100.00$
100.00$
703-836-6620
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amino acid
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                                                                                                                                   MOLECULE TYPE: peptide
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OPERATING SYSTEM:
                                                                                                                    TOPOLOGY: linear
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ZIP: 22314-3187
                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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US-08-523-373-23
TELEPHONE:
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PROCESS FOR PRODUCTION OF PROTEIN 24
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                                      Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
   Length:
Matches:
                                                                                                                                                                 1930 ACGGCCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                             Gaps:
                                                                                                                                                                                    165 ThrGlyGlyAsnSerGlySerProValPhe 174
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07 -SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          Sequence 24, Application US/08523373 Patent No. 6037145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00.
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Yabuta, Masayuki
APPLICANT: Yabuta, Kazuhiro
TITLE OF INVENTION: PROCESS FR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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100.00%
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10.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 699 Princ
CITY: Alexandria
STATE: VA
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OPERATING SYSTEM:
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                                    Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                         JS-08-523-373-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                            APPLICANT: OHSUYE, Kazuhiro
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
TITLE OF INVENTION: PROTEASES
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-UUN-1996
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Mismatches:
Indels:
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                                                                                                                                                                                                                                        ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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REFERENCE/DOCKET NUMBER: 001560-264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08523373 Patent No. 6037145
                                        Sequence 3, Application US/08657192
Patent No. 5747321
GENERAL INFORMATION:
APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
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100.00%
100.00%
1.40%
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                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meuth, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                   CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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RESULT 4
US-08-657-192-3
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US-08-523-373-5
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APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
UNMER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                              SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA:

RAPLICATION NUMBER: US/08/523,373 FTLING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILLING DATE: US/08/523,373
FILING DATE: 05-SEP-1995
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: BURNS, DOANE, SWECKER & MATHIS : 699 Prince Street
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 ThrGlyGlyAsnSerGlySerProvalPhe 298
                                                                                                                                                                                                                                                                                                                                                                                 001560-251
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07 SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08523373 Patent No. 6037145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          NAME: Meuth, Donna M. REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 0C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.332
10.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 344 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'RY: USA
22314-3187
22314-3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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Sequence 9, Application US/08657192;
Patent No. 574731;
GENERAL INFORMATION:
APPLICANT: YABUTA, Masayuki
APPLICANT: YABUTA, Masayuki
APPLICANT: WOUNCE, MAZUHITO
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
TITLE OF INVENTION: NO NO NEW STAFFET: P.O. BOX 1404
CITY: Alexandria
STATE: VIFGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392
10
0
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APPLICATION NUMBER: US/08/657,192 FILING DATE: 03-JUN-1996 CLASSIFICATION: 435 PROOR APPLICATION NUMBER: 197-170086, FILING DATE: 02-JUN-1995 ATTONREY/AGENT INPORMATION: NAME: Meuth, Donna M. REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTONNEY, FAGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-251
TELECHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                   LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .40%
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-523-373-6
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DB:
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APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532
10
0
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Matches:
Conservative:
                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                              1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIETCATION NUMBER: UP 6-28695
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08523373 Patent No. 6037145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                     0.315
10.00
100.00%
100.00%
1.40%
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10.00
100.00
: 532 amino acids
amino acid
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                                    single
                                                                    protein
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                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                      Alignment Scores:
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                                                                                  US-08-657-192-9
LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                         Score:
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us-10-008-355-1.olin2p.rai

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-UN-1996
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 035,607
REFERENCE/COCKET NUMBER: 035,607
RELEPHONE: (703) 836,6620
                                                                                                                                                                                                                                                                                                        APPLICANT: YABUTA, Masayuki
APPLICANT: OBSUYE, Azauhiro
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
TITLE OF INVENTION: PROTEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537
110
0
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AURE
TITLE OF INVENTION: PROTEASES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 0.0 Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
COUNTRY: United States
CONDUTER READABLE FORM:
    Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-008-355-1 (1-2139) x US-08-657-192-15 (1-537)
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Indels:
                                                                                  US-10-008-355-1 (1-2139) x US-08-523-373-7 (1-532)
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                                                                                                                                            289 ThrGlyGlyAsnSerGlySerProValPhe 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 67, Application US/08332562A ; Patent No. 5985599
                                                                                                                                                                                                                      US-08-657-192-15
; Sequence 15, Application US/08657192
; Patent No. 5747321
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10.00
100.008
100.008
1.408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
Best Local Similarity: 100.00%
Query Match: 1.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-332-562A-67
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Sequence 3729, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                    SCETARATOR STATEM: TO LOSS HE SON #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,562A
FILING DATE: 31-0CT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,457
FILING DATE: 27-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAMME: BENT Stephen A.
REGISTRENCE/DOCKET NUMBER: 54.70/119/GRHA
TELECOMMUNICATION INFORMATION:
APPLICANT: HIBBS, Margaret L.
APPLICANT: SCOTT, Bernadette M.
APPLICANT: BONDONNA, Lisa
APPLICANT: HULETT, Mark D.
TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN.
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0000
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1930 ACGGCCGTAACTCCGGTAGCCCCGTA 1956
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                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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100.00%
1.26%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 904136,
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                            CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-001C-3729
                                                                                                                                                        ADDRESSEE:
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Pred. No.:
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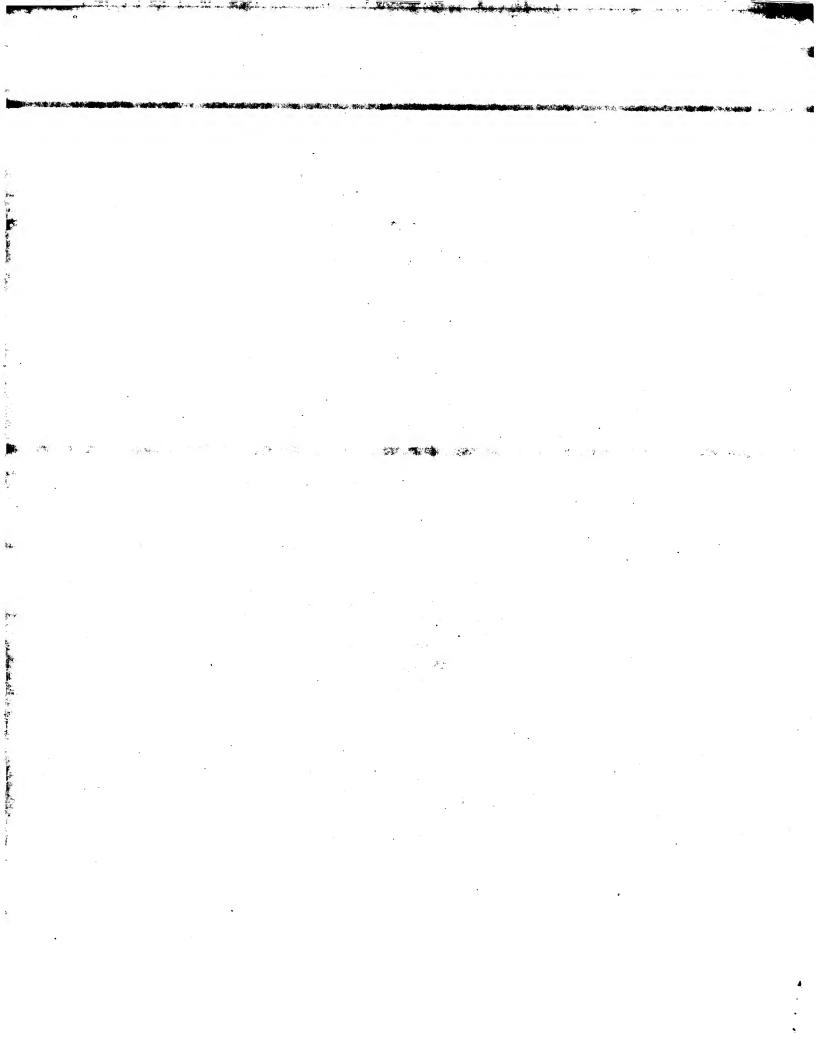
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TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       984
9
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                           US-10-008-355-1 (1-2139) x US-09-134-001C-3729 (1-311)
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROOF APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 758-4800
(212) 751-6849
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9.00
100.00%
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UNKNOWN
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 984
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3729
LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
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Best Local Similarity
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Pred. No.:
                                                                                                                               Alignment Scores
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US-08-673-789-9
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APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
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         Mismatches:
Indels:
                                                                          US-10-008-355-1 (1-2139) x US-08-673-789-9 (1-984)
                                                                                                                                                                                                                                                                                                                         ...uneSSEE: ...unesSS:
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
2.ro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Amgen Patent Operations/RBW 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                               25 CTTCTCGGAGCAGCCCTGCTGTTGGGT 51
                                                                                                               25 CTTCTCGGAGCAGCCCTGCTGGGT 51
                                                                                                                                                                                                 US-08-449-645A-19; Sequence 19, Application US/08449645A; Patent No. 5981245; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-702-367A-19
Sequence 19, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
Best Local Similarity: 100.00%
Query Match: 1.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Query Match:
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COMTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              984
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                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLAPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
                                                                                                                                                                                                            FILING DATE:
CLASSIFCATION: 435
ATONEEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 CTTCTCGGAGCAGCCCTGCTGTTGGGT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENOTH: 984 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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100.00%
1.26%
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Thousand Oaks
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
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                                         USA
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Alignment Scores:
    Pred. No.:
    Scores:
    Scores:
    Scores:
    Scores:
    Pred. No.:
    Scores:
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    Indels:
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    Scores:
    Indels:
    Indels:
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    Scores:
    Indels:
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    Indels:
    Scores:
    Indels:
    Indels:
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984 0000 000



GenCore version  $5.1.4\_p5\_4578$  Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model	7 7	712	100.0	712
Run on: May 16, 2003, 12:38:22 ; Search time 113.5 Seconds (without alignments) 5022.433 Million cell updates/sec	1 64 470 :	10	112.9	26 10 52
Title: US-10-008-355-1 Perfect score: 712 Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa 2139 ·	0 K 8 Q		4 4 4 4 .	213 214 215 336
Scoring table: OLIGO Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	10 11 13 13 15	100000	4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	344 357 392 532
Searched: 908470 segs, 133250620 residues	. 16	10	4.6.6	537
Word size: 1	11 18	ກ Ø 0	- I-I-	282
Total number of hits satisfying chosen parameters: 1687582	217	v 00 0		27
Minimum DB seq length: 0 Maximum DB seq length: 2000000000		၀ ထာ ထ	 	73 75
Post-processing: Listing first 45 summaries		ထထ	 	88
Command line parameters:	c 27 28	ထထ	г. г.	89 116
-MODEL-frame+_n2p.model -DEV-x1p -Q=/cgn2_1/USPTO_spool/US10008355/runat_16052003_110425_9716/app_query.fasta_1.2311 -DB=A_Geneseq_101002 -QFMT-fastan -SUFFIX-olin2p.rag -MINMATCH=0.1 -LOOPCL=0		<b>888</b>		116 116 116
PEXTY-0 - UNLIST-DILES - START-1 - ENDN-1 - MATRIX-01140 - TRANS-numan40.cd. THR_GCORE-quality - THR_MIN-1 - ALIGN-15 - MODE-LOCAL FFMT-pto - NORM-ext - HEAPSIZE-500 - NINLEN-0 - MAXLEN-200000000	0 0 0 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	သထထ		138 152 159
RR=US10008355_@CGN 1.1.153_@runat_16052003_110425_9716 -NCPU=6 -ICEPD=3 -XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120 	35 0 36 37	<b>ထ</b> ထ ထ		173 211 236
APOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7	38	οω	1.1	306
Database : A_Geneseq_101002:*	c 39	ထ ထ	  	312 335
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3: /SIDS2/gcgdata/geneseq/geneseqp·embl/AA1982.DAT:*	c 43	x	7.7	340 395
4: /SIDSZ/gcgdata/geneseg/genesegp-embL/AA1983.DAT:* 5: /SIDSZ/gcgdata/geneseg/genesegp-embL/AA1984.DAT:* 6: /SIDSZ/grodata/geneseg/genesegp-embL/AA1984.DAT:*	44	ထထ	 	396 413
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:* 8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*				
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* 10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*	5	17		
ii: /sibsz/gcgdata/geneseq/geneseqp-embl/AA1990.bAT:* 12: /sibsz/gcgdata/geneseg/genesego/enesego-embl/AA1991.bAT:*	AAO1520	15205	standard	Protein
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*			, במווכמד כי	
14: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1993.DAT:* 15: /SIDSZ/gcgdata/geneseg/genesegn-embl/AA1994_naT·*	AC AA	AAO15205;		
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT		05-SEP-2002	2 (first	t entry)
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT		Porphyromonas		gingivalis
<b></b>		peptidyl	peptidas	e-7; DPP
. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT : /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT		DPP-7 inhibit	or.	tif
/SIDS2/gcgda		Porphyromonas		qinqivalis
No. is the number of results predigreater than or equal to the score	_	WO200238742-A2	~~~	
and is derived by analysis of the total score distribution.	XX	0000		

			·a			SUMMARIES	
Resul No	ult No.	Score	ت نه	Let	DB		cription
1	1	712	100.0	712	23	AAO15205	Porphyromonas ging
	7	52	7	52	23	AA015206	S
	ω.	21		26	23	AA015221	
	4 n	10		10	23	AAO15228	U
	) မ	10		213	17	AAR91042	, +
	۲,	. 10		214	17	AAR91043	in
	<b>co</b> c	10		215	17	AAR91044	teas
	y 5	10		344	17	AAK23044 AAR91033	Mota-dalactoridase
	11	10		344	18	AAW22218	Protein encoded by
	12	10		357	13	AAR26842	Protease from S. A
	13	10	1.4	392	17	.AAR91034	Beta-galactosidase
	4 r	9 9		532	1 / B	AAK91035 AAW22219	Recombinant V8 pro
	16	10		537	18	AAW22220	Protein encoded by
	17	თ		6	23	AA015229	gi
	18	o 0		76	22	AAU63245	Propionibacterium
	9 5	<b>э</b>	•	282	7.7	AAG81635	S. epidermidis ope
	2 5	ν œ		27	2 5	ABE 36664 ABR96842	Staphylococcus epi
	22	∞		55	212	AAB35780	Human CART peptide
	23	80	•	73	23	ABB96626	Omega-conopeptide
	24	œ σ	٠	75	21	AAB35779	CART pep
υ	2 0	10 ac		800	27	AAUSU283 AAR35772	Propionipacterium Human truncated Ca
υ	27	ο σο		68	22	AAU66041	hibacterium
	28	80	•	116	17	AAW06814	cocaine a
	50	<b>œ</b> c		116	13	AAW78906	cocaine
	31	<b>∞</b> α		116	2 0	AAY4518U AAW81341	Human cocaine and
O	32	ထ		138	22	AAO07965	polypept
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υ	34	ထစ	•	159	22	AAM92139	Human digestive sy
C	9 0	0 00		211	2 2	ABB67468	ohila
	37	8		236	23	AAU93181	dopsi
	38	ω (		306	22	ABG27777	Novel human diagno
υ	n (	<b>x</b> 0 c	•	312	77	AAB8 / / 39	uman rzku
	7 T	0 00	٠	340	2 2	ABF30343 ABP28097	Streptococcus poly
	42	- α		340	23	ABP29857	treptococcus
υ	43	80	•	395	22	ABB52640	oì i
•	44	ω (	•	396	17	AAR97569	leukin-2 re
	4 2	ж	•	413	7.7	ABB11836	2R-asso
						ALIGNMENTS	
RES	ULT 1						
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AC	AA01	15205;					
XX							
TQ X	-50	5-SEP-2002	_	first entry	۲y)		
DE	Por	Porphyromona	S	gingivali	s di	dipeptidylpeptidase-7	(DPP-7).
Y Y		antidal	pentid:	7-0	, - dac	varido]	_
KW	DPE	DPP-7 inhibitor id	bitor	enti	icat	ification; periodontal disease	c creavaye, ease; gingivitis;
KW	per	periodontit	tis.		J	1	

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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for educing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or periodontitis). The present amino acid sequence represents the
                                                                                                                                              οf
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               1561 CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC
                                              1621 TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequencé represents the C-terminal region of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme.
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dipeptidylpeptidase for protecting an animal from periodontal
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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and on the sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the N-terminal region of the Porphyromonas gingivalis dipeptidyleptidase-7
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The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Staphylococcus aureus V8 endopeptidase enzyme.
          8888888888888
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52 AA; Sequence

0 0 0 0 0 0 0 Conservative: Mismatches: Indels: Length: Matches: Gaps: 0.618 . 10.00 100.00\$ 100.00\$ 1.40\$ 23 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Score:

US-10-008-355-1 (1-2139) x AAO15207 (1-52)

1930 ACGGCGGTAACTCCGGTAGCCCCGTATTC 1959 ò a

1 ThrGlyGlyAsnSerGlySerProValPhe 10

AAR91042 standard; Peptide; 213 RESULT 6 AAR91042

AAR91042;

Ą

mature protease (aal-2:13). (first entry) 23-MAY-1996

Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coll; transposon Tn903; aminoglycoside 3'-phosphotransferase.

Staphylococcus aureus strain V8 (ATCC 27733)

EP700995-A2

13-MAR-1996

95EP-0306235 06-SEP-1995; 94JP-0296028 94JP-0238595 07-NOV-1994; 07-SEP-1994;

(SUNR ) SUNTORY LTD.

Ohsuye K, Yabuta M;

WPI; 1996-141021/15

Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide

Example 8; Fig 14a; 44pp; English

A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active VB protease. Extension of the C-terminal end of the VB moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of 

213 10 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 0.542 10.00 100.00\$ 100.00\$ 1.40\$ 213 AA; Best Local Similarity: the host cells. Percent Similarity: Alignment Scores: Sednence Query Match: Pred. No.: Score:

US-10-008-355-1 (1-2139) x AAR91042 (1-213)

AAR91043 RESULT

AA AAR91043 standard; Peptide; 214

AAR91043;

(first entry) 23-MAY-1996

V8 mature protease (aal-214).

Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.

Staphylococcus aureus strain V8 (ATCC 27733).

EP700995-A2

13-MAR-1996

95EP-0306235 06-SEP-1995;

94JP-0296028 94JP-0238595 07-NOV-1994; 07-SEP-1994;

(SUNR ) SUNTORY LTD.

Ohsuye K, Yabuta M;

WPI; 1996-141021/15

Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide 

Example 8; Fig 14b; 44pp; English.

A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli Ompr protease to yield active VB protease. Extension of the C-terminal end of the VB moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of

214 AA; Sequence

0.541 Alignment Scores: Pred. No.:

Score:

Length: Matches:

214 10

9

Query Match: DB:

AAR91044;

AAR9104 RESULT

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The sequences given in AAR26842 and AAR29644 are proteases which were isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
   1930 ACGGCCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1.68
7.label Signal_peptide
69.336
7label Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                    165 ThrGlyGlyAsnSerGlySerProvalPhe 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 15-16; 25pp; Japanese.
                                                                                                                                                                                                                                      Protease; PCR; amplify; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-008-355-1 (1-2139) x AAR29644 (1-336)
                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91033 standard; Protein; 344 AA.
                                                                                                   AAR29644 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91JP-0024633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90JP-0040398
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10.00
100.00%
100.00%
1.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                      Protease from S. Aureus
                                                                                                                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-304938/37.
N-PSDB; AAQ27988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                         JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                   11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1992
                                                                                                                                      AAR29644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR91033;
                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                       AAR29644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR91033
                                                                     RESULT
                                                                                                                      A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature VB procease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli Ompr protease to yield active VB protease. Extension of the C-terminal end of the W motean protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                                       recombinant protein; fusion protein; beta-galactosidase;
Escherichia col1; transposon Tn903;
aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215
10
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                                                                                                                                                                                                                                                                                                                                                         protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
   Conservative:
                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus strain V8 (ATCC 27733)
                                                                                                                   1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                      US-10-008-355-1 (1-2139) x AAR91043 (1-214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-008-355-1 (1-2139) x AAR91044 (1-215)
                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 14c; 44pp; English
                                                                                                                                                                                                                  AAR91044 standard; Peptide; 215
                                                                                                                                                                                                                                                                                                                      mature protease (aal-215).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95EP-0306235
100.00%
100.00%
1.40%
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0296028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-0238595
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                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                         Linker peptide; V8
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 AA;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1994;
                                                                                                                                                                                                                                                                                      23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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336 0 0 0 0 0 0

23-MAY-1996 (first entry)

Query Match: DB:

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proteolytic activity; fusion protein; beta-galactosidase; urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                           31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1993
                                                                                                                                                                              02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                       EP745669-A2
                                                                                                                                         04-DEC-1996
                  Chimeric
Chimeric
                                                                                                                                                                                                                   Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                       Region
                                                                         Region
                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR26842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X E X B X S X B
Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification;
                                                                                                                                                                                                                                                                                           Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                     comprising
                                                                                                                                                                                                                                                                                                                                                  Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia cool beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature VB protease without or with the repeat region. The constructs were inserted into vector p69784DFCT(6)R6, yielding pVBRPT(-) and pVBRPT(+), respectively. Both constructs yielded active protease when expressed in E. coll JM101 transformants.
                                                                                       1..124
/note= "beta-galactosidase region"
125..344
/note= "mature V8 protease without the repeat
region"
                          V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli.
                                                     Chimeric Escherichia coli;
Chimeric Staphylococcus aureus strain V8 (ATCC 27733).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        344
10
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
        Beta-galactosidase-V8 protease fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by pV8RPT(-) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-008-355-1 (1-2139) x AAR91033 (1-344)
                                                                                                                                                                                                                                                                                                                                 Example 2; Page 12-13; 44pp; English.
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW22218 standard; Protein; 344 AA
                                                                                                                                                                                      95EP-0306235
                                                                                                                                                                                                        94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.518
10.00
100.00
100.008
1.408
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                                                                                                                                                                                                                                                      Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                    (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                         WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                            344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1997
                                                                                                                                                                                      06-SEP-1995;
                                                                                                                                                                                                        07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                 EP700995-A2
                                                                                                                                                                    13-MAR-1996
                                                                                                                                                                                                                                                                                                               polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                           Region
                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
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which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218) or 53 (AAW22220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 proteases lacking the prepro and C-terminal 48 amino acids linked, via a synthetic linker, downstream of the E. coll beta-galactosidase. The S. aureus portion of the chimaera was amplified by the primers AAF73254-5 from wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence. The coding sequence was then used to generate mutants of the V8 protease which retain their levels of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new mutant Staphylococcus aureus V8 proteases
                                                                                                                                                                                                                                     /note= "truncated S. aureus V8 protease portion"
                                                                                                  /note= "E. coll beta-galactosidase portion"
101.120
/note= "synthetic R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V8 protease mutants - with increased
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Matches:
Conservative:
Mismatches:
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                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 13-14; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR26842 standard; Protein; 357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease from S. Aureus ATCC12600

    Escherichia coli,
    Staphylococcus aureus.

                                                                                                                                                                                                                                                                                                                                                                                                        96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                          95JP-0170086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.518
10.00
100.00
100.00%
1.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus V8 presistance to denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNR ) SUNTORY LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
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region"
                                                                                                                  Ohsuye K, Yabuta M;
                                                                                                (SUNR ) SUNTORY LTD
                                                                                                                                  WPI; 1996-141021/15
                                                                                                                                                                                                                                                                              392 AA;
                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                    06-SEP-1995;
                                                                      07-NOV-1994;
                                                                              07-SEP-1994;
                                                                                                                                                                                                                                                                                               Aliqnment Scores:
                  EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996
                                   13-MAR-1996
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Chimeric S
Chimeric S
Chimeric S
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91035;
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR91035
The sequences given in AAR26842 and AAR29644 are proteases which were isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                     Novel protease prepd. using Bacillus or Saccharomyces host -capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125..392
/note= "mature V8 protease including the repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant protein; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus strain V8 (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "beta-galactosidase region"
                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-galactosidase-V8 protease fusion protein.
                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                               1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                        233 ThrGlyGlyAsnSerGlySerProValPhe 242
                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                         Disclosure; Page 13-15; 25pp; Japanese.
Protease; PCR; amplify; Staphylococcus.
                                         1..68
/label= Signal_peptide
69..358
/label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                              US-10-008-355-1 (1-2139) x AAR26842 (1-357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V8 protease; Staphylococcus aureus;
fusion protein; beta-galactosidase;
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR91034 standard; Protein; 392 AA.
                                                                                                                         91JP-0024633.
                                                                                                                                           90JP-0040398
                                                                                                                                                                                                                                                                                                                                                0.516
10.00
100.00$
100.00$
1.40$
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                                                                                                                                                            (SHIO ) SHIONOGI & CO LTD.
                 Staphylococcus aureus
                                                                                                                                                                            WPI; 1992-304938/37.
N-PSDB; AAQ27987.
                                                                                                                                                                                                                                                                                                                       357 AA;
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                      JP04211370-A
                                                                                                                     19-FEB-1991;
                                                                                                                                         20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                        03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR91034;
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                          Peptide
                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Region
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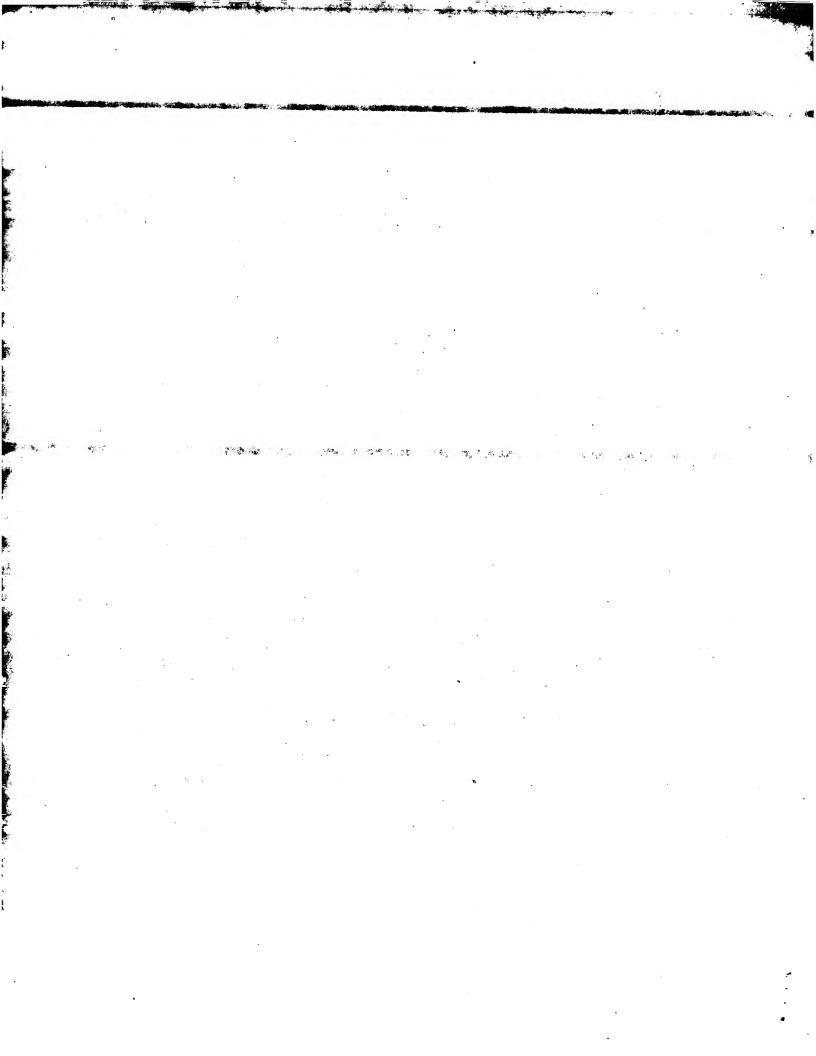
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Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal and to the S. aureus manure VB protease without or with the repeat region. The constructs were inserted into vector pG9784DhCT(G)R6, yielding pVBRPT(+) and pVBRPT(+), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic;
Staphylococcus aureus strain V8 (ATCC 27733);
transposon Tn903.
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/note= "beta-galactosidase region"
101..120
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 ThrGlyGlyAsnSerGlySerProvalPhe 298
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                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 14-15; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR91035 standard; Protein; 532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "R6 linker"
104..105
                                              94JP-0296028,
94JP-0238595,
95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.512
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100.00
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    Staphylococcus aureus.

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                                                                                                                                                      04-DEC-1996
 Chimeric
                             Region
                                                                                     Region
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                                                Region
                                                                  Region
 Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification; proteolytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                                                                                                                                         A fusion protein, VBD (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides (derived from Escherichia coli beta-galactosidase and and Th903 aminodylvoside 3'-phosphotransferase, respectively), B is Staphylococcus aureus mature VB protease lacking the C-terminal repeat region, and L is a linker peptide (AAR9103). The fusion protein is expressed in inactive form in E. coli. It is then recovered, solubilised and cleaved at the linker peptide regions with a protease intrinsic to the host cells, i.e. OmpT protease, to allow recovery of VB protease.
                                                                                                                                                                                                                                          Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                 /note= "R6 linke.
339.340
/note= "cleavage site for OmpT protease"
707..532
/note= "aminoglycoside 3'phosphotransferase
region"
"cleavage site for OmpT protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                     532
000
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Matches:
Conservative:
Mismatches:
Indels:
                  "V8 protease region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 ThrGlyGlyAsnSerGlySerProValPhe 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-008-355-1 (1-2139) x AAR91035 (1-532)
                                                                                                                                                                                                                                                                                         Example 3; Page 16-18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by pV8D construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW22219 standard; Protein; 532
                                                                                                                                                             94JP-0296028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Escherichia coli,
                                                                                                                                            95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                    0.498
10.00
100.008
100.008
1.408
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/note= "c
125..335
                           ..356
                  /note=
                                                                                                                                                                                                              Yabuta M;
                                                                                                                                                                                          (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                         532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                              07-NOV-1994;.
07-SEP-1994;
                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1997
                                                                                                     EP700995-A2
                                                                                                                         13-MAR-1996
                                                                                                                                                                                                              Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22219;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                 Region
          Region
                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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The invention relates to new mutant Staphylococcus aureus V8 proteases which have enzyme activity even under environmental conditions which proteases lacking 48 (AAW22218). 75 (AAW22219) or 53 (AAW2220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially P44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 56 amino acids linked, via a synthetic R6 linker, downstream of the E. coli beta galactosidase. Also included downstream of the E. coli beta galactosidase. Also included downstream of the E. coli beta galactosidase. Also included downstream of the E. coli beta galactosidase. Also included downstream of the E. coli beta galactosidase. Also included downstream of the Sequence is sequence (see AAW22218) by using a natural EcoRV site which removed a sequence (see AAW2218) by using a natural EcoRV site which removed a curther 8 amino acid from the C-terminus. This truncated V8 protease, designated V8D, retains its level of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                           /note="truncated S. aureus V8 protease portion"
337..360
/note= "R6 linker sequence"
361..532
/note= "aminoglucoside 3'-phosphotransferase portion"
                                             /note= "E. coli beta-galactosidase portion"
101.124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus V8 protease mutants - with increased
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Mismatches:
Indels:
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Matches:
                                                                                                                            "R6 linker sequence"
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Job time: 123.5 secs
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95JP-0170086
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                                                                                                                                                               ...336
                                                                                                                            /note= 125..336
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Query Match:
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Title: Perfect score:

Sequence:

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Scoring table:

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Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 36591, A
Sequence 36591, A
Sequence 36591, A
Sequence 367, Appl
Sequence 26, Appl
Sequence 266, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 170, Appl
Sequence 1813, Appl
Sequence 1970, Appl
Sequence 29, Appl
                    Sequence 25, Appl
Sequence 4, Appli
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Sequence 56, Appli
Sequence 9, Appli
Sequence 30, Appli
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APPLICANT Travis.
APPLICANT Travis.
APPLICANT Potempa, Jan S
APPLICANT Potempa, Jan S
APPLICANT Banbula, Agnieszka
TITLE OF INVENTION: Diopptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
NRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
SPRIOR FILING DATE: 2000-11-08
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 712
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US-09-815-242-10510
US-09-801-368-44
US-08-910-386A-18
US-08-945-749-3
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2 US-10 135-687 4

105-09-938-315-89

105-09-938-315-89

105-09-938-315-89

105-09-938-315-57

105-09-938-315-57

105-09-964-761-3943

105-09-774-639-268

105-09-774-639-268

105-09-774-639-268

105-09-774-839-214

105-09-774-860-324

105-09-764-891-5217

105-09-764-891-5217

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Mismatches:
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US-10-008-355-26
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Patent No. US20020164759A1
GENERAL INFORMATION:
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-WODEL-framet-lap, model -DEV-xlp
-Q-/cgn2_1/USPTO_spool/US1000835/runat_16052003_110429_9845/app_query.fasta_1.2311
-Q-/cgn2_1/USPTO_spool/US10008355/runat_16052003_110429_9845/app_query.fasta_1.2311
-Q-/cgn2_1/USPTO_spool/US10008355/runat_160FIX=01102p.rapb -MINMATCH=0.1
-LOOPEL-0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdl -LIST=45 -DOCALIGN=200 -THR_SCORES-quality -THR_MIN=1
-ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=560 -MINLEN-0
-MAXLEN-200000000 -USER=US10008355_GCGN_1_1_25_Grunat_16052003_110429_9845
-NCPU-6 -ICFUT-3 -NO_WMAP - LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FCAPOP=6
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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//cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
                                                                                                                                             May 16, 2003, 13:13:37 ; Search time 83 Seconds
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                - protein search, using frame_plus_n2p model
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Matches:
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            RESULT 2
US-10-008-355-8
Sequence 8, Application US/10008355
Factor No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Agnieszka
TITLE OF INVENTON: Dipeptidylpeptidases And
TITLE OF INVENTON: Dipeptidylpeptidases And
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEG ID NO 8
LENGTH: 699
701. GlnCysProArgLeuIleGlnGluLeuLysLeuIle
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TTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCG
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US-10-008-355-18
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1681 CGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGA 1740
                                                      1741 TATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCAAGGGGGTATTGGAG 1800
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APPLICANT: Tracks, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Banbula. Agnieszka
TTILE OF INVENTION: Dipeptidylpeptidases And Methods Of Use;
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 52
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82 ATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTCGGCTTT
                                                                     APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
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APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
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; Sequence 18, Application US/10008355; Patent No. US20020164759A1
GENERAL INFORMATION; APPLICANT: Travis, James
                                                                                                                                                                                                                                                                                                                ORGANISM: Porphyromonas gingivalis
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US-10-008-355-7
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APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 255.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
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PRIOR FILING DATE: 3000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/246,827 PRIOR FILING DATE: 2000-11-08 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin version 3.0
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; Patent No. US20020164759A1
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Shewanella putrefaciens
                                                   US-10-008-355-5
; Sequence 5, Application US/10008355
; Patent No. US20020164759A1
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ORGANISM: Artificial Sequence
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APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TTTLE OF TWENTON: Dipoptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION UNMBER: US/10/008,355
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
                                                                                                                                                                        APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
FILE REPERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR PPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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                                                                                              Sequence 4, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureus
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LENGTH: 52
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APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot.
APPLICANT: Ryba, Nick
APPLICANT: Weller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278Alel Family of Taste Receptors
TITLE OF INVENTION: T2R, 200/0510.332
CURRENT APPLICATION NUMBER: US/09/510,332
CURRENT FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 17
LENGTH:
                                                                                                                                                                     APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3014-2US.
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 274
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptomyces refuineus subspecies thermotolerans US-10-166-087-30
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Matches:
Conservative:
Mismatches:
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Mismatches:
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 221 TrpProArgHisThrGlyAspPheSer 229
                                                                                         Sequence 30, Application US/10166087
Publication No. US20030077767A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 ArgMetArgGluLeuGlyPheThr 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CGAATGCGTGAGCTCGGCTTTACG 144
                                                                                                                                                     APPLICANT: Ecopia Biosciences Inc
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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                                                         RESULT 12
US-10-166-087-30
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US-09-510-332-17
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REPERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: US/000-11-08
                                                                                                         GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
TILLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use;
FILE REPERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR PILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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Matches:
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662 ThrGlyGlyAsnSerGlySerProValPhe 671
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ORGANISM: Porphyromonas gingivalis
                                                                         ; Sequence 26, Application US/10008355
; Patent No. US20020164759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/10008355 Patent No. US20020164759Al GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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9.00
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US-10-008-355-26
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LENGTH: 720
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LENGTH: 9
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FEATURE:

Query Match:

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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbech, word APPLICANT: Oblsen, Kari L. APPLICANT: Oblsen, Kari L. APPLICANT: Syskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Wall, Daniel APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard J. TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
                                                                                                                                                                                                                                                            APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Alel Family of
FILE REFERENCE: 02307E-098000US
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Matches:
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US-10-008-355-1 (1-2139) x US-09-510-332-17 (1-312)
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Patent No. US20020061569A1
GENERAL INFORMATION:
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                                         1164 CTTGGCTCCTTCCTTATAAGCCTT 1141
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                                                                                                                                                           ; Sequence 51, Application US/09393634; Patent No. US20020051997A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: human GR09
                                                                                                                                                                                                                     Zuker, Charles S.
Adler, Jon Elliot
Ryba, Nick
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Best Local Similarity:
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US-09-815-242-10510
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SEQ ID NO 51
LENGTH: 312
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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR PILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SEQ ID NO 10510
; SEQ ID NO 10510
; CAGANISM: Enterococcus faecalis
; ORGANISM: ORGANIS
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c 15 8 1.1 162 2 C69495 hypothetical prote 117 8 1.1 1 24 2 A69054 thypothetical prote 118 9 2 A69054 thypothetical prote 118 9 1.1 24 2 A69149 probable molybdenu 119 24 2 A69149 probable molybdenu 119 226 2 S04752 probable molybdenu 119 226 2 S04754 protein 128 1.1 284 2 T707614 protein 128 1.1 284 2 T707614 protein 128 1.1 28 2 S70718 protein 128 2 S06947 probable beta-ketoadipyl. Co 130 8 1.1 421 2 S06949 probable protein 128 2 S06947 probable protein 128 2 S06947 probable transport 129 2 S06947 probable	ALIGNMENTS  RESULT 1  GRAGA  Hypotherical protein XF1887 [imported] - xylella fastidiosa (strain 9a5c) C.Species: Xylella fastidiosa C.Species: Xylella C.Species: Xyl
GenCore version 5.1.4_p5_4578  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - protein search, using frame_plus_n2p model Run on: May 16, 2003, 13:00:32 ; Search time 79 Seconds Title: US-10-008-355-1 Perfect Score: 120-008-355-1 Sequence: 142 Sequence: 142 Scoring table: OLIGO Scoring table: Nappop 60.0 , Yapext 60.0 Fqapop 60.0 , Yapext 7.0 Fqapop 60.0 , Papext 7.0 Fqapop 60.0 , Fqapext 60.0 Fqapop 60.0 , Fqapext 60.0 Fqapop 60.0 , Fqapext 60.0 Fqapop 60.0 , Fqapext 7.0 Fqapop 60.0 , Fqapext 60.0 Fqapop 60.0 , Fqapext 7.0 Fqapop 60.0 , Fqapext 60.0 Fqapop 60.0 , Fqapext 7.0 Fqapop 60.0 , Fqapext 60.0 Fqapop 60.0 , Fqapext	COMMand line parameters:

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A; Status: preliminary
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                                                                               Alignment Scores:
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                            C; Genetics:
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                                                                                                          Score:
                                                                                             Pred.
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                                                                                                                                                  Hypothetical protein sspA [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Sate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Sacession: G89873
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C.; Shiba, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu, Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet, 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
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Matches:
Conservative:
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-342 <KUR>
 Best Local Similarity:
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Best Local Similarity:
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C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C; Accession: S21758
R; Yoshikawa, K; Tsuzuki, H.; Fujiwara, T.; Nakamura, E.; Iwamoto, H.; Matsumoto, K.;
Biochim. Biophys. Acta 1121, 221-228, 1992
A; Title: Purification, characterization and gene cloning of a novel glutamic acid-spe A; Reference number: S21758; MUID:92287954; PMID:1599945
A; Status: preliminary
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A;Residues: 1-569 <WHI>
A;Cross-references: GB:AE001999; GB:AE000513; NID:96459316; PIDN:AAF11119.1; PID:9645
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C;Species: Deinococcus radiodurans
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F7581
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Science 286, 1571-1577, 1999
A;Cross-references: GB:BA000018; PID:g13700850; PIDN:BAB42146.1; GSPDB:GN00149, A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA *
A; Residuos: 1:357 cx705
A; Residuos: 1:357 cx705
A; Ccsduos: 1:257 cx705
C; Superfamily: staphylococcal serine proteinase
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Matches:
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C;Superfamily: staphylococcal serine proteinase
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                                                                                                                                                                                                                                                           Best Local Similarity:
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Alignment Scores:     Pred. No.:     Score:     Score:     Score:     Score:     Score:     Score:     Percent Similarity:     100.00%	RESULT 8 AF2363 hypothetical protein all4462 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A;Note: Nostoc sp. A;Note: Nostoc sp. A;Note: Nostoc sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AF2363 R;Kaneko, T: Nakamura, Y: Wolk, C.P.; Kuritz, T.; Saṣamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:2159285; PMID:11759840 A;Accession: AF2363 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-483 <kur> A;Residues: 1-483 <kur> A;Cross-references: GB:BA000019; PIDN:BAB76161.1; PID:g17133598; GSPDB:GN00179 A;Genetics: A;Gene: all4462</kur></kur>		RESULT 9 T36771 probable integral membrane protein - Streptomyces coelicolor C;Species: T3671 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Sischer commber: 221574 A;Reference number: 221574 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-684 <see> A;Crossreferences: EMBL:AL096844; PIDN:CAB50875.1; GSPDB:GN00070; SCOEDB:SCI28.01 A;Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SCI28.01</see>	Alignment Scores: 5.03 Length: 634  Pred. No.: 5.03 Matches: 9  Percent Similarity: 100.00% Conservative: 0  Best Local Similarity: 100.00% Mismatches: 0
Az toz o	AUSTOLIT 6  D75483  Hypothetical protein - Deinococcus radiodurans (strain R1)  C.Species: Deinococcus radiodurans  C.Species: Deinococcus radiodurans  C.Species: Deinococcus radiodurans  C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000  C.Accession: D75483  R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  M.; Shein, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999  A.Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  A.Reference number: A75250; MuID: 20036896; PMID: 10567266  A.Accession: D75483  A.Status: preliminary  A.Molecule Lype: DNA  A.Residues: 1-266 <whi> A</whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi></whi>	Alignment Scores:  Alignment Scores:  Score:  Score:  Score:  Fred. No.:  9.00  Matches:  9.00  Matches:  Percent Similarity:  100.004  Mismatches:  0  Ouery Match:  1.264  Mismatches:  0  Ouery Match:  1.264  Mismatches:  0  Ouery Match:  1.265  Ouery Match:  1.266  Ouery Match:  Ouery M	RESULT 7 AE1710 hypothetical protein homolog lin2224 [imported] - Listeria innocua (strain Clip11262) C; Species: Listeria innocua C; Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C; Accession: AE1710 R; Claser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mathors: Comparative genomics of Listeria species. A; Attle: Comparative genomics of Listeria species. A; Reference number: AB1077; MuID:21537279; PMID:11679669 A; Accession: AE1710 A; Molecule type: DNA	A; Residues: 1-452 <cla> A; Cross-references: GB:AL592022; PIDN:CAC97453.1; PID:g16414737; GSPDB:GN00178 A; Experimental source: strain Clip11262 C; Genetics: A; Gene: lin2224</cla>

Sun May

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C;Accession: T04804
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes submitted to the Protein Sequence Database, February 1999
A;Reference number: 215385
                                                                                        A:Cross-references: GB:AE000770; NID:92984274; PIDN:AAC07805.1; PID:92984280; GB:AE00
A:Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T36095
R;Saunders, D.; Barris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, April 1999
A;Reference number: Z21596
A;Reference number: Z21596
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-102 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL049661; PIDN:CAB41211.1; GSPDB:GN00070; SCOEDB:SCE134.13
A;Experimental source: strain A3(2)
                    preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SCE134.13 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F10M23.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Streptomyces coelicolor hypothetical protein SCE134.13
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A;Cross-references: EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                               A; Molecule type: Dn
A; Residues: 1-1116
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-984 <HIR>
A;Cross-references: GB:M18391; NID:g339716; PIDN:AAA36747.1; PID:g339717
A;Note: the sequence in GenBank entry HUMTKR, release 111.0, has the codons GCG for 398-
R;Tuzi, N.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1993
A;Description: An EGFR/eph chimeric receptor possesses ligand stimulated tyrosine kinase
A;Reference number: $44280
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A;Residues: 286-397,'A',399-580,'QRDRATDVDREDKLWLKPYVDLQAYEDPAQGALDF',583,625-984 <TU2>
A;Cross-references: EMBL:227409; NID:9482916; PIDN:CAA81796.1; PID:9482917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70476
                                                                                                                                                                                                                                                                                                                                                                                                                    #sequence_revision 22-Oct-1999 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eph gene.
                                                                                                                                                                                                                                                                                                                                    type eph 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A novel putative tyrosine kinase receptor encoded by the A;Reference number: A34076; MUID:88070650; PMID:2825356
                                                                                                                                                                                                                                                                                                                               protein-tyrosine kinase (EC 2.7.1.112) receptor type eph 1 NAlternate names: receptor tyrosine kinase eph 1 Species: Homo sapiens (man) receptor 2.5pecies: Homo sapiens (man) receptor 2.2-oct-1999 #sequence_revision 22-oct-1999 #text_cC 1.8ccssion: A34076; $44280 R:Hiral, H: Maru, Y: Hagiwara, K:; Nishida, J:; Takaku, Science 238, 177-1720, 1987 A;Title: A novel putative tyrosine kinase receptor encoded
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                 Indels:
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A;Cross-references: GDB:119875; OMIM:179610
A;Map position: 7q32-7q36
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                                                                                                                                                               28 CTCGGAGCAGCCCTGCTGGTTGGGTGCT
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Conserved hypothetical protein AF1964 - Archaeoglobus fulgidus
Cipteries: Archaeoglobus
Richer, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Filelschmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.
Nature 390, 364-370, 1997
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Alauthors: MulD:98049343; PMID:9389475
Alactession: C69495
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C;Comment: This protein plays a conserved functional role within the mammalian central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Characterization of the human cDNA and genomic DNA encoding CART: A cocaine-A;Reference number: JC4669; MUID:96194810; PMID:8647455
A;Accession: JC4669
                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Homo sapiens (man)
C; Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jul-2000
C; Accession: JG4669; G01648
R; Douglass, J; Daoud, S.
Gene 169, 241-245, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Gross references: GB:U16826; NID:g609305; PIDN:AAB08010.1; PID:g609306 R;Douglass, J.O.
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A;Accession: G01648
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-116 <D02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, January 1995
                      Length:
Matches:
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Matches:
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A; Residues: 1-116 <DOU>
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Query Match:
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A; Introns: 53/3, 81/3
Alignment Scores:
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A;Gene: CART
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                      Pred. No.:
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-162 <KLE>
A;Cross-references: GB:AE000967; GB:AE000782; NID:g2689290; PIDN:AAB89289.1; PID:g264
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Length:
Matches:
Conservative:
Mismatches:
Indels: 62.6 8.00 100.00% 100.00% 1.13% Percent Similarity: Best Local Similarity:

US-10-008-355-1 (1-2139) x C69495 (1-162)

Search completed: May 16, 2003, 13:16:20 Job time: 92 secs

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US-10-008-355-1

Title: Perfect score:

Sequence:

protein search, using

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Run on:

GenCore version Copyright (c) 1993 - 2003

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Q8ynu9 anabaena sp
Q9s282 streptomyce
Q91wb5 mus musculu
Q9x868 streptomyce
Q9s21 arabidopsis
Q9s21 arabidopsis
                                                                                                                                                                             Q8zval pyrobaculum
Q9k3j5 streptomyce
O27455 methanobact
Q9ss66 arabidopsis
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Q8tv91 methanopyru
Q39862 glycine max
Q9x246 thermotoga
                                                                                                                                                                                                                                                                                                                                                                                      Q92xm6 bacteriopha
033999 chromatium
09ngt6 leishmania
09fdk6 zymomonas m
092330 caenorhabdi
09kbd1 beacillus ha
09a166 shigella fil
                              Ogru39 deinococcus
OgajxO staphylococ
                                                                                                                                                                                                                                        Q9v4h5 drosophila
Q9pij8 campylobact
Q8wz66 homo sapien
                                                                                                                                                                                                                                                                                                                                            Q9nywl homo sapien
Q40600 oenothera b
Q93cal bifidobacte
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09f2u9 streptomyce
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    Q99v45 staphylococ
Q04186 staphylococ
                                                          Q9rwf5 deinococcus
Q929q0 listeria in
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08vlm4 escherichia
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Q8vv03 streptomyce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update) |
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Xf1887.
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Q40600
Q93CA1
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09F2U9
08U7A5
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09KBD1
09AL66
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08 Y N U 9
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Q91WB5
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                                                            Q9RWF5
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Q9FDK6
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Q8VLM4
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Q8VV03
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MEDLINE=20365717; Pubmed=10910347;
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114
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01-OCT-2000 (
01-JUN-2002 (
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Q9PC94;
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-MODEL=frame+_n2p.model -DEV=x1p
-Q-Cqqn2_110426_9734/app_query.fasta_1.2311
-Q-Cqqn2_1108PQ_spool_VGS1008355/runat_16052003_110426_9734/app_query.fasta_1.2311
-QB-SPTREMBL_21 -QFWT=fastan -SUFFIX=olin2p.rspt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STPRT=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HERSEIZE=500 -MINLER=0 -MAXER=20000000
-USER=USI0008355_@CGN_11_238_grunat_16052003_110426_9734 -NOEV=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -LONGIGG -DEV_TIMEOUT=12
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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(without alignments)
5342.240 Million cell updates/sec
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5.1.4_p5_4578
Compugen Ltd.
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SUMMARIES

score greater than or equal to and is derived by analysis of

is the

Pred. No.

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*

sp\_rvirus:\* sp\_bacteriap:\*

sp\_archeap:

sp\_invertebrate:\*
sp\_mammal:\*

sp\_archea:\* sp\_bacteria:\*

SPTREMBL\_21:\*

Database

sp\_fundi:\* sp\_human:\* sp\_organelle:\*

sp\_mhc:\*

sp\_phage:\* sp\_plant:\* sp\_rodent:\*

09PC94

716 16

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Query Match Length DB

Score 13

SO. Result

Total number of hits satisfying chosen parameters:

Word size:

Searched:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

671580 segs, 206047115 residues

, Xgapext 60.0 , Ygapext 60.0 , Fgapext 7.0 , Delext 7.0

60.0

Xgapop (Ygapop Fgapop Delop

OLIGO

Scoring table:

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Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

R. Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

Krieger J.E., Kuramae E.E., Laigert F., Lambais M.R., Leite L.C.C.,

Lemos E.G.M., Lemos M.V.F., Lopes S.R., Lambais M.R., Leite L.C.C.,

R. Marques M.V., Martins E.A.L., Martins E.M.F., Martino C.L.,

R. Martins E.A.L., Martins E. M.F., Martino C.L.,

R. Martins E.A.L., Martins E. M.F., Martino C.L.,

R. Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

R. Moon D.H., Nobreage F.G., Nunes L.R., Oliveira M.A.,

R. D.J., Moon D.H., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

R. D. Roberto P.G., Rodrigues V., de Rosa A.J.M.,

R. Gollveira M.C., de Oliveira R.C., Santelli R.V., Sawasaki H.E.,

R. Sallveira J.F., Silvestri M.L.Z., Siqueira W.J. de Souza A.A.,

R. Sallveira J.F., Silvestri M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

R. Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

R. Mature 406:151-159(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus warneri.
Bacteria; Firmlcutes; Bacillus/Clostridium group; Bacillales;
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AJ293885; CAC06168.1; -.
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EAF086E2315BBDFC CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Matches:
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InterPro; IPR000126; Ser_proteas_V8.
Pfam; PF00089; Urypsin; 1.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
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SPECIES—S. aureus (strain MuSO), and S. aureus (strain N315);
MEDLINE—21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Magai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protease; Complete proteome.
i; 5AEF42DCE01C4B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Serine protease, V8 protease, glutamyl endopeptidase.
SSPA OR SAV1048 OR SA0901.
             316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 357:1225-1240(2001).
-!- SIMILARITY: TO SERINE PROTEAȘES, TRYPSIN FAMILY.
EMBL; AP003351; BAB57210.1; -.
EMBL; AP003132; BAB42146.1; -.
MEROPS; S01.269; -.
             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                          Mismatches:
                                                                                                                                                                                                                                                   342 AA
                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                      1930 ACGGGGGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1930 ACGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; JOHNOO, SELPROCHESS, SELPROCHESSE, Try.
Interpro; IPROO0126; Selprochess_V8.
Pfam; PF00089; Lrypsin; 1.
PRINTS; PR00819; VBPROCHEASE.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS0040; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
                                                                                                                                                                      231 ThrGlyGlyAsnSerGlySerProvalPhe 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-008-355-1 (1-2139) x Q99v45 (1-342)
                                                                                                                        US-10-008-355-1 (1-2139) x Q9FBG1 (1-316)
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Protease; Serine pi
SEQUENCE 342 AA; 36977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.594
10.00
100.008
100.008
           0.599
10.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=158878, 158879;
                                                                         1.40%
                                                                                                                                                                                                                                                   PRELIMINARY;
                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                 Q99V45
Q99V45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                Pred. No.:
                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
                              Score:
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1933 GGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                                   InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
                                                                                                 InterPro; IPR004358; Bact_sens_pr
InterPro; IPR003018; GAF.
InterPro; IPR004359; HIS_KIN_sig.
             EMBL; AE001999; AAF11119.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                59182 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23667 MW;
                                                                                                                                                                                                                        PRINTS; PR00344; BCTRLSENSOR
                                                                                                                                                                                                                                                                                                         ; HATPase_c; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Staphylococcus epidermidis
Submitted (JAN-2001) to the
EMBL, AJ305145; CAC27157.1;
HSSP; P09331; 1EXF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.39
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100.00%
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10.00
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100.00%
                                                                                                                                                                                                   Pfam; PF02518; HATPase_c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                SMART; SM00065; GAF;
SMART; SM00387; HATPa
                                                                                                                                                                                                                                                                                                                                                                                                       569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Complete proteome
SEQUENCE 569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-6746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AJX0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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                Yoshikawa K., Tsuzuki H., Fujiwara T., Nakamura E., Iwamoto H., Matsumoto K., Shin M., Yoshida N., Teraoka H.;
"Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from staphylococcus aureus atcc 12600.";
EMBL. D00730; BAA00630.1;
MEROPS; S01.269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-RI;
MEDLINE-20036896; PubMed=10567266;
MEDLINE-20036896; PubMed=10567266;
MEDLINE-20036896; PubMed=10567266;
Mitce O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vannathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.E. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glutamic acid specific protease prepropeptide (EC 3.4.21.19).
Staphylococcus aureus.
                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58AA9A4E371E2577 CRC64;
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Last annotation update)
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                        357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
Pfam; Pr00089; trypsin; 1.
PRNOSTE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 ThrGlyGlyAsnSerGlySerProvalPhe 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Protease; Serine protease.
CHAIN 69 357 POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-008-355-1 (1-2139) x Q04186 (1-357)
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                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWO-component sensor, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 357 AA; 38651 MW;
                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.591
10.00
100.00%
100.00%
1.40%
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                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deinococcus radiodurans
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                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1280;
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DB:
004186
1D 004186
2C 004186
DC 004186
DT 01-NOV-
DT 01-NOV-
DT 01-MAR
DE Glutamic
OC Staphylo
OX NCBI_Ta
RN [1]
RN [1]
RN [1]
RN ASDUENC
RA YOSHIKA
RA YOSHIKA
RE EMBL; DD
R MEROPE;
DR INTEFPR
DR PROSITE
DR PROS
                                                                      004186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RU39
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09RU39
01-M
DT 01-M
DT 01-M
DT 01-J
DE 01-DE
DE 01-DE
CO DEINC
OC 
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extracellular serine proteinase.";
EMBL/GenBank/DDBJ databases.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEINASE.
Kinase; Phosphorylation; Sensory transduction; Transferase;
                                       1A6CA4F88D96A940 CRC64;
                                                                                                 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Extracellular serine proteinase precursor (Fragment)
                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
EXTRACELLULAR SERIN
FB9B886D453B8BB7
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA
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Matches:
                                                                                                                                                                                                                                                                                                                63 LeuLeuGlyAlaAlaLeuLeuLeuGlyAla 72
                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-008-355-1 (1-2139) x Q9AJX0 (1-217)
                                                                                                                                                                                                                                                   US-10-008-355-1 (1-2139) x Q9RU39 (1-569)
                                                                                                                                                                                                                                                                                            25 CTTCTCGGAGCAGCCCTGCTGTTGGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Serine protease; Signal.
NON_TER 1 1 POTENT
SIGNAL <1 1 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00673; V8_SER; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
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Hypothetical protein; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                   Aypothetical
                                                                                                                                                                                                                                                      Alignment Scores:
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Q9S282;
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Q9S282
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STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed-11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Raerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                    Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathbf{R1."}\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 protein; Complete proteome.
266 AA; 28225 MW; F7C0ED7F231ADD3C CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lin2224.
                                                                                                                                                                                   Last sequence update)
Last annotation update)
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167 GlyGlyAsnSerGlySerProvalPhe 175
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                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein DR0714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                          Deinococcaceae; Deinococcus NCBI_TaxID=1299;
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9.00
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                                                                                                                   PRELIMINARY;
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Best Local Similarity:
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Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Dlaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species."; Science 294 849-852 (2001).

EMBL, AL56G171; CAC97453.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakataki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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1883 MW; 17F82B83C39E7808 CRC64;
                                                                                                                                                                                          al protein; Complete proteome.
452 AA; 48806 MW; OCC0B8BBF765745A CRC64;
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U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein All4462.
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Mismatches:
Indels:
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MEDLINE-21595285; Pubmed-11759840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8:205-213(2001).
EMBL; AP003596; BAB76161.1; -.
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483 AA; 51883 MW
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SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
       NCBI_TaxID=10090;
                                                                                                         Strausberg R.;
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wletzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)".

Nature 417:141-147(2002).

EMBL; AL096844; CAB50875.1; -.

InterPro; IPR002055; P. Tich, extensn.

PRINTS; PR01582; KV33CHANNEL.

PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                             Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative integral membrane protein.
SCO1807 OR SCI28.01.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 10.1 kba protein.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 CTCGGAGCAGCCCTGCTGTTGGGTGCT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
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16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.45
                                                                                                   Streptomyces coelicolor
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
                                                                                                                                                                                                                                                   STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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Taylor K.,
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail N.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandraam M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the model actinomycete Streptomyces
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC016132; AAH16132.1; -...
InterPro: IPR002412; FEL_allergen. InterPro: IPR00329; Utercoglobin. Pfam: PF01099; Utercoglobin; I. ProDom; Pp019935; FEL_allergen; I.
                                                                                                                                              Hypothetical protein.
SEQUENCE 92 AA; 10080 MW; F1A7557E0F5568BB CRC64;
                                                                                                                                                                                                                                        0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SC03512.
SC03512 OR SCE134.13.
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                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                     US-10-008-355-1 (1-2139) x Q91WB5 (1-92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LeuLeuGlyAlaAlaLeuLeuLeu 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 GlyAlaAlaLeuLeuGlyAla 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 CTTCTCGGAGCAGCCCTGCTGTTG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GGAGCAGCCCTGCTGTTGGGTGCT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL049661; CAB41211.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 protein.
102 AA; 10274 MW;
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8.00
100.00%
100.00%
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100.00%
                                                                                                                                                                                                                                                                                                                                    1.12%
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                                                                                                                                                                                                                                        96.5
8.00
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                      Percent Similarity:
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Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=13773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Ketchum K.A.,
                                                                                                                                                                                   Venter J.C.;
                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 16
                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aerophilum."
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    RA
RA
RA
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SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Lecharny A., Chefdor F., Krivitzky M., Kreis M., Mewes H.W.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Bevan M., Lecharny A., Chefdor F., Krivitzky M., Kreis M., Hohelsel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8058B0ECA90F4CE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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8
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                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 12.2 kDa protein.
F10M23.150 OR AT4G26810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                           106 AA.
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Matches:
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                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12209 MW;
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                                                           PRELIMINARY;
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SEQUENCE 106 AA; 1
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EU Arabidopsis seq
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Best Local Similarity:
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                                                           095221
                RESULT 13
09SZ21
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                                                             A PART OF THE PROPERTY OF THE 
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Richardson, D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus Bu., Peterson S., Reich C.I., McNeil L., Badger J.H., Glodek A., Zhu Coverbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE000967; ABB89289.1; --
TIGR; AF1964; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                           11 protein; Complete proteome.
162 AA; 18024 MW; 46404F9FC3EE74AA CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Transport protein part 1, authentic frameshift.
                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002)
EMBL; AE009873; AAL64155.1; -.
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-008-355-1 (1-2139) x Q8ZVA1 (1-177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-008-355-1 (1-2139) x 028315 (1-162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1401 CTTGAATATATCGGGGGGGCTTGTC 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1039 GACGTGATAGGTCGTAAGCGTGCC 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 LeuGluTyrIleGlyGluLeuVal 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 AspValileGlyArgLySArgAla 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 AA; 19519 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   90.3
8.00
100.00%
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Search completed: May 16, 2003, 13:13:33 Job time: 177 secs

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Copyr  Protein se  May 16,  US-10-C  US	DB seq length: 200000000  cessing: Listing first 45 summaries  line parameters:  line line parameters:  line line parameters:  line line parameters:  line line line line line line line line	No. Score Match Length DB ID   Description

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88070650; PubMed-2825356;
Hirah H., Maru Y., Hagiwara K., Nishida J., Takaku F.;
"A novel putative tyrosine kinase receptor encoded by the eph gene.";
Science 238:1717-1720(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPA1_HUMAN STANDARD; PRT; 976 AA.
P21709; Q15405;
01-MAY-1991 (Rel. 18, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein
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EPHAI OR EPHT OR EPHT OR EPH.

Homo.sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N -> D (IN REF. 3).
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Matches:
Conservative:
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InterPro; IPR0001254; Ser_proteas_Try.
PRINTS; PR00839; V8PROTEASE.
PROSITE; PS00673; V8_SER; 1.
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Owshalimpur D., Kelley M.J.;
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                                                                                               Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS WITH A LOW AFFINITY TO EPHRIN-A1.
                                                                                                                                                                tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: OVEREXPRESSED IN SEVERAL CARCINOMAS.
-!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic structure of the EPHA1 receptor tyrosine kinase gene."; Mol. Cell. Probes 13:169\cdot173(1999).
                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 1. EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
CYS-RICH.
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SMART; SM00606; FN3; 2.
SMART; SM00604; SAM; 1.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS01186; EGF_2; UNKNOWN 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; RECEPTOR_TYR_KIN_V_1: 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1: 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_kinase.
InterPro; IPR001426; Ykase_receptorv.
Pfam; PF00041; fn3; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF001406; pkinase; 1.
Pfam; PF001404; EPH_lbd; 1.
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ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD001495; Ephrin_receptor; 1.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; FN_III.
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                                                 SEQUENCE OF 286-976 FROM N.A.
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PIR; A34076; A34076.
HSSP; P00523; 2PTK.
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Q16568;
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                        Query Match:
                                                                                                                                               CART_HUMAN
                                                                                                                                   RESULT 4
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HVTAPPMWIERTSCAEALCGTSRHTRTLHREPWTLPGGWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                 PHOSPHORYLATION (AUTO-) (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 PROTEIN KINASE
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Hypothetical protein;
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Length: . Matches:

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Diabetes 50:2157-2160(2001).

-:- FUNCTION: Satiety factor closely associated with the actions of leptin and neuropeptide y; this anorectic peptide inhibits both normal and starvation-induced feeding and completely blocks the feeding response induced by neuropeptide Y and requlated by leptin in the hypothalamus. It promotes neuronal development and survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mutational screening of the CART gene in obese children: identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kristensen P., Judge M.E., Thim L., Ribel U., Christjansen K.N.,
Wulf B.S., Clausen J.T., Jensen P.B., Madsen O.D., Vrang N.,
Larsen P.J., Hastrup S.;
"Hypothalamic CART is a new anorectic peptide regulated by leptin.";
Nature 393:72-76(1998).
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Halsall D.J., Keogh J.M., Wareham N.J., O'Rahilly S.;
"The CART gene and human obesity: mutational analysis and population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Douglass J.O., Daoud S.;
Characterization of the human cDNA and genomic DNA encoding CART:
cocaine- and amphetamine-regulated transcript.";
Gene 169:241-245(1996)
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 del Giudice E.M., Santoro N., Cirillo G., D'Urso L., Di Toro R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a mutation (Leu34Phe) associated with reduced resting energy expenditure and cosegregating with obesity phenotype in a large
                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cocaine- and amphetamine-regulated transcript protein precursor (Contains: CART(1-39); CART(32-89)].
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MEDLINE=21371766; PubMed=11478874;
LudVigsen S., Thim L., Blom A.M., Wulff B.S.;
LudVigsen Structure of the satiety factor, CART, reveals new functionality of a well-known fold.";
Blochemistry 40:9082-9088(2001).
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   Conservative:
                    Mismatches:
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                                    Indels:
                                                                                         US-10-008-355-1 (1-2139) x YK54_AQUAE (1-1116)
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MEDLINE=21413627; PubMed=11522684;
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ventrolateral part of the arcuate nucleus, in the external zone of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 602606; -.
Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues; Signal; Disease mutation; Polymorphism; Obesity; 3D-structure.
strant. 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
            the median eminence, and also found in terminals in the periventricular part of the paraventricular nucleus. INDUCTION: By leptin.

DISEASE: A defect in CART is associated with reduced resting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CART_MOUSE STANDARD; PRT; 129 AA.
P55388, 090x28.
15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cocaine- and amphetamine-regulated transcript protein precursor (Contains: CART(1-52); CART(55-102)].
                                                                                                                                                                                                                                                                                                      COCAINE- AND AMPHETAMINE-REGULATED TRANSCRIPT PROTEIN.
                                                                energy expenditure and cosegregates with obesity phenotype. SIMILARITY: BELONGS TO THE CART FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                  L -> F (IN AN OBESE PATIENT).
/FTId=VAR_012199.
S -> T.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_012200.
FC396CA2C032AA83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
8
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                               CART (42-89).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1-116)
                                                                                                                                                                                                                                                                                                                                   CART(1-39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-008-355-1 (1-2139) x CART_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 CTTCTCGGAGCAGCCCTGCTGTTG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LeuLeuGlyAlaAlaLeuLeuLeu 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₩.
                                                                                                                                                                                                             EMBL; U16826; AAB08010.1; -. EMBL; U20325; AAB08011.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.1
8.00
100.00%
100.00%
1.12%
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116
100
108
115
61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                 28
69
82
88
102
61
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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PEPTIDE
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                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
CART_MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
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                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
normal and starvation-induced feeding and completely blocks the feeding response induced by neuropeptide Y and regulated by leptin in the hypothalamus (By similarity).
SUBCELLULAR LOCATION: Scoreted (Potential).
ALTERRATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE CART FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20504483; PubMed-11016950;
MEDLINE-20504483; PubMed-11016950;
MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                           MGD; MGT:1351330; Cart.
Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                              COCAINE. AND AMPHETAMINE-REGULATED TRANSCRIPT PROTEIN.
CART(152) (BY SIMILARITY).
CART(55-102) (BY SIMILARITY).
CART(65-102) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
MISSENG (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaecta; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-129)
                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-008-355-1 (1-2139) x CART_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
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89 129
129 113
5 1121
128 66 M.
                                                                                                                                                                                                                                                                                         EMBL; AF148071; AAF24168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 CTTCTCGGAGCAGCCCTGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                Alternative splicing; Signal. SIGNAL 1 27
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8.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halobacterium sp.
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SEQUENCE
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AC DOHOSA
DT TIS_HALNI
DT 15-JUN
DT 15-JUN
DT 15-JUN
DE TTIOSE
COS HAIODE
COS HAIODE
COS NOS NOSIC
RN SEQUE
RN SEQUE
RNA MEDLI
RNA SHUKI
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Percent Similarity:
Best Local Similarity:
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P22575;
01-AUG-1991 (
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No
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YDH1_HSVSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grosskopf R., Feldmann H.; "Analysis of a DNA segment from rat liver mitochondria containing the genes for the cytochrome oxidase subunits I, II, II, ArPase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                      -!- PATHWAY: Plays an important role in several metabolic pathways. -!- SUBUNIT: Homotetramer (By similarity).
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                  Probom; PD001005; Triophos_ismrse; 1.
TIGRPAMs; TIGR00419; tim; 1.
PROSITE; PS00171; TIM; FALSE_NEG.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
                                    SUBUNIT: HOMOLEtramer (By similarity).
SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gadaleta G., Pepe G., de Candia G., Quagliariello C., Sbisa E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete nucleotide sequence of the Rattus norvegicus mitochondrial genome: cryptic signals revealed by comparative analysis between vertebrates.";
J. Mol. Evol. 28:497-516(1989).
                                                                                                                                                                                                                                                                               BY SIMILARITY.
B6DD20B1DD85D6A4 CRC64
                                                                                                                                                                                                                                                                                                                               214
8
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Matches:
Conservative:
Mismatches:
Indels:
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01-NOV-1988 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MAATP6 OR ATP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-008-355-1 (1-2139) x TPIS_HALN1 (1-214)
                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                  EMBL; AE005037; AAG19439.1; -.
InterPro; IPR003009; FNN.enzyme.
InterPro; IPR002173; PfkB.
InterPro; IPR000652; Triophos_ismrse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 AlaSerGlyValAlaLysAlaAsp 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89362487; PubMed=2504926;
                                                                                                                                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                        52 GCTTCAGGGGTAGCCAAAGCCGAC 75
                                                                                                                                                                                                                                                                               ACT_SITE 85 85 B
SEQUENCE 214 AA; 20928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6, and several tRNA genes.";
Curr. Genet. 4:151-158(1981)
                                                                                                                                                                                                                                                                                                                            27.7
8.00
100.008
100.008
1.128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                     Pentose shunt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccone C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAT
                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                               Pred. No.:
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                                                                                                                                                                                                                                                                                                                                             Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H(+)(Out).

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

SUBCELLULAR LOCATION: Integral membrane protein.

SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                       Mathews C.E., McGraw R.A., Berdanier C.D.; "A point mutation in the mitochondrial DNA of diabetes-prone BHE/cdb
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                              Speir J.A., Stevens J., Joly E., Butcher G.W., Wilson I.A.; "Two different, highly exposed, buiged structures for an unusually long peptide bound to rat MHC class I RTl-A(a)."; Immunity 14:81-92(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D -> N.
A -> P (IN REF. 2).
S -> L (IN REF. 2).
A -> V (IN REF. 2).
W; 6074E2CCAC2B586E CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 28.7 kDa protein in DHFR 3'region (ORFI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0000855
SEQUENCE FROM N.A., AND VARIANT ASN-101.
STRAIN-BHE/CDB, and Sprague-Dawley; TISSUE-Liver;
MEDLINE-96118462; PubMed-8529844;
                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 29-41.
MEDLINE=21109741; Pubmed=11163232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 AA.
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Matches:
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TIGREAMS; TIGR01131; ATP.Synt_6_or_A; 1.
PROSITE; PS00449; ATPASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-008-355-1 (1-2139) x ATP6_RAT (1-226)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000568; ATPsynt_Asub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 LeuSerMetAspLeuSerMetAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 S
205 A
25050 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00119; ATP-synt_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J01435; AAD15019.1; -. EMBL; X14848; CAA32959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF115770; AAD22965.1;
PIR; S04752; S04752.
PDB; 1ED3; 21-JUN-00.
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100.008
1.138
                                                                                                                                                                           FASEB J. 9:1638-1642(1995)
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226 AA;
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EMBL; AE010383; AAM02152.1; -.
                                            SEQUENCE
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                                                                                                                                                                                                   Query Match:
                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                             YNJ6_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                          SEQUENCE FROM N.A.
MEDLINE=90266466; PubMed=2161148;
Biesinger B., Trimble J.J., Desroslers R.C., Fleckenstein B.;
"The divergence between two oncogenic Herpesvirus saimiri strains in a genomic region related to the transforming phenotype."; virology 176:505-514(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E04BA49D27A59D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
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                Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Herpesvirus saimiri (subgroup C / strain 488).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypochhetical protein MK0939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-008-355-1 (1-2139) x YDH1_HSVSC (1-256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 ACAACGAATACTTCCTCATCGTCT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 ThrThrAsnThrSerSerSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, A34770, A34770.
Hypothetical protein.
SEQUENCE 256 AA; 28662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M55264; AAA72928.1; -.
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1.12%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                 NCBI_TaxID-10384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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P58851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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110 Y9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94150718; PubMed=7906398; Milson R., Baynes C., Berks M., Milson R., Anscough R., Anderson K., Baynes C., Berks M., Milson R., Anscough R., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hiller L., Jier M., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R., Sims M., Smaldon N., Smith A., Smith M., Vaudin M., Vaughan K., Watsston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Watsston R., Watsston A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     '2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 38.0 kDa protein R10E11.6 in chromosome III.
R10E11.6.
Caenorhabditis elegans.
Hypothetical protein; Complete proteome.
SEQUENCE 279 AA; 31379 MW; 49474EC38B012D85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862F7D9D3E3E2E2F CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 AA.
                                                                                                                                                                                                                                                                                      US-10-008-355-1 (1-2139) x Y939_METKA (1-279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wormpep; R10E11.6; CE00308.
Interpro: IPR000261; EPS15_repeat.
PROSITE: PS50331; EH; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                        301 GTGGATCACGACTATCTGCGCGAT 324
                                                                                                                                                                                                                                                                                                                                                                   224 ValAspHisAspTyrLeuArgAsp 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 표.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 229095; CAA82351.1; -.
                                                                                                     26.7
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8.00
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                                                                                                                                                                                     Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
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                                                                                                                                                        Percent Similarity:
                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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P34550;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHIONINE AND ATP (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)0 = phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'saml, a new gene coding for S-adenosylmethionine synthetase in
                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
5-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
00
                                                                                                                                                                                                    382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate + S-adenosyl-L-methionine.
-!- PATHWAY: Activated methyl cycle.
 Indels:
                                                   US-10-008-355-1 (1-2139) x YNJ6_CAEEL (1-349)
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
                                                                                                          545 CCAACAACGAATACTTCCTCATCG 568
                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                               SAM1 OR SPBC14F5.05C.
                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                METK_SCHPO
060198;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHALCONE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: PART OF THE BIOSYNTHFIIC PATHWAY FOR ALL CLASSES OF FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY OF WHICH ARE BRIGHTLY COLORED.
-!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ardi R., Kobiler I., Jacoby B., Keen N.T., Prusky D.;
"Involvement of epicatechin biosynthesis in the activation of the
mechanism of resistance of avocado fruits to Colletotrichum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA + naringenin-chalcone + 3 CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiol. Mol. Plant Pathol. 53:269-286(1998).
-!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CH?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chalcone synthase (EC 2.3.1.74) (Naregenin-chalcone synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Persea americana (Avocado).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trac
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Persea
                                                                                                                                                                                                                                                                                                                                                                                                                                    9970A9D1195C5738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
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                                                                                                                                                                                                                                                                                                                                Transferase; One-carbon metabolism; ATP-binding. NP. BIND 123 ATP (POTENTIAL). BINDING 146 146 ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                   PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1. PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
or send an email to license@isb-sib.ch)
                                                                                                                                     Interpro; IPR002133; S-AdoMet_synt.
Pfam: PF00438; S-AdoMet_synt; 1.
Pfam: PF02772; S-AdoMet_syntD2; 1.
Pfam: PF02773; S-AdoMet_syntD3; 1.
TIGRFAMS; TIGR01034; metK: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1755 CGGTGCCTGGTACAACTATCATAC 1778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 ArgCysLeuValGlnLeuSerTyr 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                    41831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AD001672; AAC98143.1; -
                                                   EMBL; AJ001705; CAA04941.1;
                                                                                 EMBL; AL023780; CAA19323.1;
HSSP; P04384; 1MXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
1.12%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.5
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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Q9ZU06;
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RESULT 14
MPPA_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungl; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
S-adenosylmenthionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase).
       Probon; PD000453; N-C_synthase; 1.
PROSTE; PS00441; CHALCONE_SYNTH; 1.
Flavonoid biosynthesis; Transferase. Acyltransferase. ACT_SITE 165 165 BY SINTLARITY.
SFOHENCE 392 AA; 42480 MW; B08D286FB80B842E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
Transferase; One-carbon metabolism; ATP-binding.
NP_BIND 127 132 ATP (POTENTIAL).
BENINING 155 155 ATP (POTENTIAL).
SEQUENCE 393 AA; 43010 MW; 88FBZF2F14B751C3 CRC64;
                                                                                                            392
8
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                                                                                                            Length:
Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                            (1-392)
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                                                                                                                                                                                                                                        1223 GTTTTGCACAGTTTGCCAACGCAT 1246
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Pfam; PF02772; S-AdoMet_syntD2; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
Pfam; PF02797; Chal_stil_syntC; 1.
                                                                                                                                                                                                                                                     385 ValLeuHisSerLeuProThrHis 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96200878; PubMed-8621082;
                                                                                                                                                                                                            JS-10-008-355-1 (1-2139) x CHSY_PERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U21548; AAB03805.1; -.
                                                                                                                                      100.00%
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                                                                                                                                                                   ..12%
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                             25.4
8.00
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                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-5191;
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                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                         METK_ASCIM
P50304;
                                                                                                                                                                   Query Match:
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90
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393

Length:

25.4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alba H., Baba T., Fullte K., Hayashi K., Inada T., Isono K., Itch T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Maxin T., Marzobuchi K., Mori T., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Mada C., Yamanoto Y., Horiuchi T., Takeuchi Y., Mada C., Yamanoto Y., Horiuchi T., Takeuchi Y., Mada C., Yamanoto Y., Horiuchi T., Dishima T., Saito N., Sait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPORT IS EFFECTED BY THE OLIGOPEPTIDE PERMEASE SYSTEM.
SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAINSTO. / MG1655,
STRAINSTO. / MG1655,
BEDITINE-91426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
R1ley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 23-32.
STRAIN=K12 / AT980;
MEDLINE=98155149; PubMed-9495761;
Park J.T., Raychaudhuri D., Li H., Normark S., Mengin-Lecreulx D. "MppA, J. a periplasmic binding protein essential for import of the bacterial cell wall peptide L-alanyl-gamma-D-glutamyl-meso-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic murein peptide-binding protein precursor.
80000
                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                               537 AA
Matches:
                                                                                   Indels:
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                                                                                                                  Gaps:
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                                                                                                                                                                                                                                     1755 CGGTGCCTGGTACAACTATCATAC 1778
                                                                                                                                                                                                                                                                309 ArgCysLeuValGInLeuSerTyr 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 180:1215-1223(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K12;
MEDLINE-97251357; PubMed-9097039;
                     100.00%
100.00%
1.12%
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         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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P77348;
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or send an email to license@isb-sib.ch)
                                         EMBL; L07045; AAA30045.1; -.
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8.00
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium-binding.
SIGNAL 1
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290
328
366
404
442
                                                              P00740;
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Extracellular.
DEVELOPMENTAL STAGE: LOW LEVELS IN UNFERTILIZED EGGS AND DURING ERARLY CLEBANGE; LOW LEVELS IN NBUNDANCE BETWEEN LATE MORULA AND MESENCHYMEN ELSTULA STAGES TO MAXIMAL LEVELS MAINTAINED THROUGH SUBSEQUENT STAGES.
MISCELLANEOUS: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryo.";
Dev. Biol. 157:526-538(1993).
-!- FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea, Echinacea; Echinoida; Strongylocentrotudae;
Strongylocentrotus.
EMBL; U88242; AAC38216.1; -.
EMBL; AE000231; AAC74411.1; ALT_INIT.
EMBL; D90772; BAA14932.1; ALT_INIT.
EMBL; D90772; BAA14932.1; ALT_INIT.
HSSP; P06202; 1JEV.
SWISS-2DRAGE; P77348; COLI.
ECGGENE; EG13376; mppA.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
22
IGNAL
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the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-FEB-1996 (Rel. 40, Last annotation update)
11-Fibropellin C precursor (Epidermal growth factor-related protein 3)
11-Fibropellin III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 CUB DOMAIN.
SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR
TO AVIDIN/STREPTAVIDIN.
                                                                                                                                                                                                                                  PERIPLASMIC MUREIN PEPTIDE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Gastrula;
MEDLINE=93273088; PubMed=8500658;
Bisgrove B.W., Raff R.A.;
"The SpEGF III gene encodes a member of the fibropellins: containing proteins that form the apical lamina of the sea
                                                                                                                                                                                                                                                                   C6A17656836DC3AC CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 ValSerSerIleSerLeuSerTyr 21
                                                                                                                                                                                                                                                                     537 AA; 59900 MW;
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8.00
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100.00%
1.12%
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                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                          Alignment Scores:
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P49013;
                                                                                                                                                                                                                                                                     SEQUENCE
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     OR OR OR CANAL STATE OF STATE 
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CALCIUM-BINDING (POTENTIAL)
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LINKED (GLCNAC. . .) (POTENTIAL).
BE665E3E1C05E6EE CRC64;
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CALCIUM-BINDING (
CALCIUM-BINDING (
CALCIUM-BINDING (
CALCIUM-BINDING (
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PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_2; 6.
Biotin; EGF_1ike domain; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBROPELLIN C.
EGF-LIKE 1.
CUB.
EGF-LIKE 2, CALK
EGF-LIKE 3, CALK
EGF-LIKE 4, CALK
EGF-LIKE 6, CALK
EGF-LIKE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
Interpro; IPR000152; Asx_hydroxyl.
Interpro; IPR000088; Avidin.
Interpro; IPR000089; CUB_domain.
Interpro; IPR0000561; EGF-like.
Interpro; IPR000742; EGF_2.
Interpro; IPR001881; EGF_Ca.
Interpro; IPR001438; EGF_E.
Fam; PF00008; EGF; 8.
Pfam; PF00008; EGF; 8.
                                                                                                                                                                                                                        PRINTS; FANOLACY, CUB; 1. SMART; SMO0042; CUB; 1. SMART; SMO0179; EGF_CA; 7. SMART; SMO0101; EGF_Like; 1. PROSITE; PSO0010; ASX_HKPROXYL; 8. PROSITE; PSO0022; EGF_LI; 8. PROSITE; PSO0777; AVIDIN; 1.
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US-10-008-355-1 (1-2139) x FBP3\_STRPU (1-570) Gaps: DB:

Search completed: May 16, 2003, 13:07:56 Job time: 48.5 secs

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

May 23, 2003, 01:38:11; Search time 3816 Seconds (without alignments) 16313.129 Million cell updates/sec Run on:

US-10-008-355-1 2139 1 atgcaaatgaaattaaaaag.....aagagctgaagttgatctaa 2139

Perfect score:

Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmb1:\* Database :

gb\_ro:\* gb\_sts:\* gb\_sy:\* gb\_un:\* gb\_ba:\* gb\_htg:\* 9b\_in:\*
9b\_om:\*
9b\_ov:\*
9b\_pat:\*
9b\_ph:\*

em\_fun:\* em\_hum:\* gb\_vi:\* em\_ba:\* em\_mu:\* em\_in:\*

em\_or:\* em\_ov: em\_pat: em\_pl:

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em\_htg\_other:\* em\_vi:\*
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em\_htgo\_mus:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	cription	AE004008 xvlella f	anthomo	AF429315 Homo sapi	Gold	AY051790 Drosophil	rosophi	rosoph	rosophi	rosophi	otryti	M15810 R.meliloti	inorhi	AF429315 Homo sapi	enopus	AC121850 Mus muscu	L24395 Emericella	AL583920 Mycobacte	X79242 Paracoccus	AC099055 Homo sapi	AC105363 Oryza sat	AC118980 Oryza sat	AL646080 Ralstonia	AC017879 Drosophil	AC007414 Drosophil	AE003831 Drosophil	AC019786 Drosophil	rosop	AL669952 Mouse DNA	lus musc	OWO.	lomo sap	AP002997 Mesornizo	AF433301 ACLINOSYN	AXIIU931 Sequence	ADZSOIUZ POUOSPOIA	AEU04/50 Pseudomon	ACIU4321 Oryza sat	AJ248283 Pyrococcu	edneuc		X66412 C.reinhardt	N.	1231 Homo sap	905 Homo s	3148 Homo sap	
COLUMNIC	Ω	AE004008	AF01173		AF4034	AY051790	AC01425	AC00823	AC00835	AE00368	-	RHMNTRE	SME5917	AF429315	AF05178	AC12185	EMEFLBA						AL646080					AC007452							AXIIO931				_	AX04110	-	U	MOCDRN	AC091231	AC01690	AC02314	,
	Le	.0 10689	9 10811	2.0 125020 9	.0 820	.0 1461	.0 76748	.0 148847	.0 162593	.0 224400	.9 720	.9 1700	.9 329100	.9 125020	.9 4314	.9 202306	.8 3060	.8 348450	.8 13155	.8 155962	.8 100986	.8 126637	.8 190050	.8 31896	.8 172904	.8 275390	.7 38408	.7 146153	.7 183213	.7 195533	.7 133691	.7 170398	.7. 329709	7 02/40	018 /.	7 10005	. / 10925 10925	./ 13/U3/ 	.7 307150	.7 349980	.7 1129	.7 1496	.7 6709	.7 95727	.7 170630	.7 185097	
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## ALIGNMENTS

Xylella fastidiosa 9a5c, section 154 of 229 of the complete genome. AE004008 AE003849 RESULT 1
AE004008/c
LOCUS
DEFINITION
ACCESSION
VERSION KEYWORDS SOURCE

Xylella fastidiosa 9a5c. Xylella fastidiosa 9a5c Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

ORGANISM

REFERENCE AUTHORS

Xylella.

1 (bases 1 to 10689)
Simpson,A.J., Relnach,F.C., Arruda,P., Abreu,F.A., Acencio,M., Alvarenga,R., Alves,L.M., Araya,J.E., Bala,G.S., Baptista,C.S., Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HQREKAEEEVWKFPKDRYALYASSTLHTVSHKRRIPKKVWSALSVCVTCSVIGLVFWH
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                                                                                                                                                                                                                                                                                      The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis Nature 406 (6792), 151-157 (2000)
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                                                                                           /translation="MCSRSFPLYFISALGLTLVISFPFCLFAQNVPPTVEVVPTSVRY
SYLSDQVSYSATFBARSTALVNGVRYTVPVDISASTICLSAKNAVNSRGMAFVNVYS
MLSGLINGAGWYDTHFEWRSCPALKEIPVGTVAWWORPGDGHYFYSVTPOFLIA
INAYGSSLSPPQPLVTSSGPSSVSSERWLYHLEGGGEVIGHLSKTDQSVPDYSSGLPP
                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKSYIDRGIAFFSLLSTSSLVFAADAAGASFDAGAAVTALGAIS
GAVALIGAAKLAPAAISVGWKWLKGAIFG"
complement(4724. .4924)
                                                                                                                                                              SVILDTDLGQLVRSDPSTVNAVLTDSQTGAVLLTPEIVSALNKLRRSLEDELKASHAP
DQQPSSGGASSPPSSSGTAWPSFCSWASVVCDFIDWVKSDEFLKKPLVPPDVPYVDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by sequence
Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAQQLMSLYCTQYDVEARTCSQQAWMVPPSLLPPISYEDVRILL
PHIVMCFLVAWGFHFLFTVVRD"
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                                                                                                                                                                                                                                                                                             /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"hypothetical protein"
/protein_id-"AAF84685.1"
/db_xref-"GI:9106970"
                                              /product-"hypothetical protein"
/protein_id-"AAF84683.1"
/db_xref-"GI:9106968"
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/protein_id="AAF84684.1"
/db_xref="GI:9106969"
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complement(4724. .4924)
/gene="XF1879"
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/gene="XF1878"
complement(4481. .4702)
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similarity; putative;
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                                                                                           1723 TACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACA 1782
                                                                                                                                                                                      1783 GGCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAAT 1842
                                                                                                                                                                                                                                                                                 1843 ATCCTCGACCTCTTCCGCACCAAAACTATGGTCGCTATGCCGA-----GAACGGTCAG 1896
                                                                                                                                                                                                                                                                                                                             8654 CTGATTAATGCGATAAAGGCAAAGAGCTACGCCAATTTAGCCGATCAGCGTATTGGCACT 8595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2017 GGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACATCCGCTACGTT 2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas axonopodis pv. citri str. 306.
Xanthomonas axonopodis pv. citri str. 306
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furla Quaggio, R.B., Monteiro Vitorello, C.B., Van Sluys, M.A., Almei Jr., N.F., Alves, L.M.C., do Amaral, A.M., Betrolini, M.C., Camargo, L.B.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comparison of the genomes of two Xanthomonas pathogens with differing host specificities Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8831 TACAACAAGAGTCATGGCAAATTTGTTTACCCAGACGCCAACTCATCATTACGTATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1957 TTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE011732 10811 bp DNA
Xanthomonas axonopodis pv. citri str. 306,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the complete genome.
AE011732 AE008923
AE011732.1 GI:21107161
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Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighleri, E.F., Franco, M.C., Groggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite, J.T., Leite, Machado, M.L., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M. B.N., Martine, E.C., Machado, M.A., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Tankita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVIGEDVLITGAGPIGIIAAGICKHIGARNVVYDVADVADFRLKLAADMGATRVVNVSKT
SLKDVMADLHMEGFDVGLEMSGNSRAFNDMLDCMYHGGKIAMLGIMPRCAGCDMDK11
FKGLTVQGIYGRKMYETWYKMTQLVLSGFPLHKVLTHQLPIDDFQKGFDLMEEGKAGK
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QDIEQLTPGSSAFKAVEKLPGVQFQSADPFGTYEWSTQVTLHGFDQSRLGYTLDGIPL
GNMSYGVTNGLHITRAIISENLGSVEIAQGAGALGTASNTNLGGTWQFYSADPQTTPG
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QWGDGNRLSLEVDTSRRKEYDYMDLSLTSQRALGWNYDYLQPDWATAVQMARAYQNTG
ATSGVANGYPQSLAGLPSDYSWLDASYYAGGGLRRDNLAGLSGTFVFGGATLDASGYY
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SPCTAVQTVGCASILSBVGAAN HSAGADLALMWRPPEGLSWLNSLSBWNSRSYDDD LINNG
VVAT SGKDVVG I PALMESSSASYQIGNLRLDLDGKY VDKRY TYFLNDSQVPSYWLENA
GARYDFGRVGGVADVALALNI SNLTDKRYFASTGTNGY VASDPDGY NQTMVVGAPRQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tränslation="mkaLvkREanKGIWLEQvPvPTPGPNEVLIKLEKTAICGTDLHI
YLWDEWSQRTIEPGLTIGHEFVGRVAELGSAVTGYQIGQRVSAEGHIVCGHCRNCRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPHLCPNTVGIGVNVNGAFAEYMVMPASNLWPIPDQIPSELAAFFDPYGNAAHCALEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
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SP 05508-900,

    .10811
/organism="Xanthomonas axonopodis pv. citri str. 306"

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Kitajima,J.P.
Direct Submission
Submitted (28-NOV-2001) Departmento de Bioquimica,
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="threonine 3-dehydrogenase"
/protein_id="AAM35905.1"
/db_xref="G1:21107162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:190486"
/note="pathovar: citri"
complement(293. .1315)
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/gene="fecA"
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/gene="XAC1024"
4369. .6450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="fecA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="tdh"
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/transl_table=11
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FAAVEAARGDTALTYFEFGTLAALMLFQQSALELÄVLEIGLGGRLDAVNIVDSDVAVI
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1936 GGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTCGAT 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7033 GGCAACTCCGGTTCGCCGGTGATGGACGCGCAAGGTGGTCGGCCTGGCCTTCGAC 7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                /note="identified by sequence similarity; putative; (
located using Blastx/Glimmer/Genemark; dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996 GGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7093 GGAAATTGGGAGTCGGTGAGCAGCAGCAGCTGGATCTTCGACCCGGCAATGACCCGCCAATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2056 AGCGTGGACATCCGCTACGTTCTTCATGATTGACAAATGGGGTCAGTGCCCCCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="16"
/map="16q4.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
complement(35581. 35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers
1. 125020
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 10811;
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 61.6; DB 1; 56.4%; Pred. No. 5e-05; Live 0; Mismatches 89;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2116 ATCCAAGAGCTGAAGTTGATCTAA 2139
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8242. .9540
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/note="XAC1029"
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                                                                                                                                                                                          /codon_start=1
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/gene="folc"
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.9
Best Local Similarity 56.4
Matches 115; Conservative
                                                                                                                                                                  synthase"
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/protein_id="Ama35907.1"
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/db_xref="G1:21107164"
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SQNTCAPLIKSIDHSWKAGHGQDPARWAEYDAWVPYKGELTMGYFQRHDIPYYHALAD
                                                                                                                                                                                                                                 GSTAGNAATTQAEHLVAAIAADVRANRLPQVSWVIPPTAYCEHPEAPPAYGESLVARL
IDALTANPEVWAKTALIINYDENDGFFDHVPAPLPALDARMGRSNVDTHGEVYDGVPI
GLGIRVPMLVISPWTRGGWVNSQVFDHTSVLRLLERRFGVAEPNISPWRRAVSGDLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MMDAQGKLVGLAFDGNWESVSSNWIFDPAMTRWIAVDGRYLRWI
MTEVAPAPQLLKELGVR"
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                                                                                                                                                                                     AFTICDGYYCSLHGPTNPNRMYLFTGTSGPSVGNVGAQAVTNADDGNWTADMARDKPG
YAALQWTTYAQRLQAAGVDWRVYQEYDNFGCNSLAYFSHYRDLRTDDERYLRARACVP
                                                                                                                                                                                                                                                                                                      VFDFRKPDDSALSALPSVDDYRÅRTAAVRDKPLPSAPAAATWPRQEPGQRPARALPYA
LYDHRVQEGAAVQLQFVRSGAAAAFNVINSARAGGGFWYXTVLGFQLDDAFTGATH
EGXVALRVHGPRGFTERFAGQPRSAAPSAAPWYDRAGGDALVLETGNAGQRACTVO
LRALDYADPSARTLSLAAGQRETIRLALAASDHWYDLVVEQPGSAFRRRLAGHLETGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MRPNLFAVSVLATLAVAASAQAGEGMWVPQQLPEIAGPPQQAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGAVVALGGCTASFVSPQCLVVTNHHCAYGAIQLNSTAQKNLIK
DGFNAVRPADELSAGPSARIYVLDAITDVTAPAKAAMATPVRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ldentified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark"
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located using Blastx/Glimmer/Genemark"
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/transl_table=11
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/transl_table=11
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7329. .7973
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/gene="XAC1025"
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6791. .7054
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/gene="XAC1025"
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/gene="pgmA"
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/rpt\_type=tandem

repeat\_region

LQIDRAVASPLSRAQATAKAALGASRQALLQTDADLQEIAHGEWEGLLASEINDKDPA RLRAWREEPDTVLMPGGESLRQVLDRSWRGLMRAADGLGAHDTLLVVAHDAVNRVILC KILGLPLSRLMSFRQAPTTLNLLEGDDVEHLEVVRLNDCAHHTPFFGEAKHRAL"

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LTGKRDBERGWYRLLSTLTKKSTPSTWYTSDWTLDTTTGLTKPPVTGFNARATVKDSAI
VWWFPAPDIATSARRAIVSPMSCVFE"
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revealed by genome characterization of Golden shiner reovirus, Grass carp reovirus, Striped bass reovirus and golden ide reovirus (genus Aquareovirus, family Reoviridae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thoses 1 to 1461)
Stapleton, M., Brokstein, P., Hong, L., Adbayani, A., Carlson, J.,
Chavez, C., Gorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,
Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K.,
Liewis, S. E., Rubin, G. M. and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-100-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:

Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1858 CGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCG 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1918 AACAACGACATCACGGGGGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTG 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744 CGCCCGACGAGGGGGGTTGCGATGTCGGGAGCGGGGAACCATAACGATGGCGGAGTC 685
                                                                                                               2 (bases 1 to 820)
Attoni,H., de Micco,P. and de Lamballerie,X.
Direct Submission
Submitted (30-30L-2001) Virologie, Faculte de Medecine de
Marselle, 27 Boulevard Jean Moulin, Marselle 13005, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                     /product="non-structural protein NS3"
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                                                                                                                                                                                                                                                                              /organism="Golden shiner reovirus"
//Ob_xref="taxon:185783"
//note="Golden shiner reovirus
segment: 11"
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                                                                      Gen. Virol. 83 (Pt 8), 1941-1951 (2002)
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PUBMED
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AUTHORS
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JOURNAL
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                                                                                                                   REFERENCE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                               /translation="MSSGGRFNFDDGGSYCGGWEDGRAHGHGVCTGPKGQGEYTGSWS
HEPVLGGYTWPSGATYQCTGTAAAGKHGIGLESKGKWYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQGYGTETYSDG" 4254 others
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                                                                                                                                                                                                               complex between plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601den shiner reovirus segment 11 non-structural protein NS3 gene, AF403408
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1 (bases 1 to 820)
Attoul, H., Fang, Q., Jaafar, F.M., Cantaloube, J.F., Biagini, P., De Micco, P. and De Lamballerie, X.
Common evolutionary origin of aquareoviruses and arthorouser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evolutionary origin of aquareoviruses and orthoreoviruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51081 KGCSGYMSMGMYGSGRTSKYCSYTGGYCSKCSAKMCKSKSTSKSCCTKSKYS----CSMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50905 MMRDMWYDKMRWKVSSGTRGYHBHSAWMCKSMSRDSDSGYSGMYHMKSYWKSSASKHMYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51141 SRWWTSSMACMYWYKGSRRKTKSMATSGCMRWGAMRSKGGMRKYWSCRYKGMRWGRWSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 GCCAAAAAAGAAAATGCAGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550 AACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 CCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACG
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                                                                                                                                                                                                                                   membrane and endoplasmic reticulum"
                                                                                                                                                                                                          /note="component of the junctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
                     .>36887)
                                                                                           .>36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 43.2; [
9.8%; Pred. No. 5.9;
                                                                                                                                       /product="junctophilin 3"
complement(<36507. .36887)
                                                                                                                                                                                                                                                                            /product="junctophilin 3"
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                     complement(<36507.
                                                                                         complement(<36507.
                                                                                                                                                                                                                                                           /codon_start=1
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  /rpt_unit-ctd
                                           /gene="JPH3"
                                                                                                                   /gene="JPH3"
                                                                                                                                                                                     /gene="JPH3"
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sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAS, and reverse transcriptae errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site chaeficity. Derkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADKOPLOEVGFINSAADHLAEMAKPŜNVLMLRVSVDGVAKAHGEKSVAVEEANKLLSA
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NIILWFWVVFGLSLLAICYAIAAMDPGRDSIIYRMTSTRIKKDN"
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TDASLNALAAELEAANEPVCDINFEQFDDGVQAWKSCFGDFEAPAAK PTKHLNPSLHT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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/db_xref="FLYBASE:FBgn0037671"
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/db_xref="GI:15291891"
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/db_xref="taxon:7227"
/map="85D8-85D9"
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E (bases 1 to 148847)

E (clniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H., K., Evans,C.A., Gocayne,J.D., Amanatideas,P.G., Brandon,R.C., Rogers,Y., An.H., Baldwin,D., Banzon,J., Bescon,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hostin,B., Moxiand,T.J., Hostin,D., Howland,T.J., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nuoco,J., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,Ho, Rubin,G.M. and Venter,J.C.
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                                                                                                                                                                                                                                      This sequence was identified as CDM:10211789 by the submitter. For further information on this sequence e-mail to fly@celera.com. * NoTE: This is a "working draft" sequence. * This sequence will be replaced * This sequence as soon as it is available and * by the finished sequence as soon as it is available and * the accession number will be preserved.
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2 (bases 1 to 148847)
Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter.E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
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                                                                                                                                                                Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
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Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
21897 a 15665 c 15830 g 23356 t
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                                                                                                      Adams, M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                          Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley abboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 17, 2001 this sequence version replaced 91:6984365. Sequence submitted by:
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Drosophila melanogaster.

Drosophila melanogaster

Eukaryota: Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases I to 162593)

1 (bases I to 162593)

1 (Claniker, S. E., Adams, M. D., Kronmiller, B., Tyler, D., Wan, K. H., Gelniker, S. E., Adams, C.A., Gocayne, J. D., Amanatides, P. G., Brandon, R. C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K. Y., Busam, D. A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001
BAC clone
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="3R"
/map="85D-85D"
/clone="BACR3ZW04 (D969)"
/clone=1bb="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAGTTTGC 1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%; Score 42.2; DB 3; Length 148847; 49.3%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                              Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCATCCTGTGGTTCATGGTCGTCTTCGGACTGTCTTCTGCTG 8162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Matches 110; Conservative
                                                                                                                                                          Rubin, G.M.
Direct Submission
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VERSION
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JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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Direct Submission

Submitted (02-Aug-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Sep 6, 2001 this sequence version replaced gi:12957666.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Borkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Gargi, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeliffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapeleton, M., Strong, R., Svirskas, K., Tector, C., Williams, S.M., Sequencing of Drosophila chromosome 3R, region 85D-85D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Calace, C., Chew, M., Cissiolka, L., Boyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
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49.3%; Pred. No. 11;
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/gene="CG9746"
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Adams, M.D., Celliker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,
Amanatides, P.G., Scherrs, S.E., Richards, S., Ashburner, M., Henderson, S.N.,
Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,
Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,
MANLOs, G.L., Abrill, J.F., Agbaylani, A., Anh, H.J.
Andrews-Ffannkoch, C., Bayter, E.G., Helt, G., Melson, C.R., Gabor
MANLOs, G.L., Abrill, J.F., Agbaylani, A., Anh, H.J.
Baxendale, J., Bayrakaragull, L., Beasley, E.M., Beson, K.Y.,
Bencos, P.V., Berman, B.P., Bhandari, D., Ballew, R.M., Beson, K.Y.,
Bencos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D.,
Bockham, R.P., Bouck, J., Brokstein, P., Brothter, P., Burtis, K.C.,
Busam, D.A., Butler, H., Cadicu, E., Center, A., Chandra, I.,
Buck, J., Bouck, J., Brokstein, P., Brothter, P., Durbir, K.C.,
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Dudn, P., Durbin, K.J., Evangelista, C.C., Ferriera, S.,
Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S.,
Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,
Gunn, P., Harnis, M. Harris, N.L., Harvey, D., Helman, T.J.,
Well, M.H., Ibeyamm, C., Jalali, M., Kalush, F., Karpen, G. H., Ke, Z.,
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Kennison, J.A., Ketchum, K.A., Liu, X., Matrei, B., McIntosh, T. C.,
Li, J., Liz, Z., Lidang, Y., Liu, X., Matrei, B., McIntosh, T. C.,
McLeod, M.P., McPherson, D., Merkulov, G., Milshian, N.V., Modary, C.,
Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden Kiamos, I.
Simpson, M., Skupski, M.P., Yang, S., Yao, G., X., Wethnert, C., Stapleton, M., Skupski, M.P., Walls, S., Yao, G., X., Wethnert, J., Wethnert, C., Wethnert, J., Wethnert, J
224400 bp DNA linear INV 05-OCT-2000 Drosophila melanogaster genomic scaffold 142000013386035 section 7 AE003682 AE002708 AE003682.2 GI:10726402 HTG.
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
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                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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On Oct 9, 2000 this sequence version replaced gi:7299142.
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/chromosome="3R"
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1. .224400
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                                                                                                                                                                                                                                         Drosophila melanogaster
Drosophila melanogaster
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complement(join(3004. 3235,3300. 3914,3972. .4605,
4986. .5199,5255. .6265,6330. .7367,7561. .7747,7809. .>7907))
/gene="CG9746"
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/db_xxref="FLYBASE:FBan00037663"
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4986. .5199,5255. .6265,6330. .7367,7561. .7747,7809. .7906))
/gene="CG9746"
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/db_xref="FLYBASE:FBgn0037664"
join(9619 ..10588,10978. .11126,12073. .12352,12809. .13132,
                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEEVAVKKRGRPSKASVGGKSSTAAVAA1SPGIKKRGRPAKNKG
SSGGGGQRGRPPPKASKIQNDEDPEDEGEEDGDGDGGSGAELANNSSPSPTKGRGRPKSS
GGAGSGSGDSVKTPGSAKKRKAGRPKKHQPSDSENEDDQDEDDDGNSSIEERRPVGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAGSVNLNISRTGRGLGRPKRRAVESNGDGEPQYPKRRGRPPQNKSGSGGSTGYVPTG
RPRGRPKANAAPVEKHEDNDDDQDDENSGEEEHSSPEKTVVAPKRGRPSLAAGKVSK
EETTKPRSRPAKNIDDDADDADSADQGGHNSKRESNDEDRAVDGTPTKGDGLKWNSDG
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WWILLSDFASFKPTYLPEDNPADYTYFFDTSRŘRTCYIAPERFVKTLASDDDGGNGN
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DLVEKHLAGIENERLRNILASMIDIHSMNRKSAİDYLDQERGQLFPEYFYSFLQSYLQ
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GLILIITVVTSCIRGLKQSNTKIAALELLQKLSKYTTSETILDRILPYILHLAQKSPA
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LAKSAVYFLEETQRNAPNDMPTPRYEAELNALHIIVRQAVLSLLTDSQPVVKQTLMES
GICDLCAFFCKEKANDVILSHIMTFLNDEDKNLRGAFYDNIAGVAGYVGWQASDILVP
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GMATATRANICSAIDVQCKINPALGAFLKAPLIOFVRFPHILLDCVHPPPPPRDIFDSVLR
FQDIHHFIRLLEARSPRSOTRQGALPOYEEMGOTLRHLFRRLSSEGITDLIEMQLLA
MNPFLISMKHKALQDLDDTASGNGRIVVSRKOVÄCHEYPLADKASKMPLDNRSSEGPT
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GGIVAMDTRMQHSAWRLQNELRHGVITTICADPTGSWLATGTSGGKHICWDLRFRLPI
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/db_xref="FLYBASE:FBan0009745"
/db_xref="FLYBASE:FBgn0000412"
complement(join(672. .1324,1643. .2057))
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/db_xref="FLYBASE:FBqn0037663"
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/db_xref="FLYBASE:FBgn0000412"
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/db_xref="FLYBASE:FBgn0037664"
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/db_xref="G1:7299144"
                                                                                                                                                                                                                                           /protein_id="AAF54341.1"
/db_xref="GI:7299143"
                                                                                                                                                               /note="D1 gene product"
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.10588,10978. .11126,12073. .12352,12809. .13132,

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CDS

24193 CATCATCCTGTGGTTCATGGTCGTCTTCGGACTGTCTGCTG 24235

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720 bp mRNA linear PLN 03-SEP-1999
nitrogen deprivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr) The cDNA library to be analyzed within the framework of this
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Sinorhizobium meliloti
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 1700)
Szetco, W.W. Nixon, B.T., Ronson, C.W. and Ausubel, F.M.
Identification and characterization of the Rhizobium meliloti ntrc gene: R. meliloti has separate regulatory pathways for activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1482 CGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGA 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1542 GAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTGCTCGCGCTATTCAGGC 1601
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                                                                                                                                                                                                                                                                           Pezizomycotina; Leotiomycetes;
                                                                                                                                                                                                                                                      Eukaryota: Fungi: Ascomycota: Pezizomycotina; Leotiomycetes
Helotiales; Sclerotiniaceae; Botryotinia.
1 (bases 1 to 720)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
Direct Submission
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R.meliloti ntrC gene, complete cds, and ntrB gene, 3' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Botryotinia fuckeliana"/strain="T4"
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHMNTRBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pp
                                                                                                                                                                                                                                               TQGNDKATHHHQQKRSTATEPESENGLMNLLPLVMQAVSSFAGPEGQSTQEKHKSHAW
VLPPFLEHIHVLMDHFSNSELADALYEKSGVNKIMKGFKGSDGKLDYDKLFESLNNQS
FRRRWIKSATLYLADWASYLANPEVYLRYFQTAQIMFNGLLKSQGYPKQTHFDPSRPG
                                                                                                                                                                                                                                                                                                             ETISNLLDHVAKHHLNVKIDSRQYVKPAVGYAKĒLKLGQARGLLQFNĀTEISDKLTD
TULEVIEPVEVKHRAYRYISKSPQCDRYVLCQLNAAALDQQEKQROHDQYQQHQPK
QSQLNRPTSASSLIAGVSPKIVKIGSMGAAIFISTETGTPFWTLFGVINAPYNCEAKY
PVDCNGFHEGEAKVTTEYIHNEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF54344.1"
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/db_xref="FLYBASE:FBGN0037665"
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                                                                                                                                                                                                   NQNGGNNGGGGGGLAGVASLIGTFMQASGKSGGAGGGGGGGGGGGGGULSGLGSTLSKS
QGGQSGGFDPSIIGNVLEMFTQGDDEEATPQQKRSNGGGSESGIGLDTILQVASAFMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESIRSLPVYQDDVWMVSYPRTGSTWAQEMVWLLGHQLDYVAAEQDLRLRSPLIELSAL
FSIDHHETVAQKFGNTVDLVRNLPRPRFARSHLPWPLLPEQFETVKPRIVYTARNPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCVSYYHYFKLLHGMNGDFEQFVDLFLEGHTPMGSYMRHVLPFWKRSQDDNVLFIKYE
DMVKDLPSVVRRCARFLGVQSLLDVSTLQKLCDHLTFDKMRANKAVNLEKLLPESSSK
FIRNGKIGDMRNHMGNEMSERFDEWTERHMRGSGLNFDYV"
                                                                                                                                                                               /translation="MYVRRALLLACLLCLQPLGPSMASEDESNPLLDMASMFFQEALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24013 GGCCGCTATCAGCCGCCTGCTTGCTGCCTCCCAGAAGTCCAGCGACTCGGTTCTGTTTGT 24072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24133 CACCACCAACAACCTGGCCGTCTACTACGGCAGCGACTACCCGGTGATCTTCAA 24192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1530 CAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTCG 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1590 CGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTT 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="FLYBASE:FBgn0037666"
join(<16163. .16213,16307. .16490,16637. .>16836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="FLYBASE:FBan0016735"
/db_xref="FLYBASE:FBgn0037666"
join(16163. .16213,16307. .16490,16637. .16836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 224400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FLYBASE:FBgn0037665"
join(14006. .14358,14503. .>15118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref""FLYBASE:FBan0016733"
/db_xref="FLYBASE:FBan0037665"
join(14024. .14358,14503. .15118)
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/db_xref="FLYBASE:FBgn0037664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="FLYBASE:FBan0016733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="FLYBASE:FBan0016735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note-"CG16733 gene product"
                                              /note="CG8420 gene product"
                                                                                         /protein_id="AAF54343.1"
/db_xref="GI:7299145"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="CT37237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="CT37245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CG16733"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           >16836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="CG16733"
13366. .13446)
/gene="CG8420"
                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CG16735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CG16735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1650
                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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/protein_id="Cac45913.1"
/db_xref="G1:15074267"
/db_xref="SPTREMBL:092019"
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GAELMIDQIGTGRIFADGHLPRSYPFGRGLNYQIRVASADALVRALTDRGIALYLPLE
ERWYRRGDEEVGNRQFVVADPDGYLLRFYEPLGRRPFTS"
                                                          \mbox{Gouzy,J.} Direct Submission Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVRORLAASPTLLARLGEITTDNLSOMPTLSMNEÖHPNDVWRLVHATGGAÏEIAHRPV
VGCSDFLILERAAIEGMGIALLPDHICERAFRTGALVPVLPEWTSGNVMVHLVFPSRH
GLLPATRALIDFLAENLIKALERCREVDPRPAASFEI"
                                                                                                                                                                                                            France, Indoordanismes, UMR215-CNR6-INRA, BP27, F-31326 Castanet, France, Laboratoire de Genetique et Developpement UMR6051-CNRS, Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes, Universitaet Bielefeld, Biologie IV (Genetik) Universitaet Bielefeld, Germany, Unite de Biochimie physiologique, D-33615 Bielefeld, Germany, Unite de Biochimie physiologique, Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6, B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr http://sequence.toulouse.inra.fr/meliloti.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MQDLNDIALFAAVVKHNGFSAAARDLNVPKSKLSKHVARLEBQL
GVRLLERSTRKLRMTEVGRIFYEHAQGLLDGVAAAEARIAAVRAEPTGVVRLACPIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPMLADILPAFHRRYPGVRLLITASNRRIDLIEERIDVALRARDQLDTDSQLIVRKFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="codon recognized: ACA; predicted by tRNAscan-SE"
/Avidence=not_experimental
complement(373..798)
/gene="SMcO4435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="miscellaneous; hypothetical/global homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(914. .1855)
/gene="SMc01330"
/function="miscellaneous; not classified regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="PUTATIVE TRANSCRIPTION REGULATOR PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="CONSERVED HYPOTHETICAL PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Product confidence : hypothetical
Gene name confidence : hypothetical
predicted by Homology"
                                                                                                                                                                                           Laboratoire de Biologie Moleculaire des Relations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Product confidence : putative
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sinorhizobium meliloti"
/strain="1021"
/db_xref="taxon:382"
152. .227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by Codon_usage_
predicted by Homology
predicted by FrameD"
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/gene="acpD OR SMc01329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(914. .1855)
/gene="SMc01330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(373. .798)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="tRNA-THR_TGT"
/product="tRNA-Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="tRNA-THR_TGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                 (bases 1 to 329100)
                                                                                                                                          EO
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                              REFERENCE
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                                                                                                                 JOURNAL
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                                                                                     TITLE
                                                                                                                                                                     COMMENT
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Rhizobiaceae: Sinorhizobium.
1 (bases 1 to 329100)
2 Capela.D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J., Boistard,P., Becker,A., Boutry,M.; Cadieu,E., Dreano,S., Gloux,S., Godie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D., Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U., Renard,G., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F. Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021
Droc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGDGLVVTDVVMPDBNAFDLLPRIKKARPDLPVLWGALSRAGYDVRITSNAATLWRWIA
AGDGLVVTDVVMPDBNAFDLLPRIKKARPDLPVLWGSAQNTFWTAIKASEKGAYDYL
PREPLUFELIGIIGRALAEPKRRPSKELDBSOGMPLVGRSAMQETTFVRLARLMQTD
LTLMTTGESGTGKELVARALIBVGKRRNGFPVAINNAAIPRDLIESELFGHEKGAFTG
AQTRSTGRFEQAEGGTLFLDEIGDMPWDAQTRLLRVLQQGEYTTVGGRTPIRSDVRIV
AATNKDLKGSINGGLRREDLYYRLNVVPLRLPPLRDRAEDIFDLVRHFVQQAEKEGLD
VKRFDGEALELMKAHPWGON RELENLVNRLTALYPQDVITREIIENELKSEIPDSPI
EKRAARGSSLGISGAVEBNWRQYFASFGDALPPSGLYDRYLAENTEIENELKSEIPDSPI
EKRAARGSSLGISGAVEBNWRQYFASFGDALPPSGLYDRYLAEMEYPLILAALTATR
                                                                                                                                                                                                                                                                                                                                                                                                        /translation="EFCVHDNGPGVPPDLLPHLFDPFITTKTNGSGLGLALVAKIIGG
HGGIVECDSQHSRTTFRVLMPASKGLAADEETPMTKGTNG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1654 GCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATG 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1714 CGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTAT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                741 ATGATCACCGGCGACCGCCACCGCAAGGAACTCGTTGCCCGTGCACTGCACTAT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 GCGCCATGCAGGAAATCTACCGCGTGCTTGCGCGGCTGATGCAGCCGACCTCACGCTG 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sinorhizobium meliloti 1021 complete chromosome; segment 6/12. AL591787 AL591688
AL591787.1 GI:15074266
of nitrogen fixation genes in free-living and symblotic cells J. Bacteriol. 169 (4), 1423-1432 (1987)
87165745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9%; Score 41; DB 1; Length 1700; 55.2%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Indels
                                                                                                                                                                                      /organism="Sinorhizobium meliloti"
/db_xref="taxon:382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                             /transl_table=11
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/db_xref="G1:152392"
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/db_xref="G1:152393"
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                                                                                                                                    Location/Qualifiers
1. .1700
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/transl_table=11
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Sinorhizobium meliloti
                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                         /note="ntrB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80; Conservative
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                                                                                                                                          FEATURES
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AADGPMPQTREHILLARQVGVPAIVVFLNKVDQVDDAELLELVELEVRELLSSYEFPG
DDIPIVKGSALAALEDSDKKIGEDAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSI
SGRGTVVTGRVERGIVKVGEEIEIVGIRPTTKTTCTGVEMFRKLLDQGQAGDNIGALL
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IDAAPEEKARGITISTAHVEYETPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGVDRNGVERGQILCKPGSVKPHRKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTD
VTGIVTLPEGTEMVMPGDNVTVDVELIVPIAMEEKLRFAIREGGRTVGAGIVASIVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD 117496 GCCGCCATGCAGGAAATCTACCGCGTGCTTGCTGCGCGGCTGATGCAGGCCGACCTCACGTG 117555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 117556 ATGATCACCGGCGAGTCCGGCAAGGAACTCGTTGCCCGTGCACTGCACGACTAT 117615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostoml Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G.; Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L. ashworth associated with Huntington disease-like 2 associated with Huntington disease-like 2 like 2 (4), 377-378 (2001)
                                                                      GGA; predicted by tRNAscan-SE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1654 GCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATG 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 1714 CGTATGAGCTACGGCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTAT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                  /function="macromolecule metabolism; macromolecule
synthesis, modification; proteins and peptides -
translation and modification"
/note="Product confidence : probable
Gene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="PROBABLE ELONGATION FACTOR TU PROTEIN"
/protein_id="CAC45918.1"
/db_xref="GI:15074272"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 329100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental/transl_table=11
                                                                                               /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:0925Y6"
                                                                                                                                                                                                                                                                                                                                           predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                   /note="codon recognized:
                                                                                                                    /gene="tufB OR SMc01326"
4602. .5777
                                                                                                                                                                                             /gene="tufB OR SMc01326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="tRNA-GLY_TCC"
/product="tRNA-Gly"
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6125. .670^
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2 (bases 1 to 125020)
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Matches 80;
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AF429315
LRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Hyporhetical Transmembrane Protein"
/protein_id="Cac45916.1"
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/brotein_id="G1:15074270"
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CACTACIRFIGDISYLARCENNINVTFWKRLQDGCPTAGLAVTIVPSAPIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="macromolecule metabolism; macromolecule synthesis, modification; rna synthesis, modification, dna transcription"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"SPTREMBL:092016"
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/traansletton="MSKDKYTHORNSARDTHYANLRRAHRDARRERGEIPTPRODKRAKL
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RSANAFDAGALITTWRHSPTESGVLAKSASGALELIPYIQITNLADTLEELHELGFMT
IGLDSEGPPDLEGTFAGDKIALVGSEGKGLRQKTRQTVKALARLDMPGAIKSLNVSN
AAALAMYAARHLKG
                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKILHIDSGILGEHSVSRRLTSAIVSQLKADRPDAEITYRDLAS
                                                                                                                                                                                                                                                                                                                                                                                                                 ERVPHLTGAQIMAPADLEGVDALLAADVRIGRQMLEEFLAADTVVVGAPMYNFSIPSQ
LKAWIDRLAVAGKTFRYTEAGPEGLAKGKKLIVASTRGGHYSVAPASAMDHQETYLRS
                                                                                                                                                                                                                                                                                             /product="PROBABLE ACYL CARRIER PROTEIN PHOSPHODIESTERASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="miscellaneous; hypothetical/partial homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product = "PUTATIVE TRNA/RRNA METHYLTRANSFERASE PROTEIN"
                                            /function="small molecule metabolism; fatty acid biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFGFFGITDIEFIRAEGLNLGPDQKQFAIAEAEKTIAEGNVLKLAS"
                                                                                        /note="Product confidence : probable Gene name confidence : putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Product confidence : putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental/transl_table=11
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                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:092017"
                                                                                                                                            predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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predicted by FrameD"
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:063. .2683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3066..3941)
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/EC_number="2.1.1.-"
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                                                                                                                                                                                                                                                                                                               /protein_id="CAC45915
/db_xref="GI:15074269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2792. .3076
/gene="SMc01328"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2792. .3076
/gene="SMC01328"
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                                                                                                                                                                                                                                                                        /transl_table=11
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/translation="wssggrpneddggsycggwedgkahghgvctgpkgggeytgsws
HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                            /note="component of the junctional complex between plasma
Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission Submitted (05-007-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17143 SYCYAKCKSMCYSCYYGMSMKGYYYACSYRGSMSKYCMRGSTYSTYGCCTTTTTCC 17202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17379 WSRCWGSMWGSASRSSCYKCYK--SMRCSMMSSKCYRCAGCMMMKGGYMRYMRCWSWKRR 17436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17319 MCYCMMRSMRSRCMSYYMYASWKSSSRGCYCTRCYWCMSSKSCYKSYYMMMRSKRMKGMK 17378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 CCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGACGAGAACCAACTCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCAT 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/chromosome="16"
/map="16q24.3; between D16S520 and WI-12410"
/mote="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 125020;
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32731 c 30696 g 28283 t
                                                                                                                                                                                                                                                   /rpt_unit=ctg
complement(<36507. ,>36887)
                                                                                                                                                                                                                                                                                                                 complement(<36507. .>36887)
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                                                                                                                                                                                                                                                                                                                                                        /product="junctophilin"3"
complement(<36507, .36887)
                                                                                                                                                                                               Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="junctophilin 3"
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/db_xref="GI:17646245"
                                                                                                                                                                                                                                  /rpt_type=tandem
                                                                                                                                                                                                                                                                                    /gene="JPH3"
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/codon_start=1
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/db_xref="G1:3328231"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OQAIEKEIKEKDAELNOKLPOYIKAKENPSHKIKKFRAAKKSLONAOKOYKKRRADMD
ELEKEMLSVEKARQEFEERMEEESOSOGRDLTLEENQVKKYHRLKEEASKRAATLAQE
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EQKNLEETLTEEVEWAKRRIDEINSELNQVMEQLGDARIDRQESSRQORKAEIMESIK
RLYPGSVYGRLIDLCQPTQKKYQIAVTKVLGKNMQAIIVDSEKTGRDCIQYIKEQRGE
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Identification of Xenopus SMC protein complexes required for sister
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SEYKINNKVVQLSEYSDSLEKLGILIKARNFLVFQGAVESIAMKNPKERTALFEEISR
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AQIQLQLFKLYHNESEIEKLNKELSVKNKGIEKDKKHMDKVEEELKDKKKELGKMMRE
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ARRIAFGGHQRHKTVALDGTLFQKSGVISGGASDLKAKARRWDEKAVDKLKEKKERLT
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Direct Submission
Submitted (03-MAR-1998) Cold Spring Harbor Laboratory, 1 Bungtown
Road, Cold Spring Harbor, NY 11724, USA
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                               17497 MCMSSYWCTCWCTSYMSYYRCTCWCKGWSSYTKSKSWSSSMSSYKKGRRKSYSMCCTSRG 17556
                                                                                    17557 AMSCWRRCCYMRGASSMRAGSMSRRRAKGRSWGGRSKWWMTGGMWRSKYYYYCTGRRMM 17616
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Xenopus laevis 14S cohesin SMC1 subunit mRNA, complete cds.
AF051784
                                                 567 CGTCTACGATGTATTCAAGGACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAA
                                                                                                                                                      627 GTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATT
                                                                                                                                                                                          family of ATPases; SMC protein"
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/db_xref="taxon:8355"
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SRNSSAQAFLGPENPEEPYLDGINYNCVAPGKRFRPMDNLSGGEKTYAALALLFAIHS
YKPSPFFVLDEIDAALDNTNIGKVANYIKEQSMSNFQAIVISLKEEFYTKAESLIGVY
PEQGDCVISKVLTFDLTKYPDANPNPND"
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                         IETKLEQKRSDRHNLLQACKMSDIKLPLSKGTWDDISQEEGSSQGEESASSSQRSSTV
YAKEALIEIDYSDLSEDLKDAVADDDIKQEMSALHQKINEQQSILQRISAPNMKAMEK
  <u>ORHMKIIDETMAQLQDLKNQHLAKKSEVNDKNHLMEDIRKKLGSANKEVTHLQKEVTA</u>
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Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC121850 202306 bp DNA linear HTG 21-1
Mus musculus chromosome UNK clone RP24-92E18, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-reminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197589 bases at least Q40
Consensus quality: 198358 bases at least Q20
Consensus quality: 198775 bases at least Q20
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Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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Mus musculus.
Mus musculus
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Center project name: M_BB0092E18
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Pred. No. 28;
0; Mismatches 5
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Unpublished
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McPherson, J.D. and Waterston, R.H.
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ilarity 58.3%;
Conservative
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Best Local Similarity
Matches 70; Conserva
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COMMENT

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Db 147941 GTACCCTTCAACTCTGACAATAGTATGTATCTTCATATGGTGGGGGGTTGGCCATCTTA 148000
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Sequence encoding

Drosophila melanog Drosophila melanog

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Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence.
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/product= "Porphyromonas gingivalis DPP-7"
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. 9 Result

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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidasa-7 (DPP-7) enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g., gingivitis or periodontils). The present DNA sequence encodes the Porphyromonas gingivalis dipeptidylepeptidase-7 (DPP-7) enzyme of the invention. oę il isolated dipeptidylpeptidase useful for identifying inhibitor dipeptidylpeptidase for protecting an animal from periodontal ase caused by Porphyromonas gingivalis Claim 11; Fig 4; 65pp; English 2002-490075/52 P-PSDB; AA015205 disease Novel the 

Sequence 2139 BP; 544 A; 543 C; 565 G; 487 T; 0 other;

ö 420 240 240 300 480 540 099 120 120 300 360 360 420 480 Gaps 9 9 1 ATGCAAATGAAATTAAAAAGTATTCTTCGGAGCAGCCCCTGCTGTTGGGTGCTTCAGGG GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGAT TATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTA TCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCCGAT CAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG GGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGC CAAGAACTGGCCAAAAAAAAATGCAGAGAGGAGAACCAACTCTGCATCGTAGAGCCTTTC TTTGCTCCTCCCAGCTCTGTAGGTAGGTTCGGAGGCGATACGGACAACTGGATGTGGCCG DB 24; Length 2139 ö Indels ; 0 100.0%; Score 2139; 100.0%; Pred. No. 0; Mismatches ; 0 Best Local Similarity 100. Matches 2139; Conservative Query Match 121 121 181 181 241 241 301 301 361 361 421 421 481 481 541 541 601 601 g ò g ò QQ 9 ò a g g ò g ò QQ ô 음 ò ò ò ç

1140 1260 1200 CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080 AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAATTCAAAGGCGACACGAAGAAG 1440 TATGAACCGCAGGACGCTGCCTGGTACAACTATCATACGACAGGCAAGGGCGTATTGGAG 1800 CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080 TATGCAGACTTCGTATTCGACAAGAGTGTGCTTCCTTATAGCGACAAGTTCCATGCCATG 1500 960 GAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATC GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAA AAGGCTTATAAGGAAGGAGCCAAGGCCAACCGTGAGATGACTTATTTGAGCGAGACGCTC TTCGGTGGTACCGAGGTGGTTCGTTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCT AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAG TATECAGACTTCGTATTCGACAAGAGTGTGTGCTTCCTTATAGCGACAAGTTCCATGCCATG CTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG CTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC TATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGGTTTGCGTGAGATGTACCCCGGA CGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCATCAAGGGA GGCTACAAGGCTGACGACTATGCCATGACCATTGGTTTCCCGGGCAGTACGGATCGCTAC CTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTT 1021 1081 1141 1201 1261 1321 1441 1741 961 1021 1081 1141 1201 1261 1321 1381 1381 1441 1501 1501 1561 1561 1621 1621 1681 1681 199 661 721 721 781 781 841 841 901 901 961 Db Dp Dp Db Db g ò Db ò δ ò g ò Ω οy ŏ g qq QQ QQ g ŏ g ò Q ò g ò ò qq õ ò δ g δ ò

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1741 TATGAACCGCAGGACGGTGCCTGGTACAATCATACGACAGGCGAAGGCGTATTGGAG 1800
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signalling and cell interactions
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                                                                      Sequence 1147 BP; 257 A; 335 C; 303 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
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Pred. No. 0.11;
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                     2316 CACCACCAATCCCTACAACCTGGCCGTCTACTACGGCAGCGACTACCGGTGATCTTCAA 2375
                                                                                                            1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
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                                                             Length 3632;
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                                                           Score 42.2; DB 23; Length
Pred. No. 0.2;
0; Mismatches 113; Indels
                                 Sequence 3632 BP; 1062 A; 799 C; 773 G; 998 T; 0 other;
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                                                           Query Match 2.0%;
Best Local Similarity 49.3%;
Matches 110; Conservative
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
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                                                                                                                                                                                                                                                                                                                                    ABL2155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                      1494 TGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGC 1553
                                                                                                                                                                                                                                                                                           1554 AGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGC 1613
                                                                                                                                                                                                                                                                                                                                                                                                           CAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTTTCTTTGCCGGTTTGCGTGAGATGTA 1673
                                                                                                                                                                                                                                                                                                                          CGTCTACTACGGCAGCGACTACCCGGTGATCTTCAACATCATCCTGTGGTTCATGGTCGT 189
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
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                                                   Length 2868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 7432
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                                                                                                                  Indels
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C; 624 G; 850 T; 0 other;
                                                      DB 23;
                                                                                                            99;
                                                                                                                  Mismatches
                                                   Score 40.6;
Pred. No. 0.
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Sequence 2868 BP; 737 A; 657
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                                                      1.9%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                  Conservative
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                                                                                    Similarity
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                                                                                                                                                                                                                                                                                    1473
                                                                                                   1294 GACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGAT 1353
                                                                                                                                                                                          1354 ATTGTACGCCGCCTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGAC 1413
                                                                                                                                                                                                                                                                                                                                                                        1474 CCTTATAGCGACAAGTTCCATGCCCATGCTCCATGGACAAGGAAAAGTTTGCCAAG 1533
                                                                                                                                                                                                                    282 ATGGGTCAGACGCTTGTGGCCTACGACAACCGGCGGACCATCCACGGCAGTAACATCCAT 341
                                                                                                                                               222 GACAATAATACGGAGTGGCTCATTTGGATGGTCGGTAATATTCCGGGCTGCGGATGTCGCC 281
                                                                                                                                                                                                                                                                                                              342 CGAATCGTCTTCCTGGCCTTCAAGCAGTATCTGGAGCTCGATTTCGACGAGACTTTCGTT 401
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      1414 AAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT
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                  Length 4013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. pantotrophus GB17 DNA encoding ORF2, ORF3 and soxXYZA.
                                                            Indels
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/transl_except= (pos:643..645,aa:Leu)
             Score 38.8; DB 23;
Pred. No. 2.1;
0; Mismatches 132;
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             Query Match 1.8%;
Best Local Similarity 47.2%;
Matches 118; Conservative
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2749..3621
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2385..2714
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This invention describes novel genes (I) of the sox (sulphur oxidation) region designated ORF1, ORF2, ORF3 (Open Reading Frame), and soxXXZA from Paracoccus pantotrophus GB17. The proteins (II) encoded by (I) are used for oxidation of reduced sulphur compounds in cellular or cell.-free systems, particularly of thiosulphate to sulphate. (I) is also used for expression of the proteins and to prepare transgenic plants or animals or transformed microorganisms. This sequence encodes the ORF2, ORF3 and the soxXXZA proteins from the P. pantotropus sox region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; sox; ORF1; ORF2; ORF3; soxX; soxX; soxA; thiosulphate; transgenic plant; transgenic animal; ds.
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WPI; 2001-497622/55.
P-PSDB; AAB86529, AAB86530, AAB86531, AAB86532, AAB86533, AAB86534.
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                                                                   New genes involved in oxidation of reduced sulphur compounds, particularly conversion of thiosulphate to sulphate, and related proteins, from Paracoccus pantotrophus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3621 BP; 650 A; 1153 C; 1186 G; 632 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 38.6; DB 22; 48.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 109;
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                                                                                                                                                            Claim 1; Page 10-14; 22pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                          6709 ATTTGTTTTCGCAGATGAACCAAGTCCTGGATGCCATGTTCGAGCGAAAGGTTCAGCCGG 6768
                                                                                                                                                                                                                                                                                                                                                  1343 CCATGCTCGATATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGA 1402
                   useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1403 ATGTAATCGACAAGAAATTCAAAGGGGACACGAAGAAGTATGCAGACTTCGTATTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GT---GACTTTATCATCGCCAGGGTGACGACGCGCATAACTTTTATGTTATTGAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                              Length 10757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 7429
                                                                                                                                                                                                                          Sequence 10757 BP; 3125 A; 2268 C; 2226 G; 3138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 7429; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                              1.8%; Score 37.8;
54.1%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL18652 standard; DNA; 9845
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.1;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1463 AGAGT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6886 AAAGT 6890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL18652
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                                                                        This invention describes novel genes (1) of the sox (sulphur oxidation) region designated ORF1, ORF2, ORF3 (Open Reading Frame), and soxXXZA from Paracoccus pantotrophus GB17. The proteins (II) encoded by (I) are used for oxidation of reduced sulphur compounds in cellular or cell.-free systems, particularly of thiosulphate to sulphate. (1) is also used for expression of the proteins and to prepare transgenic plants or animals or transformed microorganisms. This sequence encodes the P. pantotropus sox region associated proteins described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or more cell-cell
                                                                                                                                                                                                                                                                                                                                                                                         1847 TCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGAGAACGGTCAGCTCCATATCG 1906
                                                                                                                                                                                                                                                                                                                                                                                                                1907 CTTTCCTATCGAACAACGACATCACGGGGGGTAACTCCGGTAGCCCCGTATTCGATAAGA 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4133 AAGGCGGCGGTGCGGTCTTGGTCACGATCTCGACCGGTCCGCTGTCGGTTTCGATGACC 4074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
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and cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4193 CGCGTGCTGTCGTCGCGAAAGTGCCAGCCGGAATAGATCGTGTCGAACGTATCGGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide:
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster genomic polynucleotide SEQ ID NO 15907
                                                                                                                                                                                                                                                                                      DB 22; Length 4848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 15907; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                 Sequence 4848 BP; 885 A; 1584 C; 1552 G; 827 T; 0 other;
                                                                                                                                                                                                                                                                                                       Score 38.6; DB 22;
Pred. No. 2.7;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2027 AGTICGAACCCGAICTGCAGCGCACAATCAGCG 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4073 AGCCCGTCCTCGACCGGGTCCGCGAAGGCCGCG 4041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EW;
proteins, from Paracoccus pantotrophus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL21478 standard; DNA; 10757 BP
                                                                                                                                                                                                                                                                                                     1.8%;
                                      F1g 1; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-191637P.
2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                Matches 104;
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                                                                                                                                                                                                                                                                                                         Query Match
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ABL21478
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                                                                                                                        (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1354 ATTGTACGCCGGCGTATCCCTGCCGACAAGCTCCCCGATATATTCAAGAATGTAATCGAC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1294 GACAAGTACAAAGACTACCTCCCTCGCTCGACCGTAAGGTGCTGCCCGCCATGCTCGAT 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8624 GACAATAATACGGAGTGGCTCATTTGGATGGTCGGTAATATTCCGGGCTGCGATGTCGCC 8565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8564 ATGGGTCAGACGCTTGTGGCCTACGACAACCGGCGGACCATCCACGGCAGTAACATCCAT 8505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodlum merozoite surface protein-1 (MSP-1). The non-natural variants have reduced sflinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ပွဲ
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1414 AAGAAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                 Length 9845;
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                                                                                                                                                                                                                                                                              Sequence 9845 BP; 2751 A; 2130 C; 2204 G; 2760 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                       96; Indels
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                                                                                                                                                                                                                                                                                                                                    Score 37.4; DB 23;
Pred. No. 8.8;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merozoite surface protein-133 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feeney J,
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99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                                                                              1.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC68978 standard; DNA; 786
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25-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
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cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2. Compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is the MSP-133
                                                                                                                                                                                                                       1377 CGACAAGCTCCCCGATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
                                                                                                                                                                                                                                                        135 CGTTAACGTCAAGGACATTTTGAACTCCAGATTCAACAAGAGAGAAAACTTCAAGAAGGT 194
                                                                                                                                                                                                                                                                                                               195 TCTGGAGTCTGATTCCATACAAGGATTTGACTTCTTCTAACTACGTTGTTAAGGA 254
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                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merozoite surface protein; protazoacide; vaccine; malaria; ss.
                                                                                                                                                                                        Indels
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                                                                                                                       Sequence 786 BP; 245 A; 164 C; 159 G; 218 T; 0 other;
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                                                                                                                                                                                        0; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                           1497 CATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAG 1533
                                                                                                                                                     Score 37; DB 22;
Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                              Merozoite surface protein-142 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface protein-1, useful as vaccines for malaria -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC68976 standard; DNA; 1077
                                                                                                                                                      1.7%;
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                                                                                                                                                     Query Match
Best Local Similarity 52.2'
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-015762/02.
                                                                                       coding sequence.
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25-MAY-1999;
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AAC68976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                     1377 CGACAAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
                                                                                                                                                                                                                                                        1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGC 1496
                                                                                                                                                                                                     135 CGTTAACGTCAAGGACATTTTGAACTCCAGATCAACAAGAGAAAACTTCAAGAACGT 194
                                                                                                                                                                                                                                                                                                          195 TCTGGAGTCTGACTTGATTCCATACAAGGATTTGACTTCTTGTAACTACGTTGTTAAGGA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species specific, genus specific, family specific; probe, detection identification; algal, archaeal; bacterial, fungal; parasitical, microorganism; diagnosis; translation elongation factor Tu; toxin, translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catalytic subunit of proton-translocating ATPase; antimicrobial;
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                                                     Length 1077;
                                                                                                  75; Indels
Sequence 1077 BP; 338 A; 228 C; 225 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fonsecaea pedrosoi nucleotide sequence SEQ ID NO:1664.
                                                  Score 37; DB 22;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                          1497 CATGCTCAAGTCCATGGACAAGGAAAAGTTTGCCAAG 1533
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AAH01671 standard; DNA; 810 BP
                                                  1.7%;
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19-MAY-2000; 2000CA-2307010
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                                                                                                     Conservative
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                                                                        Similarity
82; Conserv
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                                                  Query Match
                                                                                Local
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least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteridecae family, Pseudomonada group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 TCTTCTCGACACCAATGTCGGGCTCGCGGCCTCAATGGCGCAAAGGGCGGAACCCATGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 cgargggagrgrcgrcgrcgraggcgraggrggaggagaggcrcacgcarcr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 TTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAGGACAGCTCAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 TGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGAT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 receargreacecresceressearceastreasgretesacrescassassas 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCGGATTCCGGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 CGACGAGCTCCAACATCTCCTTGTCCTCAATGGCATCGACCTTGTTGACGAAGACGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 810 BP; 167 A; 254 C; 228 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thierry JC, Prieur D, Dietrich J, I
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%; Score 36.8;
46.2%; Pred. No. 3.
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Querellou J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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2000-665116/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. The same patent family as WO200065062, which AAH75903-AAH75902 and AAG66436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nephrotropic; cytostatic; human; kidney disease associated; hypertension; Bartter's syndrome; Gitelman syndrome; nephrolithiasis; renal failure; renal amyloidosis; primary aldosteronism; Addison's disease; cancer; glomerulonephritis; dysplastic malformation; medullary cystic disease; medullary sponge kidney; tubular dysplasia; Alport's syndrome; ds.
                                                                                                                                                                                                                                                                                                                     168164 CGATGAGCTTGAGGATGAAGGCTTAAGGAAATCCTGGAGGTGGCTGAAAAGGTTGCAAG 168105
                                                                                                                                                                                                                                                                                                                                                         168044 GATAGATAAGCTAAAGGAGTTTGAAGAGTTCGCCAAGGGCAAGGGAAAAGAGGGACTTTT 167985
                                                                                                                                                                                                                                                                                                                                          1437 GAAGTATGCAGACTTCGTATTCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGC 1496
                                                                                                                                                                                                                                                                                                                                                                                        1497 CATGCTCAAGTCCATGGACAAGGAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGT 1556
                                                                                                                                                                                                                                                                                             1377 CGACAAGCTCCCCGATATTTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAA 1436
                                                                                                                                                                                                                           Sequence 349980 BP; 95167 A; 78444 C; 78870 G; 97499 T; 0 other;
                               New nucleotide sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yue H;
                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human kidney disease associated gene SEQ ID 7.
                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                Score 36.8;
Pred. No. 84
                                                               Claim 1; Page 183-279; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC66137 standard; DNA; 1090 BP
                                                                                                                                                                                                                                                1.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0289349
                                          proteins useful in industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                      95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 167984 CCAGCTCGCCGA 167973
                                                                                                                                                                                                                                                                                                                                                                                                                                     1557 AGAGCTTTCCAA 1568
       WPI; 2001-126236/14.
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Polynucleotides AAC66131-C66139 represent human kidney disease associated genes. Proteins AAV85678-Y85680 represent human kidney disease associated proteins. The polynucleotides have nephrotropic and cytostatic activity. The polynucleotides, encoded proteins and pharmaceutical compositions containing renal disorders such as Bartter's syndrome, treating and preventing renal disorders such as Bartter's syndrome, ditelman syndrome, autosomal dominant polystic kidney disease and nephrolithiasis. The genes and proteins are also useful for identifying biomolecules that are associated with a specific disease, regulatory pathway, subcellular compartment, call type, tissue type or species, which is useful in diagnosis, prognosis, treatment and evaluation of therapies for renal diseases for e.g. renal amyloidosis, hypertension, primary aldosteronism, Addison's disease, renal failure, chandle disease (PRD), medullary cystic disease, medullary coplycystic renal disease (PRD), medullary cystic disease, medullary sponge kidney and tubular dysplasia, Alport's syndrome, non-renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                               Novel kidney disease associated gene useful for diagnosing treating and preventing renal disorders, is uromodulin, NKCC2, NCCT, aldolase B, ROMKI, ATPIG1, PDZK1, NPT1, calbindin, kininogen or CIC-Kb -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1674 CCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCAT 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1734.CAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAGGCCAAGGGCGT 1793
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myeloma and nephrotoxic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.4; Di
Pred. No. 5.5;
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                                                                                                                                                                                                                                                   Claim 2; Page 33-34; 36pp; English.
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P-PSDB; AAY85680
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26-JUL-2001

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAAM38642-AAM42213) with nootropic, the encoded polypeptides (AAAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic acitvity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as paripheral nervous injuries, peripheral neuropathies and central nervous system diseases, auch as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                        Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.7%; Score 36.4; DB 22; Length 1292; Best Local Similarity 49.5%; Pred. No. 6; Matches 94; Conservative 0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                                                        Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1292 BP; 254 A; 422 C; 368 G; 248 T; 0 other;
                                                                                                                                                                                                                                                                                    Tang YT, Liu C, Asundi V, Chen R, Ma Y, (Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Zhao QA, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1179; 10078pp; English.
                                                                       2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                  2000US-0653450.
2000US-0662191.
2000US-0693036.
                                   26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442253/47
                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAM39820
                                                                                                                             19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                       21-JAN-2000;
25-APR-2000;
09-JUL-2000;
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1734 CAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACGGCAAGGGCGT 1793 1794 ATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATATCCTCGACCT 1853 g ò g ò q

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Gaps

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1674 CCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCTACGGCTCCAT 1733

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1854 CTTCCGCACC 1863

519 CTTCCATGCC 528

Search completed: May 23, 2003, 04:52:58 Job time : 958 secs

28 32.2 1.5 3468 3 US-29 32.2 1.5 3468 4 US-32 1.5 3468 4 US-32 1.5 3468 4 US-32 1.5 3468 4 US-32 1.5 3468 1 US-32 1.5 3468 1 US-32 1.5 1947 2 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1947 4 US-32 1.5 1947 3 US-32 1.5 1947 3 US-32 1.5 1948 1 US-32 1.5 1948 1 US-32 1.5 1948 1 US-32 1.5 1948 1 US-32 1.5 1948 1 US-32 1.5 1948 2 US-32 US-32 1.5 1948 2 US-32 US-	32 1.5 3468 3 1 1 221-017B-726 221-017B-726 Application US/09 1t No. 644799 SRAL INFORMATION:	APPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GINGIVAL NUMBER OF SEQUENCES: 1120 CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISSON & FOERSTE STREET: 755 PAGE MILL ROAD CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304-1018 COMPUTER READABLE FORM:	MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/221	CLASSIFICATION:  PRIOR APPLICATION:  PROCE APPLICATION:  PROCE APPLICATION OF PP182  FILING DATE: 31-DEC-1997  PRIOR APPLICATION DATA:  PRIOR APPLICATION DATA:  PRIOR APPLICATION NUMBER: PP546  FILING DATE: 30-JAN-1998  PRIOR APPLICATION NUMBER: PP2911  FILING DATE: 09-APR-1998  PRIOR APPLICATION DATA:	## APPLICATION NUMBER: PCT/AU98 ## FILING DATE: 10-DEC-1998 ## ATTORNEY/AGENT INFORMATION: ## REGISTRATION NUMBER: 32,430 ## REGISTRATION NUMBER: 37,430 ## REFERENCE/DOCKET NUMBER: 2734 ## TELECOMMUNICATION INFORMATION: ## TELECOMMUNICATION INFORMATION: ## TELEC TO TELECOMMUNICATION INFORMATION: ## TELEX: 706.14 ## INFORMATION FOR SEQ ID NO: 726: ## SEQUENCE CHARACTERISTICS: ## LENGTH: 1974 base pairs ## TYPE: nucleic acid ## STRANDEDNESS: double ## STRANDEDNESS: double ## TYPE: nucleic acid ## STRANDEDNESS: double ## TOPOLOGY: circular
GenCore version 5.1.4_p5_4578  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: May 23, 2003, 02:43:56 ; Search time 62 Seconds  (without alignments)  10580.348 Million cell updates/sec  Title: US-10-008-355-1  Perfect score: 2139 Sequence: 1 atgcaaatgaaattaaaaagaagagctgaagttgatctaa 2139 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0	Searched: .441362 seqs, 153338381 residues  Total number of hits satisfying chosen parameters: 882724  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%  Maximum Match 100%  Listing first 45 summaries	Issued_Patent 1: /cgn2_6/pt. 2: /cgn2_6/pt. 3: /cgn2_6/pt. 4: /cgn2_6/pt. 5: /cgn2_6/pt. 6: /cgn2_6/pt. No. is the number greater than or eq	is derived by analysis of the total score distribut  SUMMARIES  Query  Ouery  De	1717.4 80.3 1974 4 US-09-221-017B-726 Sequence 726 207.4 9.7 1317 4 US-09-221-017B-726 Sequence 326 164.4 7.7 561 4 US-09-221-017B-12 Sequence 12, 153.8 7.2 2384 4 US-09-221-017B-1045 Sequence 12, 36.4 1.7 2380 4 US-09-289-349-7 Sequence 7, 36.2 1.7 2280 1 US-08-128-15-5 Sequence 5, 36.2 1.7 2280 2 US-08-94-236-5 Sequence 5, 36.2 1.7 2280 5 US-08-894-236-5 Sequence 14, 35.2 1.6 5837 1 US-07-686-340-1	c 13 34 1.6 5837 1 US-08-104-1398-1 Sequence 1, Appl. 1 US-08-117-491-1 Sequence 1, Appl. 2 US-08-117-491-1 Sequence 1, Appl. 2 US-08-117-491-1 Sequence 1, Appl. 34 1.6 5837 2 US-08-271-364A-1 Sequence 1, Appl. 2 US-08-271-361-1 Sequence 1, Appl. 34 1.6 5837 2 US-08-22-1 Sequence 1, Appl. 35 1.6 5837 5 PCT-0896-10545A-1 Sequence 1, Appl. 33.6 1.6 5837 4 US-09-773-816-1 Sequence 1, Appl. 33.6 1.6 5037 4 US-09-105-390-45 Sequence 45, Appl. 20 33.2 1.6 1020 4 US-09-105-390-61 Sequence 61, Appl. 21 33.2 1.6 1020 4 US-09-105-390-61 Sequence 61, Appl. 22 33.2 1.6 1020 4 US-09-105-390-7 Sequence 61, Appl. 22 33.2 1.5 3468 1 US-09-105-390-7 Sequence 2, Appl. 23 32.2 1.5 3468 2 US-08-958-416-603 Sequence 2, Appl. 25 32.2 1.5 3468 3 US-08-459-448A-2 Sequence 2, Appl. 27 32.2 1.5 3468 3 US-08-459-504B-2 Sequence 2, Appl. 27 32.2 1.5 3468 3 US-08-459-504B-2 Sequence 2, Appl. 27 32.2 1.5 3468 3 US-08-459-504B-2 Sequence 2, Appl. 30-08-459-504B-2 Sequence 2, Appl. 30-08-459-4504B-2 Sequence 2, Appl. 30-08-459-4504B-2 Sequence 2, Appl. 30-08-459-4504B-2 Sequence 2, Appl. 30-08-459-4504B-2 Sequence 3, Appl. 30-08-459-4504B-2 Sequence 3, Appl. 30-08-459-4504B-2 Sequence 4, Appl. 30-08-459-4504B-2 Sequence 5, Appl. 30-08-459-4504B-2 Sequence 6, Appl. 30-08-459-4504B-2



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                                                                              Score 1717.4;
Pred. No. 0;
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DNA (genomic)
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              ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS
                                              NAME/KEY: misc_feature
LOCATION: 1...1974
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MOLECULE TYPE HYPOTHETICAL:
                                                              US-09-221-017B-726
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TITLE OF INVENTION: P. GINGIVALIS
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
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    366 GAAGTACCTGCAAAAGTTGGCTGACAAGAAGGCCGGCAAGAACTTTTCTGCCAAGAATCC 425
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Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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23-DEC-1998
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STREET: 755 PAGE MILL ROAD
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APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
FILING DATE: 23-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 755 PAGI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-221-017B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                        qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AGTGTCCGATCAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 GGAGCTTCCGATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 CCAAAGCACGGTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 TCACAGCACGCTCGAGCATAACTATCTCGAAAATGGATTTTGGGCGATGAGAGAAAGCGGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 CAAGGTAGAAGGACAGCTCAAGGGTATCACTGA-------CGAGATGGAGCGTCT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GAATCTGGATCGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 CGACAAGCCGTCCATTGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCAC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 CGTTTCCGATCGCGGACTGGTACTGACCAATCACCACTGCGGGATACGATATGATCCAGGC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 207.4; DB 4;
Pred. No. 5e-56;
0; Mismatches 421;
                                                            SYSTEM: Windows
FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27340-20021.00
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 10-DEC-1998
APPLICATION NUMBER: PC7AU98/01023
ATTORNEY/AGEWT INFORMATION:
ANAME: ACCOUNTY OF A STANDAME ATTORNEY/AGEWT INFORMATION:
ANAME: ACCOUNTY OF A STANDAME ATTORNEY/AGEWT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                        MBER: US/09/221,017B
23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MODIOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.1%;
Matches 498; Conservative
                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERICS:
LENGTH: 1317 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: 1...1317
US-09-221-017B-382
                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULL
HYPOTHETICAL: NU
HYPOTHETICAL: NU
                                                          OPERATING SYSTEM:
                                                                                                                                           FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 CGAATGCGTGAGCTCGGCTTTA--CCTCCCGTGGATTCGCTCTACAGTTTCGACAAGCCG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGCAAATGAAATTAAAAAGTATTCTTCTGGAGCAGCCCTGCTGCTTGGGTGCTTCAGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1045, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
FAPELICANT: ROSS, BULCE C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISSON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.7%; Score 164.4; DB 4; Length 561; Best Local Similarity 95.7%; Pred. No. 1.7e-42; Matches 180; Conservative 0; Mismatches 6; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                     NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: PORYPHYROMONAS GINGIVALIS
                                     PCT/AU98/01023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/221,017B
FILLING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
LECULE TYPE: DNA (genomic)
                                                                                                                                                                              TELEFAX: 650-494-0/32
TELEX: 706141
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
Annhe
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1...561
                                                                                                                                                                                                                                                                                                          double
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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1544 AAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCGCGCTATTCAGGCCG 1603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1664 GTGAGATGTACCCCGGACGTGCTCTGCCGAGCGATGCCAACTTCACCATGCGTATGAGCT 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1724 ACGCCTCCATCAAGGGATATGAACCGCAGGACGGTGCCTGGTACAACTATCATACGACAG 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1784 GCAAGGGCGTATTGGAGAAGCAGGATCCTAAGAGCGATGAGTTTGCCGTACAGGAGAATA 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1844 TCCTCGACCTCTTCCGCACCAAAAACTATGGTCGCTATGCCGA---GAACGGTCAGCTCC 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1901 ATATCGCTTTCCTATCGAACAACGACATCACGGGCGGTAACTCCGGTAGCCCCGTATTCG 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAGAACGCCCGTCTGATCGGTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTG 2020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 TGAAAGCCGTATACGAGCGTAAAGACTTCGGGCGTTATGCCGATCGCAGCGCTCGCATGC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 Argercaagreaaggecraficaccegracaargrifacracgacarcaaaccacar 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 TGGATGGTGTGTGGAAAAAGAAGATCCCGATAATTGGGAATTTGTAGTCGATCCCAAGC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AACTTGGTCCCTATGACGATCCTATTGTAAGGGCACAAACGCACCTACATTGCAGGTCTCT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 AAGATCCTATGGTACTCTTCGCCTCTTCGGTTTTTCGACGAGTACCGCAAACTCTACAACG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 153.8; DB 4;
55.0%; Pred. No. 1e-38;
tive 0; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                            27340-20021.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                              PCT/AU98/01023
                                                                                                                                                                                                                                                                                                                 NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1045
SEQUENCE CHARACTERISTICS:
                                                        APPLICATION NUMBER: PP1546
                                                                                                                                  APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                  30-JAN-1998
FILING DATE: 31-DEC-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2384 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1...2384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2
Best Local Similarity 55.0
Matches 324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                  FILING DATE: 30-JAN-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1
US-09-221-017B-1045
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ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
computer: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 908-594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822..1937
                                                                           OPERATING SYSTEM:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-415-818-5
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APPLICANT:
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 136 CCTGGACCGTGTCTTCACCACCTACAAGCTCATGCACACGCACCAGACAGTGGACTTCGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                          ; Sequence 7, Application US/09289349; Patent No. 627574; GENERAL INCPMATION:
; APPLICANT: Walker, Michael, G.; APPLICANT: Volkmuth, Wayne; APPLICANT: Volkmuth, Wayne; APPLICANT: Yolkmuth, Wayne; APPLICANT: Yue, Henry ITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY; FILE REFERENCE: PB-0010 US; CURRENT APPLICATION NUMBER: US/09/289,349; CURRENT APPLICATION NUMBER: US/09/289,349; NUMBER OF SEQ ID NOS: 12; SOFTWARE: PERL PROGram; SEQ ID NO 7; LENGTH: 1090
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                                                        2081 TCATGATTGACAAATGGGGTCAGTGCCCCCGTCTCATCCAAGAGCTGAA 2129
                                                                                 571 TTGTGATAGACAAAGTAGGCGGTTGCCAACGCCTGTTGGATGAAATGAA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.4; DB 4; Length 10
Pred. No. 0.23;
0; Mismatches 96; Indels
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ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
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APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cascieri, Margaret A. APPLICANT: Linemeyer, David L. APPLICANT: MacNeil, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08415818 Patent No. 5621079 GENERAL INFORMATION:
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MacNeil, Douglas J.
Shiao, Lin-Lin
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US-09-289-349-7
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Best Local Similarity 49.55
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                    US-09-289-349-7
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409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCT 468
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                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,818
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P.O. Box 2000, 126 E. Lincoln Ave.
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APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
ATTORNEY,AGENT INFORMATION:
NAME: APPOllina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390
TELECOMMUNICATION INFORMATION:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cascieri, Margaret A.
Linemeyer, David L.
MacNeil, Douglas J.
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Patent No. 5939263
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 55.v.
71; Conservative
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409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCT 468
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                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DOCHUER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
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55.0%; Pred. No. 0.44;
tive 0; Mismatches
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                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/01444
                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION UNBER:
FILING DATE:
O3-FEB-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
O3-APR-1995
ATTORNEY_AGENT INFORMATION:
NAME:
APPOILING MAIY A:
REGISTRATION NUMBER:
TELEFENCE/DOCKET NUMBER:
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                     Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.0°
Matches 71; Conservative
                                                                                                                                                 CURRENT APPLICATION DATA:
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; LOCATION: 822..1937
PCT-US96-01444-5
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55.0%; Pred. No. 0.44;
tive 0; Mismatches 58; Indels 0
                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Linemeyer, David L.
APPLICANT: Marchal, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
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P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                      PILING DATE:
CLASSIFICATION: 435
PILOR APPLICATION DATA:
APPLICATION NUMBER: 08/38,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTONEY/ABOTI INFORMATION:
NAME: APPOLITIA, WAS 34,087
REGISTRATION NUMBER: 34,087
REGISTRATION NUMBER: 19390Y
TELEPHONE: 908-594-3462
TELEPHONE: 908-594-3462
INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    APPLICATION NUMBER: US/08/894,236
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COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PAPEAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.0%
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-894-236-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-01444-5
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Sequence 1, Application US/07686340 Patent No. 5322785
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5: & CUSHMAN
130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.7'
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 449 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 ATTACGACATTAAAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542 ATTCCAACAACGAATA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASSACHUSETTS
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: PROSTUTO8
CLONE: 1654275
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APPLICANT: Comb, 1
     Palo Alto
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                                                                                                 TYPE:
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                                                           94304
                         ^{CA}
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US-07-686-340-1/c
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                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 7218;
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: COFACTOR A-LIKE PROTEIN
UNMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Pharmaceuticals, Inc.
                                                                                                                                                 APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AGG-1991 ATTONEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08825782
Patent No. 5834239
GENERAL INFORMATION:
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Best Local Similarity 3.2%; Matches 12; Conservative 20.
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                                                                                                                                                                                                                                                                                                                                                                                    7218 base pairs
                                                                                                                                                                                                                                                                                                          (703)683-4109
                                                                                                                                                                                                                                                                                                                            TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7218 base rayser TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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IMMEDIATE SOURCE:
                                                                                                                                     FILING DATE:
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89 GACAGATCAAGATCAAGACCGGCGTGGTGAAGCGGTTGGTCAAAGAAAAAGTGATGTATG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 GACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCC 481
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APPLICANT: Perler, Francine
APPLICANT: Rucera, Rebecca
APPLICANT: Jack, William E.
TITLE OF INVENTION: Purified Thermostable DNA Polymerase
TITLE OF INVENTION: Obtainable From Thermococcus Litoralis
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FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                        PF-0263 US
         SOFTWARE. CONTROL DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,782
FTT.ING DATE: Filed Herewith
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Gaps

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Indels

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3686 GTCATCGTCCAGAGTTAGTGCTTCAACCTTCGAGAATGCAGTATTCTTTTTCGCCAAT 3627
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Patent No. 5500363
GENERAL INFORMATION:
APPLICANT: Comb, Donald G.
APPLICANT: Comb, Donald G.
APPLICANT: Rucera, Rebecca
APPLICANT: Nucera, Rebecca
APPLICANT: RECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERS FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: 6 CUSHMAN
                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 5837;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1465 AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCA 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3626 GCTGTAGTCCACCTTAGAGAAAAGATCCTTTATTTTCACAAATCTA 3581
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,491
FILING DATE: CSFP-1993
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                         1.6%; Sco. 57.5%; Pred. No. 4...
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APPLICATION NUMBER: US 07/811,421

FILING DATE: 12-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,340

FILING DATE: 17-APR-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057

FILING DATE: 11-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
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                   REFERENCE/DOCKET NUMBER: 42188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFA: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5837 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
  REGISTRATION NUMBER: 34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 WATER STREET
                                                                                                                                                                                                                                   SS: double not relevant
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Best Local Similarity
Matches 61; Conserva
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                                                                                                                                                                                                                                STRANDEDNESS:
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US-08-004-139B-1
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APPLICANT: PERLER, FRANCINE B.
APPLICANT: XU, MING-QUEN
APPLICANT: XU, MING-QUEN
APPLICANT: JACK, WILLIAM E.
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 39
CORRESPENDENCE ADDRESSE:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: OUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 34; DB 1; Length 5837;
57.5%; Pred. No. 4.1;
tive 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1465 AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCA 1510
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  39296-CIP-II
                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 39296-CIP-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
            SOFFWARE: PALLCATION DATA:
CURRENT APPLICATION NUMBER: US/07/686,340
TITLE DATE: 19910417
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FILING DATE: 09-DEC-1992
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ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 523-3400
TELERAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5837 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 57.5 Matches 61; Conservative
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CLASSIFICATION:
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STRANDEDNESS:
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US-08-271-364A-1/C
Sequence 1, Application US/08271364A
Patent No. 5756334
GENERAL INFORMATION:
APPLICANT: PERLER, FRANCINE B.
APPLICANT: SOUTHWORTH, MAURICE W
TITLE OF INVENTION: RECOMBINANT THEROMSTABLE DNA POLYMERASE
TITLE OF INVENTION: RECOMBINANT THEROMSTABLE DNA POLYMERASE
TITLE OF INVENTION: RECOMBINANT THEROMSTABLE SEQUENCES:
UNMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                               DB 1; Length 5837;
                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 583
Pred. No. 4.1;
0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1465 AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCA 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3626 GCTGTAGTCCACCTTAGAGAAAAGATCCTTTATTTTCACAAATCTA 3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRATION DATA:
APPLICATION NAPER: US 07/811,421
FILING DATE: 18-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,340
FILING DATE: 17-APR-1991
PRIOR APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-APR-1990
ATTONINY/AGENT INFORMATION:
ANAME: ALITITAME CREATION NUMBER: US 07/513,994
FILING DATE: 26-APR-1990
ATTONINY/AGENT INFORMATION:
ANAME: ALITITAME CREATION NUMBER: US 07/513,994
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REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-101
TELEPHONE: (617) 523-3400
TELERAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5837 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEPHONE: (508) 927-5054
TELEPAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          Query Match 1.6%;
Best Local Similarity 57.5%;
Matches 61; Conservative
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US-08-117-491-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 01915
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VENTION: MODIFIED PROTEINS, METHODS OF THEIR
VENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
                                                                                                                                                                                                                                                                                                                        1405 GTAATCGACAAGAATTCAAAGGCGACACGAAGAAGTATGCAGACTTCGTATTCGACAAG 1464
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                                                                                                                    Length 5837;
                                                                                                                                                                                               45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    1465 AGTGTGGTTCCTTATAGCGACAAGTTCCATGCCCATGCTCAAGTCCA 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3626 GCTGTAGTCCACCTTAGAGAAGATCCTTTATTTTCACAAATCTA 3581
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,492
                                                                                                                DB 1;
                                                                                                                Score 34; DB 1
Pred. No. 4.1;
0; Mismatches
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REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC\_DOS/MS\_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us 08/580,555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: JACK, WILLIAM E.
APPLICANT: XU, MING-QUN
APPLICANT: NOREN, CHRISTOPHER J.
APPLICANT: ADAM, ERIC
APPLICANT: ADAM, ERIC
APPLICANT: SOUTHWATH
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US-08-811-492-1/C
; Sequence 1, Application US/08811492
. Patent No. 5834247
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                                                                                                                Query Match 1.6%;
Best Local Similarity 57.5%;
Matches 61; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1995
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CLASSIFICATION: 435
    not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MODITALE OF INVENTION: PROJUCE OF INVENTION: PROJUMBER OF SEQUENCES: 155 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASSACHUSETTS: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 29-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BEVERLY
STATE: MASSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 01915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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; TOPOLOGY:
US-08-271-364A-1
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Search completed: May 23, 2003, 04:44:48 Job time: 122 secs

GenCore version 5.1.4_p5_4578	Compugen Ltd.
version	- 2003
GenCore	(c) 1993
	Copyright

OM nucleic - nucleic search, using sw model

May 23, 2003, 03:33:01; Search time 529 Seconds (without alignments) 5339.261 Million cell updates/sec Run on:

US-10-008-355-1 2139 1 atgcaaatgaaattaaaaag.....aagagctgaagttgatctaa 2139 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

828747 seqs, 660231138 residues Searched:

1657494 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_NA:\* •• Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Onerv				
	Score	Match	Match Length DB	DB	ID	Description
-	2139	100.0	2139	. 6	US-10-008-355-1	Sequence 1, Appli
7	40.8	1.9	867	σ	US-10-123-155-20	Sequence 20, Appl
ო	36.2	1.7	345	σ	US-09-738-626-2081	Sequence 2081, Ap
4	36.2	1.7	2281	10	US-09-900-497-1	Sequence 1, Appli
S	36	1.7	292	10	US-09-294-093B-856	Sequence 856, App
9	36	1.7	369	10	US-09-878-574-5240	Sequence 5240, Ap
,	35.2	1.6	671	6	US-10-184-644-346	Sequence 346, App
œ	35.2	1.6	671	6	US-10-184-634-346	Sequence 346, App
6	35	1.6	1896	6	US-10-213-990-53	Sequence 53, Appl
10	35	1.6	2060	σ	US-10-213-990-52	Sequence 52, Appl
11	34.4	1.6	489	6	US-10-184-644-116	Sequence 116, App
12	34.4	1.6	489	6	US-10-184-634-116	Sequence 116, App
13	34	1.6	268	10	US-09-923-876-5908	Sequence 5908, Ap
14	34	1.6	50000	თ	US-10-152-724A-22	Sequence 22, Appl
15	33.6	1.6	50937	6	US-09-808-880-1	Sequence 1, Appli
16	33.4	1.6	802	σ	US-10-184-644-312	Sequence 312, App
17	33.4	1.6	802	σ	US-10-184-634-312	Sequence 312, App
18	33.2	1.6	256	10	US-09-878-574-9837	Sequence 9837, Ap
19	33.2	1.6	607	σ	US-10-123-155-344	Sequence 344, App

434,	Sequence 273, App Sequence 332, App	<	Sequence 568, App Sequence 1515, Ap	Sequence 1183, Ap	Sequence 2041, Ap	Sequence 4, Appli	Sequence 346, App	Sequence 346, App	Sequence 596, App	Sequence 9, Appli	1, 4	7		Sequence 278, App		'n	Sequence 4, Appli	٦,	Sequence 4, Appli	8	10,		
US-10-184-644-434 US-10-184-634-434	US-09-754-853A-273 US-10-184-644-332	US-10-184-634-332	US-09-910-943-568 US-09-738-626-1515	US-09-974-300-1183	US-09-974-300-2041	US-09-754-853A-4	US-10-184-644-346	4	US-09-770-445-596	US-10-032-717-9	US-10-108-580-1	US-09-988-462-2	US-09-918-995-6839	US-10-123-155-278	US-10-090-455-3	US-09-988-462-3		S	US-09-988-462-4	-988-46	US-09-988-462-10	US-09-988-462-12	
999			0 6	10	10	6	0	6	10	12	6	6	6	6	6	6	6	6	6	6	6	6	
55 55 55	171 520	520	846	987	1011	513509	671	671	860	2010	2169	3468	418	491	1941	1947	3455	3455	3468	3468	3546	3546	
2.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	
	32.4 32.4	32.4	32.4	32.4	32.4	32.4	32.2	32.2	32.2		32.2		32	32	32	32	32	32	32	32	32	. 32	
	c 53				c 28		30	31	32	33	34	35	c 36	37	38	39	40	41	42	43	44	4.5	

## ALIGNMENTS

RESULT 1
US-10-008-355-1
; Sequence 1, Application US/10008355
; Patent No. US20020164759A1
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S
; APPLICANT: Banbula, Agnieszka
; TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Us
; FILE REFERENCE: 235.00440101
; CURRENT APPLICATION NUMBER: US/10/008,355
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/246,827
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Porphyromonas gingivalis US-10-008-355-1

se

GTAGCCAAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAAATCAGGAGAATCTGGAT 120 Gaps 1 ATGCAAATGAAATTAAAAAGTATTCTTCTCGGAGCAGCCCTGCTGTTGGGTGCTTCAGGG 60 ; Length 2139; Indels ; 0 100.0%; Score 2139; 100.0%; Pred. No. 0; Live 0; Mismatches Best Local Similarity 100. Matches 2139; Conservative Query Match 61 61 Db δŻ qq δ

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DB 9;

CGAATGCGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCG 180 121 121 181 δ QQ ò

181

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us-10-008-355-1.rnpb

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APPLICANT: Sherwood, Steven; APPLICANT: Smith, Victoria	1321 CTCGACCGTAAGGTGCTGCCCGCCATGCTCGATATTGTACGCCGGCGTATCCTGCCGGC 138	. 0
; APPLICANT: Goddard, Audrey; APPLICANT: Godowski, Paul J.	dy         1261         GATGCTCARGCCGGTATCCTCAAATCGCTTGACGACAAGTACAAGACTACCTCCCCTCG         1320           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	<i>y</i> a
; APPLICANT: Desnoyers, Luc ; APPLICANT: Filvaroff, Ellen ; APPLICANT: Gao, Wei-Giang · APPLICANT: Gerritsen, Mary E.	<pre>Oy 1201 TTCGGTGGTACCGAGGTGGTTTGCACAGTTTGCCAACGCATTGGCTACAAATCCT 1260</pre>	5 0
GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen APPLICANT: DeForde. Laura	1141 AAGGCT 	3 0
RESULT 2 US-10-123-155-20 Sequence 20, Application US/10 Publication No INSONANORPOAR	Oy 1081 GACTGGATCCGTAAGAACGGCAAGAGTGCTGTCTATGGCGATGTATTGTCTTCTCTCGAA 1140 1111111111111111111111111111111111	<del>о</del> о
UY 2101 CAGTGCCCCGGTCTCATCCAAG	OY 1021 CGCGGTCTCGCTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCA 1080	J A
2041	Oy     961     AAATATGCAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAAC     10.20       DD     961     AAATATGCCAGCAAGTATGCTCAGAGTGCTAATTGGAAGAATTCGATCGGTATGAAC     10.20	5 11
1981 GGTCTTGCTTTCGATGCCAAC	QY     901     CGCGGTATCAAGCAAGGAAGGAAGGAAGCCATGAGCCCAGATCAGGCTACCCGTATC     960       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	J 1
1921 AACGACATCACGGG	OY 841 CTCACTTCTTGGGGTGTGGAAGATCGTATCGAAAACAAAC	<u>υ</u> α
1861	OY 781 GGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGGCAGTACGGTTGCTAC 840	0 0
1801 AAGCAGGATCUTAN 	OY 721 GAATACAGGAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA 780	0 0
1741	OY 661 CGTCACACGGGCGACTTCAGCGTATTCCGGGTGACGGTGCCGACAACGGGCGGCC 720	<b>3</b> A
1681 CGTGCTGTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	OY         601         TITGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGCGATACGGACAACTGGATGTGGCCG         660           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	<b>G D</b>
1621 TATGCC 111111 1621 TATGCC	QY       541       TATTCCAACAACGAATACTTCCTCATCGTCTACGTGTATTCAAGGACGTTCGTATGGTA       600         Db       541       TATTCCAACAACGAATACTTCCTCATCGTCTACGTGTATTCAAGGACGTTCGTATGGTA       600	0 0
1561 1561	OY 481 CAAGAACTGGCCAAAAAGAAAATGCAGAGGAACCAACTCTGCATCGTAGAGCCTTTC 540 .	Ο Δ
1501	Oy       421       GGACAGCTCAAGGGTATCACTGACGAGATGGAGGTCTGGGCAAAGCTCAGGAGGTATGC       480         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0 0
1441	Oy 361 ATTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAA 420 	0 0
1381	OY 301 GTGGATCACGACTATCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGGCTTCCG 360 	σд
Db 1321 CTCGACCGTAAGGTGCTGCCCG	Qy       241       CAGGGCCTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACG       300         10       111111111111111111111111111111111111	<b>υ</b> Δ

TCCGGTAGCCCCGTATTCGATAGAACGGCCGTCTGATC 1980 CGTCTTTTCTTTGCCGGTTTGCGTGAGATGTACCCCGGA 1680 AACTICACCATGCGTATGAGCTACGGCTCCATCAGGGA 1740 TGGTACAACTATCATACGACAGGCAAGGCGTATTGGAG 1800 AATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAG 1440 AAGAGTGTGCTTATAGCGACAAGTTCCATGCCATG 1500 AAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAG 1560 TGGTACAACTATCATACGACAGGCCAAGGGCGTATTGGAG 1800 GAGITIGCCGTACAGGAGAATATCCTCGACCTCTTCCGC 1860 GCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAAC 1920 GACATCCGCTACGTTCTCTCATGATTGACAAATGGGGT 2100 GCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC 1620 GCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCC GAGCTGAAGTTGATCTAA 2139 GAGCTGAAGTTGATCTAA 2139

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 CGTGAGATGACTTATTTGAGCGAGACGCTCTTCGGTGGTACCGAGGTGGTTCGTTTTGCA 1230
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                                                                         APPLICANT: Wood William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCENETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
CURREMY APPLICATION NUMBER: US/10/123,155
CURREMY PTLING DATE: 2002-04-15
PLIOR APPLICATION NUMBER: 2502-04-15
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 SSILTGKYVHNHNTYTNNENCSSPSWQAQHESRTFAVYLNSTGYRTAFFGKYLNEYNGSY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 VPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                931 GCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCAGAGTGCT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 MEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 KLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAP 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     692 KDKVWLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTS 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 GTGTATGCCGGTGCCGACAACCGGCCGGACGAATACAGCAAGGACAATAAAACCCTATAAG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 CCCGTTTACTTCGCTGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACC 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 ATCGGTTTCCCGGGCAGTACGGATCGCTACCTCACTTCTTGGGGTGTGGAAGATCGTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 MPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDT
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1.9%; Score 40.8; DB 9; Length 8
Best Local Similarity 7.6%; Pred. No. 0.01;
Matches 55; Conservative 237; Mismatches 427; Indels
Stewart, Timothy A.
                                                  Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-155-20
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                                                  APPLICANT:
APPLICANT:
APPLICANT:
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521 TCTGCATCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTAT 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 TCACTGGTCTTGGTCTTGGATCCTCTGAAATCCCCTAGGAACCTTCGGA 345
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APPLICANT: Allen, Keith D.

TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NDY6-R

TITLE OF INVENTION: WEUROPEPTIDE RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: R-639

CURRENT APPLICATION NUMBER: US/09/900,497

CURRENT FILING DATE: 2000-07-06

PRIOR APPLICATION NUMBER: US 60/216,260

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
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55.0%; Pred. No. 0.65;
tive 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.2; DB Pred. No. 0.21; 0; Mismatches
                                                                                                                                                                                             APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATETSHI, NAOKO
APPLICANT: SENCH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Corynebacterium glutamicum US-09-738-626-2081
Sequence 2081, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09900497 Patent No. US20020082232A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.7%;
Best Local Similarity 57.5%;
Matches 65; Conservative
                                                                           APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                       ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin ver. 3.0
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Matches 71; Conservative
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SOFTWARE: Patentin ver. 3.
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TYPE: DNA
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409 GACAAGGTAGAAGGACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCT 468

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RESULT 3 US-09-738-626-2081

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1577 TAGCTGCTGCTCGCGCTATTCAGGCCGATGCGATGGCCAATGCCTATGCCATTGAGAAGG 1636
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                                                                                                                                                                                                                                                               1513 GACAAGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430F1C27
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                                                                                                                                                                                                   142 GAGGAAGAAGAAATTGAGGTTCCAGTTTACAAAGAACCTGCAGAGAAAATTCCAAGATG 201
                                                                                                                                                                                                                                                                                                                                                                                                                      202 GAAACTGATGAAGCTCCTGCTGATGCTGCTGCTGCTGCAACTCCTAGCAACAATGAC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 TY.Y.YHSC.YH.B.C.YBSHD.H.SSCGY.C.SHYC..D.MH.TS.CM.SAT.CNB.
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Pred. No. 0.25;
0; Mismatches 55; Indels
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SEQ ID NO 346
                                                 ORGANISM: Glycine max
CTHER INFORMATION: Clone ID: LIB3028-035-Q1-B1-H8
US-09-878-574-5240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
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                                                                                                                                                      1.7%;
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Best Local Similarity 7.1%; Matches 29; Conservative 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US20030044930A1
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Goddard, Audrey
Godowski, Paul J.
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                                                                                                                                                         Query Match · 1.79
Best Local Similarity 55.69
Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan, James
Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication No. US2 GENERAL INFORMATION
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  LENGTH: 369
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: US/09/878,574
FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL.
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CUBRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
WHICH APPLICATION NUMBER: 60/082,567
WHICH APPLICATION NUMBER: APIL 21, 1998
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502 GACAAGGAGGATCAGAAGCTTAAGGACATCATTTTGTACATAGTGAGTTTGAGGAAAGCT 561
                                                                                                     Gaps
                                                    469 CAGGAGGTATGCCAAGAACTGGCCAAAAAAGAAAATGCAGACGAGGAACCAACTCTGCATC
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700343414H1
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51.9%; Pred. No. 0.22;
iive 0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                         Sequence 856, Application US/09294093B Patent No. US20010051335A1 GENERAL INFORMATION:
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; Patent No. US20020110548A1
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Best Local Similarity 51.9
Matches 81; Conservative
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SOFTWARE: PERL PI
SEQ ID NO 856
LENGTH: 292
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LOCATION: 111
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SEQ ID NO 53
LENGTH: 1896
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US-10-213-990-52
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                                                       1877 GCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACACGACATCACGGGCG 1936
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CURRENT APPLICATION NUMBER: US/10/184,634
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420 SSS...MMTSMMT.Y...T...SHSSS...CYCYCMYCYMMB...HH.Y...HCSSCCSCY.T. 361
                                                                                  360 CYHTY.YYY.M.,M.,Y.YY......YYYYT., YYYT.HYYMW.S.YHB.HSHSSS 301
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                                                                                                                                                            SS..Y..M.MYCY.M...M.T.MYCY...MMBSBHSHSSSSSSSSSSTSYTK 250
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Best Local Similarity 7.1%; Pred. No. 0.67;
Matches 29; Conservative 138; Mismatches 244; Indels
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                                                                                                                                                                                                                                                                       Application US/10184634
o. US20030068684A1
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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ORGANISM: Homo Sapien
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US-10-184-634-346/C
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APPLICANT: Jiang, Bo.
APPLICANT: Disary, Bo.
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Cornins, Reg
APPLICANT: Cornins, Reg
APPLICANT: Neemer, Terry
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
                                                                                       APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Scener, Terry
TITLE OF INVENTION: UUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.5;
0; Mismatches 105; Indels
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Pred. No.
Sequence 53, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
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Best Local Similarity 48.3 Matches 98; Conservative
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Best Local Similarity 48.3
Matches 98; Conservative
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; LOCATION: (1)...(1896)
US-10-213-990-53
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CORGANISM: Aspergillus
US-10-213-990-52
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Aspergillus
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Watanabe, Colin K.
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Gurney, Austin L.
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Smith, Victoria
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US-10-184-634-116
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                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
PLIOR APPLICATION TEMOVED - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 TGCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGG 245
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                                   1091 CGATTCGTTCGCTCGGTCTACGCGATCAACTCCGGCATCCCACAGGGCGCTGCCGTTTC
                                                                         705 CGACAACCGGCCGGAATACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGC
                                                                                                                                                     765 TGCCGTATCCATGCAAGGCTACAAGGCTGACGACTATGCCATGACCATCGGTTTCCCGGG
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1.6%; Score 34.4; DB 9; Length 489;
Best Local Similarity 8.3%; Pred. No. 1;
Matches 37; Conservative 116; Mismatches 291; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                 Sequence 116, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     1271 CATCACCAGCACCTCCCTCGCCT 1293
                                                                                                                                                                                                                                 825 CAGTACGGATCGCTACCTCACTT 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-116
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US-10-184-644-116
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426 GCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Heappyevlsvreqleherirectistleatlyilchifltrekkpaeftyddedatv 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430816217 CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT APPLICATION NUMBER: US/10/206-28 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 116, Application US/10184634 Publication No. US2003006868481
                                                                                                                                                               486 ACTGGCCAAAAAAGAAATGCAGA 509
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0; Mismatches

Length 50000,

Score 34; DB 9; Pred. No. 23;

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362 TTCCGGGTCTTTCCGTGAAGTATCTGCGCAAGATCGTGAAGGTAACGGACAAGGTAGAAG 421
                                                                                                                                                                                                                                                                                                                                                             422 GACAGCTCAAGGGTATCACTGACGAGATGGAGCGTCTGCGCCAAAGCTCAGGAGG 475
                                                                                                                                                        1.68;
56.18;
                                                                                                                                                                                Best_Local Similarity 56.13
Matches 64; Conservative
                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-10-152-724A-22
  SEQ ID NO 22
LENGTH: 50000
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APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYDECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT APPLICATION NUMBER: US/09/923,876
PRIOR FILING DATE: 2001-08-06
PRIOR PRILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SSCTUMAR: PROGRAM
SEC ID NO 5908
LENGTH: 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 ATCACTGACGAGATGGAGCGTCTGCGCAAAGCTCAGGAGGTATGCCAAGAACTGGCCAAA 495
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APPLICANT: HOLMES, Gregory
APPLICANT: HOLMES, Gregory
APPLICANT: KOLLE, Gabriel
APPLICANT: TAMADA, TOSHIJA
APPLICANT: GEORGAS, Kylie
APPLICANT: GEORGAS, Kylie
APPLICANT: GEORGAS, Kylie
APPLICANT: WILKINSON, Lorine
TILLE OF INVENTION: NO. US20030082714A1el Nucleic Acid and Polypeptide
FILE REFERENCE: P22378
CURRENT APPLICATION NUMBER: US/10/152,724A
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/10/152,724A
PRIOR FILING DATE: 1999-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 TACTTCCTCATCGTCTACGATGTATTCAAGGACGTTCGTATGGTATTGCTCCTCCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700457955H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 34; DB 10; Length 268;
48.4%; Pred. No. 0.98;
tive 0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: unsure
; LOCATION: 13, 50, 69, 179
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5908
                                                                                                                         Sequence 5908, Application US/09923876 Patent No. US20020013958A1 PATENT NORMATION:
APPLICANT: Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/10152724A Publication No. US20030082714A1 GENERAL INFORMATION:
421 LGDFGRFNWLGNFYIVFLYNAAFA 444
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Best Local Similarity 48.45
Matches 91; Conservative
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US-10-152-724A-22/C
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US-09-808-880-1
                                                                                                                                                                                                                       APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: ADGaniel, Robert
APPLICANT: ADGaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/4808,880
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/1928
PRIOR APPLICATION NUMBER: 60/120,28
PRIOR APPLICATION NUMBER: 60/120,24
PRIOR PILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1998-10-29
Length 50937
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Best Local Similarity 47.2%; Pred. No. 31;
Matches 102; Conservative 0; Mismatches 114;
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Job time : 741 secs,
                                                                                                                                             Sequence 1, Application US/09808880 Publication No. US20030027287A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 3
SEQ ID NO 1
LENGTH: 50937
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5.1.4_p5_4578 Compugen Ltd.		Search time 2048 Seconds (without alignments) 16915.110 Million cell updates/sec	.aagagctgaagttgatctaa 2139		Ŋ	: 32308132										·		results predicted by chance to have a l to the score of the result being printed, of the total score distribution.		Description	BH388186 AG-ND-124 BH392840 AG-ND-162 BH386991 AG-ND-148 BH375201 AG-ND-173 BH400391 AG-ND-147 BH375688 AG-ND-120
GenCore version 5.1 Copyright (c) 1993 - 2003 Comp	search, using sw model	. 2003, 02:45:01 ; Search t (with	US-10-008-355-1 2139 1 atgcaaatgaaattaaaaag	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	16154066 seqs, 8097743376 residues	satisfying chosen parameters	length: 0   length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	EST:* : em_estba:* : em_esthum:*	em_estin:* em_estivu:* em_estivv:* em_estipl:*	em_estro:* em_htc:* gb_est1:*	<pre>9b_est2:* 9b_htc:* 9b_est3:* 9b_est4:*</pre>	gb_est5:* em_estfun:* em_estom:*	gb_gss:* em_gss_hum:* em_gss_inv:*	em_gss_pln:* em_gss_vrt:*	em_gss_mam:* em_gss_mam:* em_gss_mus:*	em_gss_other:* em_gss_pro:* em_gss_rod:*	o bi⊬	SUMMARIES	Query Match Length DB ID	537 17 BH388186 591 17 BH392840 500 17 BH386991 418 17 BH375201 426 17 BH400391 697 17 BH375688

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1 (bases 1 to 500)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
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                         Fax: 301 838 3543
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AG-ND-162P14.TF ND-TAM Anopheles gambiae genomic clone AG-ND-162P14
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Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
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to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                            /organism="Anopheles gambiae"
%tatrain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-124P3"
/clone="NG-ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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BH400391 426 bp DNA linear GSS 11-DEC-2001
AG-ND-147H4.TF ND-TAM Anopheles gambiae genomic clone AG-ND-147H4,
                                                     Koo, H., Collins, F., Gardner, M. and Loftus, B.J. BAC-end sequences from Anopheles gambiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 CAACTGAATACCTTCCTTCAATTGCTGTAGAAAAGATCATCAACGÁTACAGATCCTGCTA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
1 81 c 70 g 122 t
                                                                                                                                                                                                     9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0208
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Anopheles gambiae"
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                                                                                                        Unpublished (2001)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:7165"
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                                                  Shetty, J., Malek, J.,
Direct Submission of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partial digest.
Seq primer: M13 Rev
Class: BAC ends.
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                                                                  Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
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9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3343
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minmize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas ASM Universty BAC Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 TCGTAGAGCCTTTCTATTCCAACAACGAATACTTCCTCATCGTCTACGATGTATTCAAGG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 TGGTGAAGGATTTCTTCAAAGGAAATGAGTTTTACTACTTTGTATTCCAGGATTTCAAAG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587 ACGTTCGTATGGTATTTGCTCCTCCCAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647 ACTGGATGTGGCCGCGTCACACGGGCGACTTCAGCGTATTCCGCGTGTATGCCGGTGCCG 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 ATGCCAATCCTGCTGAATATTCAGCTAACAACGTTCCTTTAAAGCCTAAGCATCATTTAC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other_GSSs: AG-ND-148L11.TF
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Pred. No. 4.7e-20;
0; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="Av ..../clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
inf c 90 g 162 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7165"
/clone="AG-ND-148L11"
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Best Local Similarity 57.6%;
Matches 194; Conservative
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Seg primer: M13 Rev
Class: BAC ends.
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ORGANISM

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AUTHORS TITLE JOURNAL COMMENT

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Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0348
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Email: bjloftus@tigr.org
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DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC.
Library was constructed at Texas ARM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                     Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 AAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGAATCTGGATCGAATGCGTGAGCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 GGAGGAATGTGGATTCCTACAGAGTTAAATGAAAAGGA------AATGAAGGAATTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 GGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATTGCCAATGCC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 GGCATGAAGATTTCTGCGAAAGATATTTTCAATACTCAAAAACCTAGTATTAAAGATGCT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 GTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTTT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 ACCAACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTAT 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 AAAAACATCCTATTAGCACTAGCTTTACTCCCCGCAGTGACGGCTTTTGCTCAACAGGCG 416
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                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Pred. No. 9.1e-08;
0; Mismatches 186;
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Contact: Brendan J Loftus
                                 African malaria mosquito.
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Seg primer: M13 Rev
Class: BAC ends.
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Best Local Similarity 50.3'
Matches 197; Conservative
                                                          Anopheles gambiae
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                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3043
Fax: 301 838 3043
Email: bloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is Gerived from miscroorganisms that inhabit
the gut. The DNA is Gerived from miscroorganisms that inhabit
University, College Station, Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
Seg primer: M13 For
Class: BAC ends.
                                                                                                                                                                                                              Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH375688 697 bp DNA linear GSS 10-DEC-2001
AG-ND-120J9.TR ND-TAM Anopheles gambiae genomic clone AG-ND-120J9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1756 GGTGCCTGGTACAACTATCATACGACAGGCAAGGCCGTATTGGAGAAGCAGGATCCTAAG 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1816 AGCGATGAGTTTGCCGTACAGGAGATATCCTCGACCTCTTCCGCACAAAACTATGGT 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1876 ---CGCTATGCCGAGAACGGTCAGCTCCATATCGCTTTCCTATCGAACAACGACATCACG 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1933 GGCGGTAACTCCGGTAGCCCCGTATTCGATAAGAACGGCCGTCTGATCGGTCTTGCTTTC 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 GGTATCAAGCAGAATTACTATACCACAATGGAAGGTATGATGATTAAGAAGTACAAGAAAGGT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea;
Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72.4; DB 17; Length 426;
Pred. No. 1.2e-09;
0; Mismatches 106; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7165"
/clone="AG-ND-14744"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
79 c 76 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                               Other_GSSs: AG-ND-147H4.TR
                                                     African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence.
BH375688
BH375688.1 GI:17321830
вн400391.1 GI:17346607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain-"PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1993 GATGGCAACTGGGAAGCT 2010
                                                                                                                                                                                        (bases 1 to 426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GACGGAAACAGTGAAGCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.8
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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вн375688/с DEFINITION

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RESULT LOCUS

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ACCESSION VERSION

Gaps

9.

GSS 24-SEP-2001

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/strain="HM1:IMSS"
/db.ref="taxon:5759"
/db.ref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="vector: PH051; Site_l: Bst I; Constructed at The
/note="vector: PH051; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Dlamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: blloftusetigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
MDA library
Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                          1005 bp DNA linear GSS 24-SEP-200
Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                          Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 CGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGCCTGATCTT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 TACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGATCACGACTA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17; Length 1005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 9543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCGCGATGGTTTCGTTTCTCGCACGATGGGTGAGGAGCTTCCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GATCACTGGTGGCTTCATCGCCAACGCCCGTGCCGACGACGACGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1005
/organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%; Score 49.2; DB 56.0%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                   Eukaryota, Entamoebidae, Entamoeba.
1 (bases 1 to 1005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 15
High quality sequence stop: 487.
Location/Qualifiers
    307 CACGACTATCTGCGCGATGGTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                BH164253.1 GI:15737691
                                                                                                                                                                                                  genomic, DNA sequence.
BH164253
                                           268 CAAAATCATTTAAAAAATGGTTT
                                                                                                                                                                                                                                                                                            Entamoeba histolytica.
                                                                                                                                                                                                                                                                                                                   Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                               ENTTG63TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                       GSS
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                                                                                                                                   BH164253/c
                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                              ORGANISM
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KEYWORDS
SOURCE
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                                           g
      δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                 ESTs from roots of Medicago truncatula after Rhizobium inoculation
Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                       1 (bases 1 to 398)
VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Seedling roots"
/dev.stage="3 days post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGCCGACAAAGGCATGTGGCTCCTCAACGAACTCAATCAGGAGATCTGGATCGAATG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 CGTGAGCTCGGCTTTACGCTCCCGTTGGATTCGCTCTACAGTTTCGACAAGCCGTCCATT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 CTGATCTTTACCAACCACCACTGCGGATACGGTGCTATCCAGAGCCAAAGCACGGTGGAT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
TTE: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 AGAGCCGATGAAGGAATGTGGTTCCTGATGTTTATCGAAAGATTAAATCACAGGGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 GCCAATGCCGTGGTTATCTTCGGTGGCGGATGTACCGGTATCACAGTGTCCGATCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 2.6%; Score 55; DB 10; Length 39 Local Similarity 50.6%; Pred. No. 0.00013; nes 133; Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               More information is available at...
http://chrysie.tamu.edv/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR sequence name: MTEBG14TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kvandenb@cbs.umn.edu
Texas A&M EST name:T258226e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="pKV3-24C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="KV3
                                                                                                                            AW774807.1 GI:7718724
                                                                                                                                                                                                  Medicago truncatula
                                                                                                                                                                             barrel medic.
                                                                                                                                                                                                                                                                                                                                                                               Fraser, C.M.
                                                                                                                                                                                                                                                                                         Medicago.
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                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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JOURNAL
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                                                                                                          ACCESSION
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AW774807
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Gaps

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Indels

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BH400866/c DEFINITION

RESULT 9

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

ACCESSION VERSION

KEYWORDS

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BH391233 721 bp DNA linear GSS 11-DEC-2001
AG-ND-141L2.TF ND-TAM Anopheles gambiae genomic clone AG-ND-141L2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_swage="adult"
/lab_host="nH5 - alpha"
/note="vorgan: head, Vector: pOT2; Site_1: EcoR1; Site_2:
/note="vorgan: head; Vector bOT8 were directly ligated into
pOT2. Plasmid cDNA library." I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 721)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
1 (bases 1 to 692)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1590 CGCTATTCAGGCCGATGCGATGCCCAATGCCTATGCCATTGAGAAGGGCAAGCGTCTTT 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1470 GGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACAAGGAAAAGTTTGC 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1530 CAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAATAGCTGCTGCTCG 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 CACCACCAATCCCTACAACCTGGCCGTCTACGACGGCGACTACCCGGTGATCTTCAA 433
                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
Plate: 252 row: D column: 6
High quality sequence stop: 496.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH25242"
/clone="GH25242"
/clone="Lb="GH Drosophila melanogaster head pOT2"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loffus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1650 CTTTGCCGGTTTGCGTGAGATGTACCCCGGACGTGCTCTGCCG 1692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                      Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42.2;
                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Other_GSSs: AG-ND-141L2.TR
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                                                                                                                                               Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.3%;
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AUTHORS
TITLE
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VERSION
             REFERENCE
                                       AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
University, College Station, Texas 77843-2123, USA using a HindIII
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                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 555)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae (Unpublished (2001))
Other_GSSs: AG-ND-125M4.TF
                                                                    GSS 11-DEC-2001
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                                                          BH400866 555 bp DNA linear GSS 11-DEC-200
AG-ND-125M4.TR ND-TAM Anopheles gambiae genomic clone AG-ND-125M4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 ATGAAAATATGCGTACTGATAATGCAACCCGTATTAAATATGCATCTAAATATGCATCCG 488
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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0
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Pred. No. 0.6;
0; Mismatches 32; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7165"
/clone="AG-ND-125M4"
/clone_lib="ND-TAM4"
/note="Vector: pECBAC1; Site_1: HindIII"
105 c 94 g 204 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          986 GTGCTAACTATTGGAAGAATTCGATCGGTATGAA 1019
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                                                                                                                                                                                                                    African malaria mosquito.
                                                                                                                                                                 BH400866.1 GI:17347082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI405287
AI405287.1 GI:4248374
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66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                partial digest.
Seq primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Conservative
                                                                                                                                                                                                                                                   Anopheles gambiae
                                                                                                                    DNA sequence.
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Best Local Similarity
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source

FEATURES

BASE COUNT ORIGIN

Matches

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KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

VERSION

RESULT 10

AI405287

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BH371846

822 bp DNA linear GSS 10-DEC-2001
AG-ND-162M17.TF ND-TAM Anopheles gambiae genomic clone AG-ND-162M17
, DNA sequence.
BH371846.1 GI:17317971
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Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library Genomic Research
CILIS and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from "microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&W University BAC Center
Dantersly, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1044 GATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCCGTAAGAACGGCAA 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CAAAGCTGTTTATGGAAATGTATTAGCAAATACTGATGCATACTACAAGCAAATTTCTAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 GAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAGCAAGTATGCTCA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles:
1 (bases 1 to 822)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus
Direct Submission of BAC-end sequences from Anopheles gambiae
Other_GSSS: AG-ND-162M17.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 GAAGAAGCATATGGATAAAGACGATGCTACAAGATTAGCTTACGCGTCTAACTATGCAAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41.2; DB 17; Length Pred. No. 2.1; 0; Mismatches 138; Indels
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="AG-ND-14112"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
122 c 147 g 183 t
                                                                                                                                                                                                                                                                                                                                                              /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .721
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                                                                                                                                                                                                                                                                                                                                                                                        /strain="PEST
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Similarity 47.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 124; Conservative
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COMMENT
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AL728310 606 bp mRNA linear EST 18-APR-2002 AL728310 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BNOAA0982A08 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
This clone is from an A. gambiae BAC library (ND-TAM) provided by P.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII Seq primer: MI3 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 606)
coinbra, W., Well,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Welssenbach,J. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="BNOAA098ZA08" /clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2007 AGCTATGAGTGGTGACATCGAGTTCGAACCCGATCTGCAGCGCACAATCAGCGTGGACAT 2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 822;
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                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7165"
/clone="AG-ND-162A17"
/clone_lib="ND-TAM"
/note="Vector: pFCBAC1; Site_1: HindIII"
142 c 155 g 290 t
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/note="subtracted cDNA library"
100 c 157 g 169 t
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                                                                                                                                                                                                                                                                                                          /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.4; DE
Pred. No. 7.6;
0; Mismatches
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Pred. No. 8.2;
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/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2067 CCGCTACGTTCTCTTCATGATTGACAAAT 2095
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                                                                                                                                                                                                                                                                                                                                  /strain="PEST
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Unpublished (2002)
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                             RESULT 15
AW375157
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BOGZL67TR BOGZ Brassica oleracea genomic clone BOGZL67, DNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1457 TCGACAAGAGTGTGGTTCCTTATAGCGACAAGTTCCATGCCATGCTCAAGTCCATGGACA 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1517 AGGAAAAGTTTGCCAAGGCTATCGAGAAAGATCCGGCAGTAGAGCTTTCCAAGAGCGTAA 1576
                                                                                                                                                          972 CAAGTATGCTCAGAGTGCTAACTATTGGAAGAATTCGATCGGTATGAACCGCGGTCTCGC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1032 TCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGCATTCGCAGACTGGATCC 1090
                                 852 GGGTGTGGAAGATCGTATCGAAAACGAGAACAATCCTCGTATCGAAGTTCGCGGTATCAA 911
                                                               116 GGAAGAGGCAGATTATAAGAGACTACATAACTTTCCTCTTATAAGGCATACTGATATGCC 175
                                                                                             912 GCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATCAAATATGCCAG 971
   Gaps
                                                                                                                                                                                                                                            /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers' 117 c 159 g 202 t
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Pred. No. 12;
0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 687)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea (Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA
Mismatches 125; Indels
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/organism="Brassica oleracea"
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/clone="BOG2L67"
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   Location/Qualifiers
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llarity 53.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea
Brassica oleracea
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Fax: 301-838-0208
   Conservative
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OV2-CT0121-280999-001-e01 CT0121 Homo sapiens cDNA, mRNA sequence. AW375157.1 GI:6879811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be set on the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?ti=QV2&t2=QV2-CT0121-
280999-001-e016.13=1999-09-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 88.
Location/Qualifiers
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                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612 CAGCTCTGTAGGTAAGTTCGGAGGCGATACGGACAACTGGATGTGGCCGCGTCACACGGG 671
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                                                                                                                                                                                                                                                                                     HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Pred. No. 5.7;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/db_xref="taxon:9606"
/clone_lib="CT0121"
/dev_stage="Adult"
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Job time: 2069 secs
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                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                     (bases 1 to 184)
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Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brazil
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on:

May 23, 2003, 08:43:01; Search time 3929.8 Seconds (without alignments) 5272.840 Million cell updates/sec

3719 1 MOMKLKSILLGAALLGASG......LFMIDKWGQCPRLIQELKLI 712 US-10-008-355-2 Title: Perfect score:

Sequence:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% 'Maximum Match 100% Listing first 45 summaries DB seq length: 0 DB seq length: 200000000 Minimum [ Maximum [

'YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

gb\_ba:\* gb\_htg:\* gb\_in:\* GenEmbl:\* Database :

gb\_om:\*
gb\_ov:\*
gb\_pat:\*
gb\_ph:\*
gb\_pl:\*
gb\_pr:\* gb\_sts:

gb\_sy:\*
gb\_un:\*
gb\_vi:\*
em\_ba:\*
em\_fun:\*

em\_pat: \*
em\_ph: \*
em\_pl: \*
em\_ro: \*
em\_ro: \*
em\_sts: \*
em\_un: \* em\_in:\* em\_om:\* em\_or: em\_ov: еm\_mu:

RESULT

ALIGNMENTS

em\_htgo\_other: em\_htg\_inv:\* em\_htg\_other: em\_htg\_mus:\* em\_htg\_pln:\* em\_htg\_rod:\* em\_htgo\_mus:\* em\_htgo\_hum:\* em\_htg\_hum:\* em\_htg\_mam:\* em\_htg\_vrt:\* em\_vi:\* em\_sy 229::330::332::334::336::336::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::34600::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::3460::34600::3460::3460::3460::3460::3460::3460::3460::3460::3460::34600::34600::3460::34600::34600::34600::34600::34600::34600::34600::3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	. Description	AEOOAOOR XVIOLE F	016590 Homo s	1732 Xanth	150	5549	333	69 Oryza s	M.sp 207	128 S	45 S	ο.	A81135 Sequence 1	AR0657,82 Sequence	E26074 Novel vals.	AE013500 Methanosa		D13791 C. perfring			AC084652 Caenorhab	AP003135 Staphyloc	AP003363 Staphyloc	AE009964 Streptoco	AC006884 Caenorhab			AE013596 Methanosa			AE0093:39 Agrobacte	_	AFUSYSTS MOFAXELLA	ABUTUOSO MELIIGIUSA	DO/338 MELIABOCOCC	AEUUI/61 Inermoted	ALI62/52 Neisseria		3695 S	95	U35629 Lactococcus	St	5169 L	01514	AX413017 Sequence	17045 Sequenc
SOFIMARIES	ID	AE004008	۰-	AE011732	AE014150	AE006549	AE000733	OSJN00169	MSP207AAM	28	~	AE009858		AR065782	E26074	AE013500	AE010493	CLOCOLA	BD003707	AE007366	CBRG45011	AP003135	AP003363	AE009964	AC006884	AF497482	LAU62096	AE013596	AE014138	AE008276	AE009339	AF106581	AFU39313	RECIOCAL	00/330	AEUUI/01	NMA122491	AX41541/	AX413695	AF296095	U35629	939	П	151	AX413017	AX417045
	DB	-	10	2 ←		г	Н	80	Н	-	7	П	9	φ.	9	٦	Н	-	9	7	m	П	П	П	~	Н.	-	٦,	-	٦.	- 0	უ ,	٦.	٦,	٦,	٠,	٦,	٥	9	14	-	П	-	Н	9	9
	Ä	10689	253217	10811	50372	10889	15569	162754	4004	10292	11362	14169	2652	2652	2652	9827	10029	4141	6004	11280	26703	291150	342600	11264	193188	90348	3084	11925	52900	9389	11199	36380	10000	70001	10290	10101	340806	4/16	4731	7009	7858	10826	239050	299850	49980	499
æ	Query Match	24.4		4.7										•	•	•		•	٠	•		•	•	٠.	٠.	•	٠.	•	٠.				n .			٠	•	٠				٠			3,3	3.3
	Score	07.		, –	47.	46.	144.5	37.	33.	m	Н	131.5	130	130	130	130	130	129	129	129	129	128.5	128.5	128	_	126.5	126		125.5	124.5	124.5	٦ ;	123.3		٠, د	123	٦ ;	7	122.5	22.	122.5	122.5	122.5	$^{\circ}$	2	7
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/LTAISTALLION="MINLYTGAPGNGKTLYAVDWLIRQIEIDKSLVKSGAVPRSFYTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to SPIP03626 (percent identity: 36 %/query alignment coverage: 88.0 %/subject alignment coverage: 105.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYSPAHLSEAASSVAGASGQASLRAAPASLSSSRSLVSGMRTYAVLETESAPTLSGCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1839, .2918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="XF1875"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2918. .3202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVLRHVLTQRQQKRKASP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="XF1874"
1351. 1662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson,A.J.G., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M., Alvarenga,R., Alves,L.M.C., Araya,J.E., Bala,G.S., Baptista,C.S., Blaros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.S., Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.S., Bueno,M.R.P., Camargo,A.B., Colombo,C., Costa,F.F., Costa,M.C.R., Costa,Met.P., Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C.R., Docena,C., Franco,C., Franco,C., Franco,C., Franco,C., Fronme,M., Facincan,A.S., Franca,S.C., Franco,M.C., Frohme,M., Fullan,L.R., Garnier,M., Goldman,G.H., Goldman,M.H.S., Gomes,S.L., Kitajima,J.P., Krieger,J.S., Kranca,S.C., Franco,M.C., Kemper,E.L., Kitajima,J.P., Martins,B.H., Madeira,M.B.M., Madeira,M.B.M., Madeira,M.B.M., Madeira,M.B.M., Madeira,M.B.M., Martins,E.M.E., Matsukuma,A.Y., Menck,C.F.M., Miracca,E.C., Martins,E.M.E., Matsukuma,A.Y., Menck,C.F.M., Miracca,E.C., Nascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.A., Nobrega,F.G., Nunes,L.R., Oliveira,M.A., Ge Oliveira,M.C., de Oliveira,R.C., Palmieri,D.A., Perica,M.B., Reixoto,B.R., Pereira,G.A.G., Pereira,J., de Sawasaki,H.E., de Silveira,M.E., Silqueira,W.J., de Sawasaki,H.E., de Silveira,M.F., Tuffil,D., Tsai,S.M., Tsuffil,D., Tsais,S.M., Tsuhako,M.H., Vallada,H., Van Sluys,M.A., Veriovski-Almeida,S.
Yylella fastidiosa 9a5c, section 154 of 229 of the complete genome. AE004008 AE003849
AE004008.1 GI:9106961
                                                                                                                                                                                                                                                                                                                                            Alvarenga, R. Alves, L. M. Araya, J. E., Baia, G. S., Baptista, C. S., Alvarenga, R., Alves, L. M., Araya, J. E., Baia, G. S., Baptista, C. S., Barros, M. H., Bonacorsi, E. D., Bordin, S., Bove, J. M., Briones, M. R., Camargo, A. A., Camargo, L. E., Carraro, D. M., Carrer, H., Colauto, N. B., Colombo, C., Costa, F. F., Costa, M. C., Costa-Neto, E., Oceta, M. C., Costa, C. M., Facincani, A. P., Ferreira, V. C., Pocena, C. H. Dias, Nato, B. J. S., Franca, S. C., Franco, M. C., Frohme, M., Furlan, L. R., Goldman, G. H., Goldman, M. H., Gomes, S. L., Gruber, A., and Marino, C. L., Kemper, E. L., Kitajima, J. P. and Marino, C. L., Kitajima, J. P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The genome sequence of the plant pathogen Xylella fastidiosa. The Sylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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Xylella fastidiosa 9a5c
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               AE004008/c
                                                                      DEFINITION
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MEDLINE
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JOURNAL
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                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                   KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ACTCATGCGGCGAAGGCATGTGGGTTCCACAACAGCTT---CCGGAAATTGCTGGC 10389
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135
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Mismatches:
Indels:
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/gene="XF1877"
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10388 CCTCTAAAGCAGGCTGGCCTACAACTGTCACCAGAACAATTGTCAATTTGACAGGTGAC 10329
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                                                                                                                                                                    10274 GAAGGACTGGTGATCACTAACCATCATTGCGCTTATGGTGCGATTGAATTGAACTCTACG 10215
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                                                                                                                                                   81 GlnGlyLeuIlePheThrAsnHisHisCysGlyTyrGlyAlaIleGlnSerGlnSerThr
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                                                                                                                                                                                                                                                                                                    121 Ile---ProGlyLeuSerValLysTyrLeuArgLysIleValLysValThrAspLysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 IleGluValArgGlyIleLysGln-------GlyIleTrpLysGluAla
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                                                                        SerIleAlaAsnAlaValValIlePheGlyGlyGlyCysThrGlyIleThrValSerAsp
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ACO16590/C LOCUS DEFINITION ACCESION VERSION VERYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT COMMENT
938   LyshlawankrgoluwerthriytlewSerGluthricaphediyGlyThriCluvalval   407     934   AndroAdankraGoluverthriytlewSerGluthricaphediyGlyThriCluvalval   1111     920   ArghbaldclipheAlabanhalabahla   112   1111     921   AndroAdankraGoluverthrigolyArghalabahlaryands   1211     922   GOTTINGGGGTANARCTGROADANTCHGANARTGANGCOCAAGT   9211     923   GOTTINGGGTANARCTGANGCOCAAGTTGANGCOCAAGTTGANG   9211     924   AndroAdantCharthrigolyGoluverthriandCharthrigolyGolupySerJeaneng   1311     925   GOTTINGGGTANARCTGANGCOCAAGTTGANGCOCAAGTTGANGCOCAAGTGGG   9211     926   GAACCGGANARCTGACCCAAGTTGGANGCACCAAATTCAAGTGGG   9211     927   CAAGGGTANARCTGAGCCCCAAGTTGANGCAAGTTGANGCAAGTGGG   9212     928   GAACCGGANARCTGACCCAAGATGAAGCAAGTGGAAGTGGAAGTGGG   9212     929   GAACCGGANARCTGACCCAAGAACTGGAAGCAAGTGGAAGTGGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGAAGTGAAGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTG

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t 3820 others
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gap of unknown length
contig of 6088 bp in length
gap of unknown length
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Location/Qualifiers
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of 3755 bp in length
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Mismatches:
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/chromosome="19"
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(bases 1 to 10811)

(a Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R. Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,
camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,
Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,
Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C.,
Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,
Madeira,A.M.B.N., Martinaz Rossi,N.M., Martins,E.C., Meidanis,J.,
Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,
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Xanthomonas axonopodis pv. citri str. 306
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                  4819 -AACGTAATGCGGAAGACTGAAGAACTGGCCGGTCAAGATCCACGCAAAGCTATGCCAAC
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                                                                     SerLys --- SerVallleAla - AlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAl
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AE011732.1 GI:21107161
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4280 AACCTGCTGAAAGAAATG 4263
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                                                                                                                                                                                                                                                                                                                          da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.S., L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Machira, A.M.B., Martins, E.C., Machado, M.A., Machira, A.M.B., Martins, E.C., Machadis, J., Mancira, A.M.B., Mayaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Tamura, R.E., Taita, M.A., Tamura, R.E., Taita, M.A., Tamura, R.E., Taita, E.F., Setubal, J.C., and Kitajima, J.P., Tsai, S.M., White, F.F., Setubal, J.C., and Kitajima, J.P., Tsai, S.M., White, F.F., Setubal, J.C., and Kitajima, J.P.,
Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J. A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Taritta, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.
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Alatilpvisoaatpadpaavaparaltadaaanatoldalnuvsogstrovoriso
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GnwsygvtnglhitpaliseNicsvetagogaalgyravinicgtwofysbottpo
Arlvotvgsdatrrtevradtgdrdglsaxlsyanastdkwkgygdotseoanlktvy
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RPHLCPNTVGIGVNVNGAFAEYWVMPASNIJWPIPDQIPSELAAFFDPYGNAAHAALEF
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SKGLTVQGIYGRKMYETWYKMYQLVLSGFPLHKVLTHQLPIDDFQKGFDLMEEGKAGK
VVLGWN
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located using Blastx/Glimmer/Genemark"
/codon_start=1
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                                                                                                                                                                  Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (28-NOV-2001) Departmento de Bioquimica,
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo,
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/protein_id="AAM35905.1"
/db_xref="G1:21107162"
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/protein_id="AAM35906.1"
/db_xref="G1:21107163"
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JOURNAL
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FEATURES

CDS

cps.

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LEHVVILMQENRSFDHYFGALRGVRGFGDPRALQLRDGHAVWSQPTPDGRRVLPPFD
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YAALQWTTYAQRLQAAGVDWRVYQEYDNFGCNSLAYFSHYRDLRFDDERYLRARACVPG
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IDALTANPEVWAKTALIINYDENDGFFDHVPAPLPALDARMGRSNVDTHGEVYDGVPI
GLGIRVPMLVISPWTRGGWVNSQVFDHTSVLRLLERRFGVAEPNISPWRRAVSGDLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQVHARVQEGAAVQLGFVNSGAAAARNVYNSAAGGGPWYYTVLPGTQLDDAPTGATH
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PSCTAVQTASLISBVGAAVHSAGADLALMWRPFGLSALNSLSSWNRSBYTQDDI_LNNG
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GARYDEGRVGGVADVALALNISNLTDKRYFASTGTNGYVASDPDGYNQTMVVGAPRQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFDFRKPDDSALSALPSVDDYRARTAAVRDKPLPSAPAAATMPRQEPGQRPARALPYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mmDAQGKLVGLAFDGNWESVSSNWIFDPAMTRWIAVDGRYLRWI
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/transl_table=11
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6791. .7054
/gene="XAC1026"
6791. .7054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGIATPAAQGLAAASKDIPVVMSAVSDPVGSRLVÄQLDQPEANVTGLSNKVPVKQTID
LMKKLTPHVKTVGILYASNEDNSLSQVKEFRRLAFKKGYQVISYAVPSTNEVPATMSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLGKVDAVFIPQDNTIASAFSSVMTTSKAAKIPVÝTSVDRMVEKGGLAAISONQYDLG
VQTANQVLKLIKGKRVVDVPVKVVDIGQPLINKNÝAAELGIAINREDFPSASFIEN"
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                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, MT 59840, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb|AAK99779.1| (AE008470)
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                                                                      Genome sequence of a serotype M3 strain of group A Streptococcus: Phage-encoded toxins, the high-virulence phenotype, and clone
     Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
Musser,J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SpyM3_0654"
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hypothetical protein [Streptococcus pyogenes M1 GAS]"
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substrate [Streptococcus pneumoniae R6]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative ABC transporter membrane-spanning permease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC transporter substrate-binding protein - unknown substrate [Streptococcus pneumoniae R6]"
                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)
2 (bases 1 to 50372)
Beress,S.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,
Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptococcus pyogenes phage 315.1"
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208. .1206

    .34426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="group: A" 34427. .>50372
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                                                                                                                              emergence
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                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
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                                                                                                                                                JOURNAL
                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                           TITLE
                                                                                                                                                                                                                                                                                                               LQIDRAVASPLSRAQATAKAALGASRQALLQTDADLOETAHGWEGLLASEINDKDPA
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                                                                                                                                                                                                                                                                  /db_xref="G1:21107168"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686 SerValAspIleArgTyrValLeuPheMetIleAspLysTrpGlyGlnCysProArgLeu 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 GlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIle
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Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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32
16
16
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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AE014150 AE014074
AE014150.1 GI:21904382
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7329. .7973
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175.00
75.00%
50.00%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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SOURCE
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.nous="best blastp hit: gb|AaK33919.1| (AE006547) putative
ABC transporter (ATP-binding protein) (Streptococcus
pyogenes MI GAS)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MITLOGNKLERSFSGDVLPQNISLQVDERDRIALVGPNGAGKSTLKTLAUGEFPTSGEVNTKKDLTLSYLAQNSRFESDKTIYEEMLKYPEALRQDEKRLR
OLKKLJVGEFFTSGEVNTKKDLTLSYLAQNSRFESDKTIYEEMLKYPEALRQDEKRLR
OMEMDMATUSGQDLTRLMMDYDLLAERFRQGGGFTYBAEITATLNGFKFDESMWQMTI
AELSGGGONTRLALARMLERPELLVLDEPTHHLDIEFITAMLENYLANYGGALITUSHD
RYFLDKVATVTLDLTPHGLDRYVGNYSRFMTLKAEKLVAEEKQFDKQQKEIAKLEDFV
/translation="MKQLLAIILWLPKLIVKMFWHLIKGFLQTILLVTIIIIGLMYYS
NHSDSVLANKISIVTEQVVQIFDILTQKPSAKTRHGSGNSHSTFLVSAKEGNQRLKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYDQTOSHLISSNTVLEELWODFSTTPEVDIRNRLGAFLFSGDDVKKSVAMLSGGEKA
KLLAKLSWENNELVLDEPTNILLDIDSKEVLENALLDPGTLLFVSHRRYFIRRLAT
KVLEITENGSTLYLGYDYYYLEERELEELRLAAGFTVEFTKEASATDYQLANQK
ERRRLIRRYEEIEARLETIEERIGAIQEDMHASNDTAQLIAWQKEWDQLDQEQEALME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="best blastp hit: gb!AAK33920.1| (AE006547) putative acetoin dehydrogenase (TPP-dependent) alpha chain [Streptococcus pyogenes M1 GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKNIVRASTIKRAQARRKOLEKIERLDKPTSARKSAHMTFQADKPSĞNVVLTVEKAAI
GYNQHVLSEPINLDVHKLDAIAIVGPNGIGKSTLIKSVIGQIPFIKGEVKYGANVEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVTVSKEQHLDMFLKMERIREFDSRINKLVRRGFVQGMTHFSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative ABC transporter (ATP-binding protein)"
/protein_id="AAM79267.1"
/db_xref="GI:21904390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative acetoin dehydrogenase (TPP-dependent) alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CTCTTTGATGATAAGGTGATGAAACAGCTTAAAACGTCGCCGTTATACTGGTTGG 30335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30335 GGACGTTGTCTCGAAAATTGATTAATGGTATTAGGGATAAGCAATCTGGCAAAACAATA 30395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 AsnGlnGluAsnLeuAspArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeu 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 GlyIleThrValSerAspGlnGlyLeu-----IlePheThrAsnHisHisCysGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GlnSerGlnSerThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50372
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAM79268.1"
/db_xref="GI:21904391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-008-355-2 (1-712) x AE014150 (1-50372)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SpyM3_0661"
8552. 9520
/gene="acoA"
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                                                                                                                                                     /gene="SpyM3_0660"
                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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/gene="acoA"
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147.50
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Pred. No.:
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                                                                                                                                                                                                                                                2417. .3175 // Action 1975 // Action
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5173. :5958
5473. :5958
fape="esta"
/note="best blastp hit: gb|AAK33917.1| (AE006547) putative
tributyrin esterase [Streptococcus pyogenes M1 GAS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"putative tributyrin esterase"
/protein_ld="AAMY9255.1"
/db_xref="G1:190438"
/translation="MASIAIEYHSVVLGMERKVNVIYPDQSEIPKKDQGDKDIPVLYL
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LAARPENMYQKREKTPAGLSGMEQGYGAFKMALKSNRESYAASFSGALDFSPETLEGN
LGELAYWQGVFGOFDDPDLDKHYLKNNWAESDGKTKFYAMCGYEDFLFARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MTDIKMIALGGVREYGKNFYLVEINDSMFILDAGLKYPENEQLG
YDLYDNLDYVENGYVENGGFLSHGHDALGGLFYLLAESASPAFVEGSELTIELAKLF
VKSNNSTKKFNNFHYNDSDYEIERPKDGLYBFRTTHBIPESWGIVLGTDKGNLYYTGD
FKFDQAAREGYQTDLLRLAEIGKEGVLALLSDSVNATSNDQIASESEVGEEMDSVISD
                                       granlglightkriodclppsidlnslitgijtyvivisvliyfelythigoaytatgdn
KDMAKSFGINTDWMEVMGLVVSNSIIALSGALVSQODGYADVSKGIGVIVIGLASIIV
KDVIXSTGITLLERLIAIVIGVSILYQPLISVVIMLGPPYRSYIKIISALVLALCIMIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTK11EL1NATVDVDNGFEDAKT1LDNVTLT1YEHDFLT1LGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGKSTLFNVIAGTLSLTRGQIRILGGDVTYWPAEKRALYLSRVFQDPKMGTAPRWTV
RELLIARDROGERKSIASRKTTEHLASFEDLVKRTGNGLEKHLETPAGILSGGQRQAL
SLLMATLKREALLLIDEHTAALDPRTSHSLMQLTDEFVTKDGLTALMITHHMEDALTY
GNRLIVWKDGNIIKDLNQMEKEQLTITDYYQLFD
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LIKPKDMSKFEDHELIILEAGRMGEPINSLQKMAAGRHRYVQIKEGDLVYIVTTPSTA
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TAAARALAEBEVGIFPENIHILKRGDIHVUNDSGETHEGGVPASDVMIDGNAIGBVGNI
VLRDRKVLSEDGI FVAITVSKREKRIISKAKVNTRGFVYVKKSHDILRESAELVNTT
VGNYLKKDTFDMGELKGNVRDDLSKFLFEQTKRRPAILPVVMFVR"
VTAISLGWNPFLSTLLGMLSGALAGFLTGLLYTKGKMPTLLAGILVMTSCNSIMLMVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3379. 5040 // Gene="SpyM3_0657" // Johne="best non-GAS blastp hit: gb|AAK74765.1| (AE007370) metallo-beta-lactamase superfamily protein [Streptococcus pneumoniae TiGR4], andgb|AAK99342.1| (AE008432) Conserved hypochetical protein [Streptococcus pneumoniae R6]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative ABC transporter (ATP-binding protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [Streptococcus pyogenes M1 GAS]"
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/gene="SpyM3_0659"
/note="best blastp hit: gb|AAK33918.1| (AE006547)
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5988. .6314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
/protein_id="AAM79264.1"
/db_xref="GI:21904387"
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/protein_id="AAM79266.1"
/db_xref="GI:21904389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAM79263.1"
/db_xref="GI:21904386"
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3379. ,5040
                                                                                                                                                                                            2417. .3175
/gene="SpyM3_0656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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/gene="estA"
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Sun May 25 15:40:28 2003

125 30512 130 30572 142 30632	150 30692 167 30752 186 30788	201 ' 30848 221 30848 241	30863 261 30893 281 30926 301	321 31046 341 31076 358 31136 31136	368 31256 368 31316 368
ThrMetGlyGluGluLeuProll	ATCGTTATTGAAATGGCACGTGAAAATCAGACAACTCAAAAGGGCCAGAAAATGCGT GluArgLeuArgLysAlaGlnGluValCysGlnGluLeuAlaLysIysGlu IIIIII:::::::::::::::::::::::::::::::	PheLeulleValTyr	TyrSerLysAspasnLysProTyrLysProValTyrPhealaalaValSerWetGlnGly	GlylleLysGlnGlylleTrpLysGluAlaMetSerAlaAspGlnAlaThrArgIleLysGltLeLysGlnGlylleTrpLysGluAlaMetSerAlaAspGlnAlaThrArgIleLysGltLeLysAaAAGATGAAAAAAGTGAAAAAAAGTGAAAGTTAATCACTCAAGGTAAAGTTAALaSerLysTylAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArgTTTAACAAAAGCTGAAGGTGAAAAGTTTTAACAAAAGCTGAAGGTGAAAAGTGGAAATTTAACAAAAGCTGAACGTGGAAAAAGAAAAAAAA	GATAAACTTATTCGAGAGGTTAGAGTGATTACCTTAAAATCTAAATTAGTTTCTGACTTC
	143 30633 151 30693 168 30753	187 30789 202 30848 222	30849 242 30864 262 30894 282 30927	302 30987 322 31047 342 31077 359	368 31197 368 31257 368
	2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	90 00 00 00 00 00 00 00 00 00 00 00 00 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	oy oy

qq	31317	GCGTATCTTAATGCCGTCGTTGGAACTGCTTTGATTAAGAAATATCCAAAACTTGAATCG	31376
Qy	369	SerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyr	383
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qq	31437	CAGGAATAGGCAAAGCAACGCAAAATATTTCTTTTACTCTAATATATCTTCTTC	31496
δγ	40	GlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAs	421
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QY	441	uAspArgLysValLeuProAlaMetLeuAspIleValArgArgArg	456
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QQ	31664	AGGCGGATTCTCCAAGGAGTCAATTTTACCAAAAGAAATTCGGACAAGCTT	31715
δλ	465	ePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPheVa	485
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Qγ	485	PheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLysSerWetAs	505
qq	31758	- TITGATAGTCCAACGGTAGCTTATTCAGTCCTAGTGGTTGCTAAGGTGGAAAAAGG	31813
Qy	502	pLysGluLysPheAlaLysAlaIle	513
QQ	31814	GAAATCGAAGAAGTTAAAATCCGTTAAAGAGTTACTAGGGATCACAATAATGGAAAGAAG	31873
δλ	514	GluLysAspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAl	531
QQ	31874	CTCTTTTGAAAAAGATCCGATTGACTTTTTAGAAGCTAAAGGATATAAAGGA	31924
Οy	531	alleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGl	546
QQ	31925	AGTTAGAAAAAGACTTAATCATTAAACTACCTAAATATAGTCTTTTTGAGTTAGAAAACGG	31984
٥y	546	yLysargLeuPhePheAlaGlyLeuArgCluMetTyrProGlyArgAlaLeuPr	564
QQ	31985		32044
Óγ	564	oSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLySGlyTyrGl	582
qq	32045	AAGCAAATATGTGAATTTTTATATTTAGCTAGTCATTATGAAAAGTTGAAGGGTAG	32101
οy	582		865
QQ	32102	TCCAGAAGATAACGAACAAAACAATTGTTTGTGGAGCAGCATAAGCATTA	32152
οy	298	1LeuGluLysGlnAspProLysSerAspGluPheAlaValGln	612
QQ	32153	TAGATGAGATTATTGAGCAAATCAGTGAATTTTC	32212
Qy	612		612
qq	32213	CAATTTAGATAAAGTTCTTAGTGCATATAACAAACATAGAGACAAACCAATACGTGAACA	32272
ΟŸ	61	GluasnIleLeuAspLeuPheArgThrLysAsnTyrGly	625
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δλ	626		636

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/Lranslation="MPYKGYLIDLDGTIYOGKNRIPAGERFIKRLQERGIPYLLVTNN
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2695. 3459
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3459. 5 KD PROTEIN IN GLPD-CSPB INTERGENIC RECION

391/7475050|pir||A69822 hypothetical protein yhce -

341/75050|pir||A69822 

341/75050|pir|

341/75050|pir||A69823|

341/75050|pir||A69823|

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341/75050|pir||A69823|

341/75050|pir|

341
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SWLFDPLKDSVIWILDFEVFFLHCFLFFMIVYEIILWSLVGLARWQRLNVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Best Blastp hit = pir!H70023 N-acetyl-glucosamine catabolism homolog yutF - Bacillus subtilis spil263726|emb|CAB15219.1| (Z99120) similar to N-acetyl-glucosamine catabolism [Bacillus subtilis]"
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Best Blastp hit = gb[AAB71730.1| (U65643) acyl-ACP
thioesterase [Myristica fragrans]"
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2695, 3459
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4571. .8677
/gene="SPy1046"
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                                                                                                                                                                                                                                        Street 10889 bp DNA linear BCT 01-JUN-2001 Street Coccus pyogenes M1 GAS strain SF370, section 78 of 167 of AEO06549 AE004092
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mqeklpslsimysqessklpyqbqgpVllakqckpgnendsdycqlvkyfskp
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Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primedux,C., Sezate,S., Surorcv,A.M., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 10889)

Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
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SL Young Blvd,
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           32333 ATATTTTGATACAACAATTGATCGTAAACGATATACGTCTACAAAAGAAGTTTTAGATGC 32392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative coproporphyrinogen III oxidase"
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/db_xref="GI:13622189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes M1 GAS.
Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-APR-2001) Department of Microbiology University of Oklahoma Health Sciences Center, 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Streptococcus pyogenes Ml/strain="SF370"
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                                                                                      645
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Location/Qualifiers
                                                                           636 aPheLeuSerAsnAsnAspIleThrGly
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98. 720
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LINREDILIRKORT FEDISOSMORY ACTIOGGASQUEET KET KPILERMOGTEELLY
YOP ELARGOR FERMORT SEDTIT PWINEE VUDGGASAQUET ERMIT NEDKIL FRY IT YET YOU WENDERLY BY THE YOUNG SET TO FWINEE VUDGGASAQUET ERMIT NEDKIL ER LIT FRI IN YOU SELY SET TO FWINEE VUDGGASAQUET ERMIT NEDKY ULL FEDRAMIT SECH SELY SET TO FWINE WAS LATT AND LIKE IN TO KNOW LIT SECH SELY TO HILD STAFF AND LIKE THE SEL SELY TO THE SELY SHILE DOWN YOU SELY WAS CHARLY BY TO YOU SELY TO THE SELY SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE SHILE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Best Blastp hit = pir||E81299 hypothetical protein c151522c [imported] - Campylobacter jejuni (strain NCTC 11168) >q11696946|emb|CAB73942.1| (AL139078) hypothetical protein Cj1522c [Campylobacter jejuni]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVV
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322 TyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArg 341
                                                                                                              δ
            10889
172
103
223
363
44
           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                       Gaps:
                                                                                              US-10-008-355-2 (1-712) x AE006549 (1-10889)
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31.98%.
20.00%
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Best Local Similarity:
Alignment Scores:
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Query Match:

Pred. No.:

Score:

Qy Db·	35 AsnGlnGl    :::    6395 AATGAAG	AsnGlnGluAsnLeuAspArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeu    ::             :: ::::                ATGAAGAAAATGAAGATATCTTAGAGGATATTGTTTTAACATTGACTTATTTGAA	54 6451
δy	55 TyrSerP	PheAspLysProSerIleAlaAsnAlaValValIlePheGlyGlyGlyCysThr	74
qq	6452		6493
Qy	75 GlyIleTh	eThrvalSerAspGlnGlyLeuIlepherhrAsnHisHisCysGlyTyr	92
3 6			
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Qy	102 AspHisAs	spTyrLeuArgAspGlyPheValSerArg	
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δÿ	. 114	ThrMetGlyGluGluLeuProIleProGlyLeuSer	125
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δλ	126		130
qq	6725 AGTTTACA	ATGAACATATTGCAAATTTAGCTGGTAGCCCTGCTATTAAAAAAGGTATTTA	6784
٥٧ م	131 Lysileve	eValLysValThrAspLysValGluGlyGln	142
3 ,		יייייייייייייייייייייייייייייייייייייי	,
oy Ob	143 6845 ATCGTTA		150
Q	151	euArgLysAlaGlnGluValCysGlnGluLeuAlaLysLysGlu	-
ф	05		9
Οy	sn	GluAsnGlnLeuCysIleValGluProPheTyrSe	186
QQ	6965 CATCCTGTI	GAAAATACTCA	.7000
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Dp	7001 CTCTATC	:: ICTATTAT	7060
οy	202 AlaProPi		221
Dp	1060		7060
δy	222 HisThrGl	yAspPheSerValPheArgValTyrAlaGly	241
Dp	7061		7075
οχ	yrSei	sAspAsnLysProTyrLysProValTyrPhe!     :::	261
Dp	7076 TATGATG	1 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7105
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QQ	7106 TTCCTTA		7138
οy	282 ThrserT	.yValGluAspArgIleGluAsnGluAsnAsnAroArgIleGluVa	301
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δý	322 TyrAlaS	SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArg	341

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	LysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGly 402	536 aMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGl 556 11 ::: :::

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in 11

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AACO7286.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15569 bp DNA linear BCT 25-MAR-1998 on 65 of 109 of the complete genome.
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similarity to a protein of unknown function.
ifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Gaasterland,T., Young,W.G., Lenox,A.L.,
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, Short,J.M., Olson,G.J. and Swanson,R.V.
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                                                                                                                                                                          ||||||||||::: ||||||||
TGAACAAGCAGAAATATTATTCATTTATTTACGTT 8514
                                                                                                                                                                                                                                                                                       AGATGCCAATTTAGATAAAGTTCTTAGTGCATATAA 8454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTAAATATTTTGATACAACAATTGATCGTAAACG 8574
                                                                                                                                                                                                                                        ------ 612
                                                                                                                                                                                                                                                                                                                                   -----GluAsnIleLeuAspLeuPheArgTh 621
                                                                                                                                                                                                                                                                                                                                                                                                                              ------Ar 626
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                                                                                                                                          sGlyValLeuGluLysGlnAspProLysSerAspGl
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9. .1497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANKEV PEPLLNKRVVALDLAALVAGTKYRGQFEERLKNILKELEKANNVILFIDELHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="ATP-dependent Clp protease"
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gene

CDS

gene

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144.50 Matches: 170 34.18% Conservative: 111 Conservative: 757	qq	
Indels:	ΟŸ	277 rAspArgTyrLe
.,733 (1-15569)	QQ	4618 GGAAAGGTACT
LeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAla	oy D	289 gIleGluAsnGl   ::: 4678 GCTCCTGACA
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LysalaaspLysGlyMetTrpLeuLeuasnGluLeuasnGlnGluasn 38              :::  GTCGCGGACAAGTATTTGAGGTTTACACACTTTTCAGCTCTAACGGAAGAGAA 3939	d d	:::   :: 4733AAAGGTGT
	Qy Db	318 rArgileLysTy     :: 4789 AAGGCTCGTGAG
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54 LeurTyrSerPheaspLysProSerIlealaasnalaValValIlePheGlyGlyGly 72 ::: :::::   :::	7 원 ·	
73	Qy Dp	344 aArgLeuAspVa :::1   4909 AAAGCTGAAAA
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	Qy Db	384 sGluGlyAlaLy        5026 AAACGGTATTAA
TRGGTGCGGGCGTGAGGAGAATAGTGGCACAAACGGGAAGGTGG 4221	ΟY	404 rGluValValAr
	qq	
MetGlyGluGluLeuProileProGlyLeuSerValLysTyrLeuArgLysIleValLys 134	oy O	424 aGlylleLeuLy :: 5105AG
	Qy	sValLeuPr
AAAATTGAAGAACTTAAGGAAGAATCAAAGACAGAGAAAAAAAA	qq	
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	Qy	484 evalPheAspLy  :::       5272 TTTATTTATAAA
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οy	231	ValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLysProTyrLys 250
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Qy	318	rarglleLysTyrAlaSer1327
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Qy	327	AsnArgC
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qq	4909	TCGAGGGTGTGTGAAACATAGAGCAAGTTGTTGACAAAG
Qγ	364	gLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLy 384
qq	4969	GGTACGCCCTGCCCGAGGTGTTTCACTATAGCGAAGGTTT
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ογ	404	rGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAl 424
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qq	5155	TGA
QY	464	pllePheLysAsnVallleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPh 484
qq	5215	Ą
Qy	484	eValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLysSerMe 504
qq	5272	TAAGAGACAT
δλ	504	tAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLysSe 524
QQ	5312	ACAGAAAGGCAAG
οy	524	rValileAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGl 544

COMMENT On Jul 19, 2002 this sequence version replaced gi:17998481.	mbly	NOTE: This is a complete sequence.  Genes were identified by a combination of several methods: Gene prediction programs including Figenesh (http://www.softberry.com/), genscan (http://ccR-081.mit.edu/GENSCAN.html), GeneMarkHMM		FEMIUNES LOCALION/VARILIEES  Source 1. 162784  /organism="Oryza sativa"  /variety="Nipponbare"	/sub_species="japonica" /db_xref="taxon:4530" / chromosome="a" / /clone="0SJNBa043124"	/clone_lib="CUGI-OSJNBa" BASE COUNT 45645 a 36513 c 35782 g 44812 t 2 others ORIGIN	Alignment Scores: 256 Length: 162754 Pred. No.: 256 Matches: 147 Percent Similarity: 36.64% Conservative: 115	: 20.56% Mismatches: 3.70% Indels: 8 Gaps:	US-10-008-355-2 (1-712) x OSJN00169 (1-162754)  QY	Qy 67 ValilePheGlyGlyGlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThr 86	Qy 87 AsnHisHisCysGlyTyrGlyalaTleGInSerGlnSerThrValAspHisAspTyrLeu 106	Oy 107 ArgAspGlyPheValSerArgThrMetGlyGluGluLeuProIleProGlyLeuSerVal 126	Oy 127 LysTyrLeuArgLysIleValLysValThrAspLysvalGluGlyGln 142 ::	Oy 143 LeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGlu 162            :::::   Db 53362 CTGAAAGGTGTAAGC53348	Oy 163 LeualaLysLysGluAsnalaAspGluAsnGlnLeuCysIleValGluProPheTyrSer 182 ::::: :::!    ::::	Qy 183 AsnAsnGluTyrPheLeuIleValTyrAspValPhe 194	Qy 195 LysaspvalargmetValPhealaProProSerSerValGlyLysPheGlyGly 212 ::         ::	Oy 213 ASPThrAspAsnTrpWetTrpPrOArgHisThrGlyAspPheSerValPheArgValTyr 232
5338 AGTTATCTTGAGGGCGAGGGAAGAAGCCCTCGAGCTGGGACACAGCTACTT 5388	544 uLysGlyLysargLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuPr 564	564 oSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluPr 583 	583 oGlnaspGlyalatrpTyrasnTyrHisThrThrGlyLysGly 597	597 597 5558 ATAGAGTITGCAGTTGAAGAAGGGAGAATTCTTCACCACCAGTTCGTAGGTCCCGAACAC 5617	598ValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGl 613 	uAsnIleLeuAspLeuPheArgThrLysasnTyrGlyArgTyrAlaGluAs                                   AGGAGCTTTGGACTGGAGGAGTACTTCAACTACTGGAGGA	630 nGlyGlnLeuHisIlealaPheLeuSerAsnAsnAsplleThrGlyGlyAsnSerGlySe 650	650 rProValPheAspLysAsnGlyArgLeulleGlyLeuAlaPheAspGlyAsnTrpGl 669 	ualaMetSerGlyAsplieGluPheGluProAspLeuGlnArgThrileSerValAspil : :::	689 eArg 690 :111 5875 AAGA 5878	7 [69/c OSJN00169 162754 bp DNA linear PLN 17-JUL-2002 TON Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0043L24,		Oryza sativa. Oryza sativa Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;	VCE 1  NRS Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J., Zhang,L.,	Li,T., Zhang,Y., Hu,H., Jia,P.X., Chang,Y., Lu,F., Zhou, Li,T., Zhang,Y., Hu,H., Jia,P.X., Chan,Y.M., Ying,K., Zhou,B., Chen,Z.H., Hao,P., Zhang,L., Wu,M., Zhang,R.Q., Guan,J.P., Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F., Tu,Y.F.,			
Dp 23	Oy :	Qy :	. da	0y 13	Qy Db 5.		Oy 00	Oy Dp 2.		Oy Dib	RESULT 7 OSJN00169/C LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS		E E	JOURNAL	REMARK

Sun May 25 15:40:28 2003

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circular BCT 26-APR-1993
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                                                                                                   ACTGAAGGAGGCATCCATTTCTGGTATCATATCTGTTTATTCTCATTTTGA 52018
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                                                                  sGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAl 562
                                                                                                                                                                                                                                                                                                                                                   oLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHi 634
                                                                                                                                                                                                                                                                                                                                                                                                                       eLeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAs 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yyetales; Micrococcineae; Micrococcaceae; Micrococcus.

des 1 to 4004)

T. and Horthoshi, K.

Heotide sequence of an alpha-amylase gene from an sygbrotrophic Micrococcus sp
crobiol. Lett. 71, 35-42 (1990)

Location/Qualifiers
                                                                                                                                                                                                           eLysGlyTyrGluProGln---AspGlyAlaTrpTyrAsnTyrHisThrTh
                                                                                                                                                                                                                                                                               ValLeuGluLysGlnAspProLysSerAspGluPheAlaValGluAs
                                                                                                                                                                                                                                                                                                                                                                     ccus sp.
ccus sp.
a, Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                       :AspAlaAsnPheThrMetArgMetSerTyr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [-----GGGAAATGG 51753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgLeuIleGlyLeuAlaPheAspGlyAsnTrp 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4004 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-amylase gene.
TyrAlaIleGlu----
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DVGTDEVVGELAGLPDFITEDPNVRKQIIDWQTDWIEKATTENGNTIDYFRVDTVKHV EDATWMQFKNALTEKMPEFKMICEAWGAKVDNTLGYLETGTMDSLLDFGFKETARSFV NGSLEAANASLTARNAKLDNTATLGQFLGSHDEGFLHSLAGDKGKLQVAATLQATAK GQPVITYGELGQTGANNYPQYGNRYDFAWDQVEGNEILAHYTKILNFREGYSKVFRK GQPVITYGGELGQTGANNYPQYDNRYDFAWDQVEGNEILAHYTKILNFREGYSKVFRK GERTLVGGSDKOQFLLFSRDYQDQVKYVGLNVARESKAVTLTVDSADAVYTDAYSGTF NYKNYGAMLWNDASPSANWPYGATWERTYDSYGATIDVLADGANIGELWDITA GDAGKDGGDKGFTISSPQANETWIGGSBVKYTYFEVUDLPANTYRIHYKRED GIWNWGDVASPSDGWPTGAVNFDGTDRYGAYPDIKLTEAAKEIGFLLVNEKTQEKDAG GIWNWGDVASPSDGWPTGAVNFDGTDRYGAYPDIKLTEAAKEIGFLLVNVEKTQEKDAG DKSFKLLDKFWHLMIKQGDDTVYVSPYDEVASGLGSAEVVSENTLLLRFNSTDGFTSE KLVAGLAIQDADSAAL"  1239 a 724 c 1028 g 1013 t	ores: 5.35 Length: 4004 133.50 Matches: 138 larity: 34.94% Conservative: 94 imilarity: 20.78% Mismatches: 259 Indels: 173 3.59% Indels: 35	•	GIYGINLƏNLYSGIYILƏTINASPGIUMƏTGIUARGLUŞSALAĞINGIUVALCYS 160 	GlnGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPhe 180 :::	TyrserasnasnGluTyrPheLeuIleValTyraspValPheLysaspValargMetVal 200     ::     ::    GTGGAAACATTAAGTACGATGTTCGTTATTAC 1541	PhealaProProSerSerValGlyLySPheGlyGlyAspThrAspAsnTrpMet 218	TrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsn 237	ArgProAlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaVal 257      ::      CGCAACATGAAAATTATGGTCGAT	SerMetGlnGlyTyrLysalaAspAspTyrAlaMetThr1leGly 272 :::	PheproglySerThraspargTyrLeuThrSer		AsnProArgIleGluValArgGlyIleLysGlnGlyIleTrpLysGluAlaMetSerAla 314	AspGlnAlaThrArgIleLySTyrAlaSerLySTyrAlaGlnSerAla 330 :::	ASNTYTTPLYSASNSETILEGlYMEtASNArgGlyLeualaArgLeuaspValileGly 350 :: :: :: :: :: ACGTGGATGCAGTTAAAAAATGCATTAAAAATGATCGGAATTTAAAATGATCGGT 2048	ArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAla 370
COUNT.	Alignment Scores: Pred. No.: Score: Bercent Similarity: Best Local Similarity Query Match:		431	161 GlnGl	181	201 Pheal 542 GAAAC	219	238 ArgPr      659 CGCAA	258 692	273 752	284	295 AsnPr      872 AACGT	315 AspGl ::: 929 GAAAA	331 AsnTy :: 989 ACGTG	351 ArgLy
BASE CC	Alignment S. Pred. No.: Score: Percent Sim Best Local Query Match DB:	-10	OY DP 14	Qy ]	Oy 3	Oy	Oy	Oy .	Oy .	Oy	Qy 10	Oy 11	Qy Dp 1	Oy Db 1	ογ

qa o	2049	CTGIVASDVAIJABSPTSPTIABGIUJASAJATYTIVSGIUGIVAJ
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Oy Db	496	LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515
Qy 4	in u	32
an i	, ע	AGACGCTGTT 26
Qy Db	533	GInAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLySGlyLysArgLeuPhePhe 551        :::  GTGACCGATGCCTATTCGGGTACGGAATATACAGCAACAGGAGGAAA 2696
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Qγ	581	
qq.	2805	GTATAAAAC 28
Qγ	591	hrThrGlyLysGlyValLeuGluLysGln !!!
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ΟŊ	611	ValGlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGlu 629
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Qy Dp	630	
· À	64	SerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGly 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="spr0487"
1942. .2196
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                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT 13-SEP-2001
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Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S.,
Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S.,
Beblefff,B.S., Estrem,S., Fritz,L., Fru,D.-J., Fuller,W., Geringer,C.,
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Noris,F.H., O'Gara,M., Peery,R., Robertson,G.T., Rockey,P.,
Sun,P.-M., Winkler,M.E., Yang,Y., Young-Bellido,M., Zhao,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                AE008428 10292 bp DNA linear BCT 13-SE. Streptococcus pneumoniae R6 section 44 of 184 of the complete
                                                 667 AsnTrpGluAlaMetSerGlyAsp-----IleGluPheGluPro---AspLeuGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Glass,J.I.
Genome of the bacterium Streptococcus pneumoniae strain R6
J. Bacteriol. 183 (19), 5709-5717 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae R6.
Streptococcus pneumoniae R6
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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5143 GATGTTTTCAAGCCTTCAGGCGATCAAAAGGCTAAGCCTTATTCAATCGTTATTCCACCA 5202
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                                                                                                                                                                                                                                                                                 204 ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5446 ACCATCAAGGAACAATGGGGCAAGATGGGGCTCTCTGTAGACTATTCTCGTGAGCGTTTC
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                                                                                                                                                                                          --- LysAspValArgMetValPheAlaPro
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CHSLRNYSQHTDLPINEVRAVSPDDETVIIDFYIDLDYLLNSNFKWKLKGELIKLNO
ESKIDALAVKEYFNALTELYGNYNKLFLKINHNTLVDIKSKLESLKLKHSRYYISK
ISKYDLKYNGNYTMSPLAAFAEIEEIYIELSKIGLVKIVNKSN"
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KQSRGELTYEQVYEDATAYHHTIDASTEEADLVSLRIVELLSRRGFSFSPATLLAIHK
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ALWPFSTMGWPEVDSEDFKRYFPTSTLVTGYDIIFFWVSRMIFQSLEFTGRQPFQNVL
IHGLIRDEQGRKMSKSLGNGIDPMDVIEKYGADALRWFLSNGSAPGQDVRFSYEKMDA
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TENFDKFEFGVAGHILYNFIWEEFANWYVELTKEVLYSDNEDDKVITRSVLLYTLDKI
LRLLHSIMPFVTEEIFGQYAEGSIVTAAYPTVNPAFEDLAAHTGVESLKDLIRAVRNA
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LDDIPKLVLIDNPLKHFEFKKNIIKNEIIEYRSVEDLY"
                                                                                                                                                                                                          /translation="MSDVKEEVSSLSEKQLRQIDVEYAELNDSDIIERLAYLEINNNE
KRIVISDIEPTKEIMSVSDQIFEIQKNFQKIKNMFELFISDVSDFLSIKNKLESKELE
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TRPETMFGDVALAVNPEDPRYKDLIGKNVILPIANKLIPIVGDEHADPEFGTGVVKIT
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KIEKRVHSVGHSERTGVVVEPRLSTQWFVKMDQLAKNAIANQDTEDKVEFYPPRFNDT
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VITGAEIFLPLVOLLNVEEELARLEKELAKWQKELDMYGKKLSNERFVANAKPEVVOK
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EIVKMLLASEGKRTGITIVEKPIVRTKFKRLQETGMEAENYFILHFDKEEKFQGGQLT
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ISRYDLGRESFLTKVWEWKDEYATTIKEQWGKMGLSVDYSRERFTLDEGLSKAVRKVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Conserved hypothetical protein"
/protein id="AAK99297]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Valy1-tRNA synthetase"
/protein_id="AAK99296.1"
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/db_xref="GI:15458065"
                                                                                                                                    /product="Hypothetical protein"
/protein_id="AAK99295.1"
/db_xref="GI:15458062"
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/transl_table=11
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/g774...85.4
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5068. .7719
/gene="vals"
                                                                                           /transl_table=11
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8827, .9630
/gene="spr0491"
1094. .5056
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/gene="spr0491"
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/qene="spr0493"
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/gene="spr0494"
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/gene="vals"
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TGTCTGCAGAAGAAGCTGCTAAGCAAATTCAAAATAAAATA 4980
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TTGTCA------AAAGCTGTTCG 4485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECCTTACGTGGTGGGGTATTACGCGTTATGACCTAGG 4629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGTCTGGGAATGGAAAGAC------GAATATGC 4581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGGCAAGATGGGGCTTTCTGTAGACTATTCTCGTGAGCG 4521
                                                                                                                                                                                                                                                                                                                                                                                                                            spLysValGluGlyGlnLeuLysGlyIleThrAspGluMet 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGluProPheTyrSerAsnAsnGluTyrPheLeuIleVa 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LysAspValArgMetValPheAl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHi 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTy 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrLysProValTyrPheAlaAlaValSerMetGlnGlyTy 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetThrIleGlyPheProGlySerThrAspArgTyrLeu-- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGl 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspArgIleGluAsnGluAsnAsnProArgIleGluValAr 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAl 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSe 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleArgLys-----AsnGlyLysSerAlaValTy 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ValLeuSerSerLeuGluLysAlaTyrLys----- 384
                                                                                                                                                             3 others
ganism="Streptococcus pneumoniae"
rotype="19F"
xref="taxon:1313"
e="654"
                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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IDIISABAGBLPFTPRWFPQLTDDAIRBALKAGVLQGYBVLVERSKGFVAQFEDTVYV
GENEVYPLVRTLEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAMTSWGGKISETVKEYFADLAVKAVLQVAEERNGKWYVDLDNIQIVKKHGGSLLDT
QLVYGIVVDKEVVHAAMPKRVVNAKIALLDAPLEVEKPEIDAEIRINDPTQMRAFLEE
EERILRGYVDKLKSLGVTVLFTTKGIDDIAQYYLAKAGILAVRRVKRSDIEKLVRATG
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ERNLDDALSVVSDVVEDPYILPAGGAAEIEAAKAVRAFAPKVGGREQYAVEAFARALE
VIPKALAENAGLDPIDILTELTHKHEQTDGWKYGLDVYQGKVVDMYSLGLVEPLTVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFKYLSLALLALGVLLSRRVLRNAEEKIRKFMANVEREAMARRYFATLKEYYNPIDYL
TKLYAEPTIEDPIIAAEKKKIRASTYLFSQSITAĻRAKNRLVITITALTISIPHLVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKPAFPVNVSVNEVAAHYTAKRGDSLKIPKTGLVKIDVGAQRDGYIVDAAVTVTLGPV
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                                              Fitz-Gibbon, S.T., Ladner, H., Kim, U.J., Stetter, K.O., Simon, M.I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSQAVLTQIGGVPVLVLKEGTQRAFGKEALRLNIMIARAIAEVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTTLGPKGMDKMLIDSLGDITITNDGATILDEMDYQHPIAKLLVEISKSQEEEAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MLAEYVAQRVALIQERAYHRLVVILSATSMSSVMMSGLALFFEP
                                                                                         Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PAE2117"
/note="Protein fate; Protein folding and stabilization"
                                                                                                                                                                         2 (bases 1 to 14169)
Fitz-Gibbon,S.T., Ladner,H., Kim,U.-J., Stetter,K.O., Simon,M.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Protein fate; Protein modification and repair"
                                                                                                                                                                                                                                       Direct Submission
Submitted (12-DEC-2001) Microbiology and Molecular Genetics
University of California, Los Angeles, 405 Hilgard Ave, Los
Angeles, CA 90095-1489, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="thermosome (chaperonin) alpha subunit"
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                                                                                                                                   Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002)
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                                                                                                                                                                                                                                                                                                                                                               /organism="pyrobaculum aerophilum"
/strain="IM2"
/db_xref="taxon:13773"
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/db_xref="GI:18160618"
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complement(2706. 3257)
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/gene="PAE2119"
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        Pyrobaculum.
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/transl_table=11
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1060, 2700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PAE2116"
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Pyrobaculum aerophilum strain IM2 section 113 of 201 of the
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4241 CTACAAGGACTTGATTGGTAAAAGGTCATCCTTCCA---ATCGCTAATAAACTCATCC 4185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3713 AATCCCTGCCTGGTACAAT----GCTGATGGTGAAATGTATGTCGGCGAAGAAGCTCC 3660
  CTGGGACCCAGCACCTCGCACACCCTTTCTGATATTGAGGTGATTCACAAGGATGTAGA 4365
                                                                                                                                                                                                                                                           ----GCGGTTGCGATTAATCCAGAA-------GACCCGCG 4242
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4364 AGGTGCCTTCTACCACATGAATTACATGCTGGAAGATGGTTCACGCGCCCTTGAAGTTGC 4305
                                                                                                                                                                                                                                                                                                        447
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                                              ------GluGlyAlaLysAlaAsnArgGluMe 393
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                                                                                                                                 tThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAl
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Pyrobaculum aerophilum
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
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AGAAGGTGACGGATGGACTCAGGACGAAGACGTCTTGGAT 3620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDAVLLPGSEVVRGTSSYLSOTFTYWALAKDRIGLVRVYPSEEGLKPMMRVEGKYTEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 AlaLys-----LysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GlyLeu
                                                        /note="Hypothetical; Conserved within genome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PAE2128"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Hypothetical; Conserved within genome"
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138
112
247
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36
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Conservative:
Mismatches:
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                                                                                                                                     /transl_table=11
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Best Local Similarity:
Query Match:
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(5m-like)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5207. .5641
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CDS

CDS

QQ	10374	AACGAGCCTCTAAAATGCC	10394
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qa	10455	TACGGCGACTACGAAATTCACGTGCCTGTTGAATCGTATACAAAAGCTTTGGAAGCCTTG	10514
Qγ	501	Æ	520
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Οÿ	601	LysGln	614
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qo	10761	CTTGAGGATGTGCTGAGGCGCCGCCCACAAAGGCTGAAAGGCTGATTGAA	10817
ΟŸ	635	IleThrGl	652
qq	10818	GTGTTGACGCCGGCGAGGAGGAGGGGACGATAGATTTACCGCTAGAAGTG	10868
Qγ	653	PheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSer	672
qq	10869	CGCGACGAAAGGGGCAACGTGGTAGCCCGCGTTGTGGACTTGAGGTATGAATTCGTAATG	10928
ογ	673	GlyAspIleGlu	919
qa	10929		10988
ΟY	677	PheGluProAspLeuGlnArgThrIleSerValAspIleArgTyrValLeuPheMetIle	969
Dp	10989	-	11039
QY	697	AspLys 698	
QQ	11040	   AAGAAA 11045	
RES LOC LOC DEF VER	RESULT 12 A81135 LOCUS DEFINITION VERSION SERVICES	~ 0, ~ ~	JAN-2000
Son	OURCE ORGANISM		
REE 1	REFERENCE AUTHORS TITLE JOURNAL	1 (bases 1 to 2652) Brown,J.R. and Wang,M. Valyl ERNA synthetase (EC 6.1.1.9) from Streptococcus pneumon patent: EP 0909818-A 121-APR-1999;	noniae
		SMITHALINE BEECHAM CORP (US)	

FEATURES Sou	ES ource	Loc 1.	ation/Qualifiers .2652 ganism="unidentified"				
BASE COUNT ORIGIN	73.	3 a 6	db_xrer="taxon:32644" 612 c 621 g 68	36 t			
Alignment Sepred. No.: Score: Percent Sim Best Local; Query Match	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match:	: Lty:	5.67 Length: 130.00 Matches: 32.81% Conservati 20.70% Mismatches 3.50% Indels: 6 Gaps:	n: es: rvative: cches:	2652 106 162 178 25		
US-10-008	-355-2 (1	-712)	) x A81135 (1-2652)				
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Oy 204 Db 136		rValG      TACAG	ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHi    ::	spAsnTrpM	etTrpProArgHisThr     - CACCTT	223 162	
Oy 224 Db 163		Serv	GlyaspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer       GGTCACGCT	laAspAsnA	rgProAlaGluTyrSer	243	
Oy 244 Db 172		LysP	LysAspasnLysProTyrLysProValTyrPhealaalaValSerMetGlnGlyTyrLys 	laalavals:	erMetGlnGlyTyrLys              GCATGCAAGGTTTTGAT	263 228	
Qy 264 Db 229		pTyrA	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr	LySerThra:     Garggacc.	SpArgTyrLeuThr ::: ACGCAGGGATTGCCACT	282	
Oy 283 Db 271		rva1G         GTAG	SerTrpGlyValGluAsparglleGluAsnGluAsnProArglleGluValArgGly	snAsnProA    CATTTCCC	rgileGluvalargGly 	302 330	
Oy 303 Db 331		TTGA	IlelysGlnGlyIleTrpLysGlualaMetSeralaAspGlnAlaThr 	<b>a</b> .	MetSerAlaAspGlnAlaThr :::        GAATATGCCACT	318 378	
Oy 319 Db 379		aTyra    GAAC	ArglleLysTyrAlaSerLysTyrAlaGInSerAlaAsnTyrTrpLysAsnSerIle 	erAlaAsnT    :::  TGTAGACT	yrTrpLysAsnSerIle     ::: ATTCTCGTGAGCGTTTC	337 .	
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Oy 397 Db 655	ACTCGT	rGluT        GAGA	SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAl          ACTCGTCCTGAGACCATGTTTGGGGACGTT	lvalArgP	heAlaGlnPheAlaAsn	414	
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|||||||
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                                                                                                                                                                                                                                                                                                                                                       SerIleLysGlyTyrGluProGlnAsp 585
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AspLysSerValValProTyrSerAsp 495
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                                                                                                                                                                                                                                    GlyLysArgLeuPhePheAlaGlyLeu 554
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GGAT 1335
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::: היידה את	י אל	35	476	Db 895 AACGA	Qy 496 LysPh	:::     Db   946 CGTTT	Qy 516 AspPr	Db 991 GGTGC	Qy 532	Db 1051 GTTGT		1111	555	1144	Oy 566 AspAL         1904 GACTE	286	1246	Qy 606 SerAs	11 Db 1300 GGTGA	RESULT 15 AE013500 LOCUS AEC	DEFINITION Met	ACCESSION AEC VERSION AEC KEYWORDS	Σ	ALC Met	AUTHORS Dep	Bru Bha	Gun TITLE The	JOURNAL J.			. JOURNAL Sub
						203 13E		223	102	171	263	228	282	270	302	330	318	378	33/	357	474	373 534	388	594	396	654	414		717	448	455
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	5.67	130.00	20.70% 3.50%	o 2) x E26074				GIYLYSPDEG          	ValobeardV	6	ProTyrLysP	::: ACTTTGCAAG	AlaMetThrI	ACCC	GluAspArgI	GAGGAGCGCT	IleLysGlnG	ACGAAAGTCT	AIASELL    CAATGGGGCA	GlyLeuAlaA       ::	.GGTTTGTCA-	TrplleargL :::  ::TTTACAAGA	ValL	cecacaecec	MetThrTyrL	ATGAATTACA	ThrLeuPheG     :::      ACCATGTTTG	AsnProAspA	AACCCAGAA-	GGTAAAAATG	
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Mismatches:
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                                                                                                             gene
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EIGDEEKASVYHRQALERFEQIIAEQSGNPEILILTSGKAFFSGMSLLEKLESENKDS
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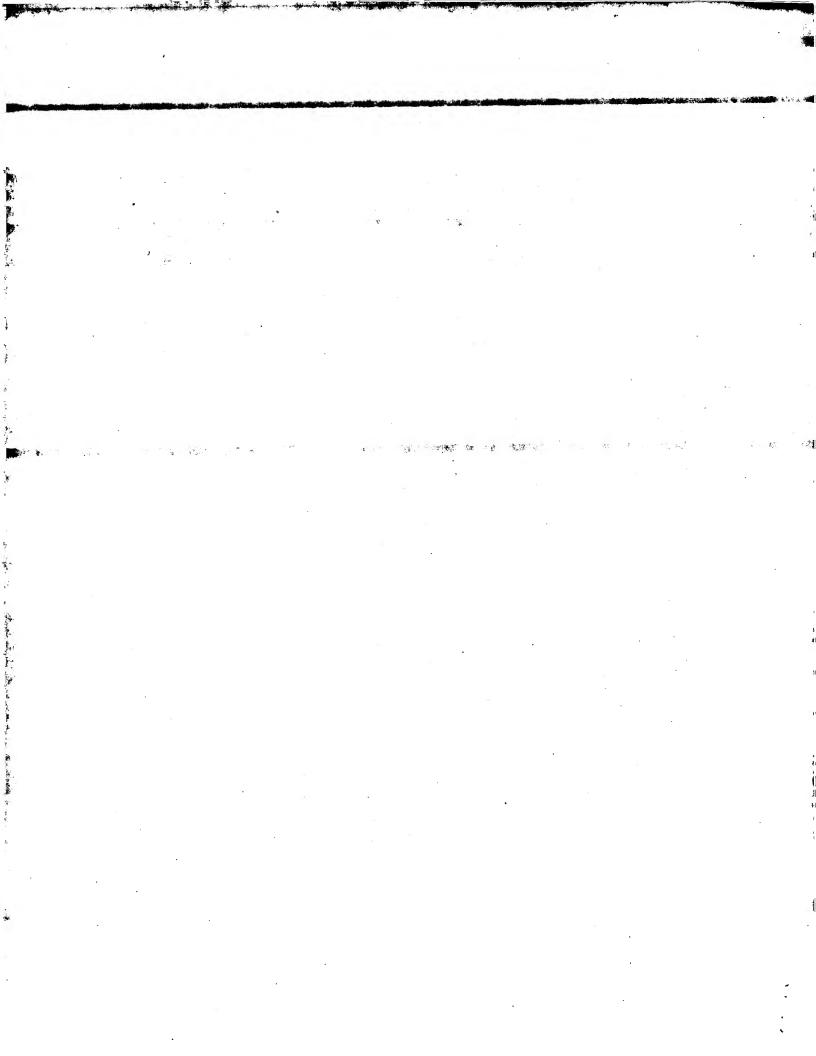
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                             FEATURES
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⋩	59	LysProSerIleAlaAsnAlaValValIlePheGlyGlyGlyCysThrGlyIleThrVal 78	
ð	3192		
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ą	3246	GCTTTTTCCGAAATCGTTGATGCAGCCAGCAATTGTAAGTTTAAAGACTGCACCCACC	
ž.	93	GlyAlaIleGInSerGlnSer 99	
ą	3306	GACCAGCCGGGCTGTGCCGTACTGAAAGCTGTTAAGGATGGGATTATTCCTGAGG	
⋩	100		
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λ	137	AspLysValGluGlyGlnLeu	
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q	3546		
χ	168	AsnAlaAspGl	
q	3582		
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λ	208		
q	3663	TCTATGTCAAGGAAGCTACAGGATTCT 3689	
χ	228	ValPheArgvalTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLys 247	
ą	3690		
λ	248	ProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyr 267	
ą	3735		
×,	268		
q	3753	::: III::: 	
<b>≿</b>	288	AsparglleGluAsnGluAsnAsnProArglleGluValArgGlylleLysGlnGly 306	
ð	3771		
<u>~</u>	307	IleTrpLysGluAlaMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyr 326	
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ą	3906		
λ	362	TrpIleArgLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLys 381	
ą	3948		

Oy Dp	382	AlaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPhe 4	401
0	0	1vGlvThrGluValValArcPheAlaGluPheAlaAsnAlaLeuAlaThrAsnProAsp	21
7 a		AAAAAACGGTTCTGGGTTTTGAAAGTTATTGGAGTCAGATCCCGAAAATCCGGAG	
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Db	4164	GTTCCACTTTTGATAAAAATTCGATCTC	4208
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٥y	459		459
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ΟŸ	460	AspLysLeuProAspIlePheLysAsnValIleAspLys	472
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ογ	492	sPheAla	510
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οy	511	val	519
og o	4506	ATT	4565
٥y	. 520	laMetAlaAsn	539
qa ,	4566	TTCCGAAAACATACAGTTCCCAAAAATATTCTTTTTTTTT	4625
Qγ	540	IleGluLysGly	. 949
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ó.	547		561
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Οy	635	Asp	554
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111 4992 AAAGAA 4997	ArgThrIle	4998 ATCGAAAATTTACGAAAATCTTCACCCAGCAGAAGCCGATAAACTCATGTTAGAAGCTAAT 5057	695 MetileAspLysTrpGlyGlnCysProArgLeulleGlnGlu 708	5058 AAAGCCGATACCTGGAACCAGATTGGAAGGCTGTATGCAGAA 5099	
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Search completed: May 23, 2003, 11:33:15 Job time: 4235.8 secs



GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

May 23, 2003, 07:32:23 ; Search time 316.182 Seconds Run on:

nucleic search, using frame\_plus\_p2n model

OM protein

(without alignments) 5071.208 Million cell updates/sec

US-10-008-355-2 3719 1 MQMKLKSILLGAALLLGASG......LFMIDKWGQCPRLIQELKLI 712 Title: Perfect score: Sequence:

Xgapext **BLOSUM62** Scoring table:

0.5 7.0 7.0 Ygapext Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0,

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2185239 seqs, 1125999159 residues Searched:

4370478 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

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	7	46.	w.	4104		ABN68149	ທ
	<b>~</b> ) <			2823		AAX91/54	Porphorymonas ging
	4 ռ		9 6	2652	2 6	AAS55647	Streptococcus preu
	9	130		2652		702	
	7	3		2652		81	. pneumoniae val
	ω	m		2652		136	0)
	σ	3		2652		ABK52414	Stre
O	10	2		6004		AAV52160	
	11	12		2652		AAS55949	
	12	26.		4110		- (	treptococcus p
	13	23.		2142		₼	rhalis st
	14	22.		4716			innocua
	15	22.		•		ABQ67873	innocua
	91,	22.		495269		ABQ67195	O
	17		m (	2649	24	ABN66404	4
	18	21.		2155561		ABN71527	S.
	13	12		2646		ABN66405	Q.
	20	91.		•	22	AA164839	
	21	117.5		1664976		AAV21209	Methanococcus jann
O	22	I,		w	٦,	90	nilus infl
	5.73	16.		15424		AAC81763	Lelystad
	24	٠,		15424		AAC81764	Porcine Lelystad v
	52	Ξ,	۳. ۲.	3598		AAC77776	ര
	26	115.5	3.1	6822		ABN71008	
	27	15	3.1	6834		ABN68971	Streptococcus poly
	28	Ξ;		4853		13	Alpha-D-glucosyltr
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	30	112		2175		AAS81718	encoding
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ပ	42	$\vdash$		4411529		966	
	43	110.5	3.0	3279		AAQ51556	Sequence encoding
	44	0	•	12665	1	22	Streptococcus pneu
	45	10.		15450	7	AAA27809	North American por

ALIGNMENTS

AAL43635 standard; DNA; 2139 AAL43635;

RESULT 1 AAL43635 BP

(first entry) 05-SEP-2002

Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence.

Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis.

Porphyromonas gingivalis.

Location/Qualifiers 1..2139

Key

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CGCGGTCTCGCTCGTCTTGACGTGATAGGTCGTAAGCGTGCCGAGGAAAGAGAGATTCGCA 1080
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            PheAlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpPro
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                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyleptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                  periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present DNA sequence encodes the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.
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            DPP-7"
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1441 TATGCAGACTTCGTATTCGACAAGAGTGTGGTTCTTATAGCGACAAGTTCCATGCCATG 1500
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                                                                                       CTTTCCAAGAGCGTAATAGCTGCTCGCTCGCTCGTTTCAGGCCGATGCGATGCCCAATGCC
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                        LeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGlu
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2001GB-0005640.
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07-MAR-2001;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to cilogical sample. (I) is used to detect Streptococcus in a compound binds to cilogical sample. (I) is used to detect streptococcus in a compound binds to composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be caid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity of promatography, immunoassays, and distinguishing/identifying
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2095 gatgatagtttgacatttaaagaagacattcaaaagcacaagtgtctggacaaggcgat 2154
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                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infe or disease caused by Streptococcus bacteria, such as meningitis, for detecting a compound that binds to the protein -
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   Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Margarit Ros YI,
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                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 3578; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 1458 A; 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00104
146.50
31.98%
20.00%
3.94%
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ò	131	LysIleValLysValThrAspLysValGluGlyGln	142
qa	2215	CAGACTGTAAAAGTTGTTGATGAATTGGTCAAAGTAATGGGGCGCGTAAAGCCAGAAAAT	2274
Οÿ	143		150
QQ	2275	ATCGTTATTGAAATGGCACGTGAAAATCACACAACTCCAAAAAGGGCCAGAAAAATTCGCGA	2334
δ		GluArgLeuArgLysAlaGlnGluValCysGlnGluLeuAlaLysLysGlu        :::::::: :::	167
g G	2335 (	GAGCGTATGAAACGAATCGAAGAAGGTATCAAAGAATTAGGAAGTCAGATTCTTAAAGAG	2394
0,	168	AsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyrSerAsnAsnGluTyr	186
Q D	2395 (		2430
ò	187	PheLeulleValTyr	201
qq	2431 (	CTCTATCTCTATTATCTCCCAAAATGGAAGACATGTATGT	2490
οy	202	AlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArg	221
q	2490		2490
ó	222	HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGlu	241
QQ	2491	AATCGTTAAGTGAT	2505
٥y	242	TyrSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGly	261
qq	2506	TATGATGTCGATCACATTGTTCCACAAAGT	2535
οy	262	TyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu :::	281
qq	2536	TTCCTTAAAGACGATTCAATAGACAATAAGGTC	2568
οy		ThrSerTrpGlyValGluAspArglleGluAsnGluAsnAsnProArglleGluValArg	301
Q	2569	TTAACGCGTTCTGATAAAAATCGTGGTAAATCGGATAACGTTCCAAGTGAAGAAGTAGTC	2628
ó	302 (	GlylleLysGlnGlylleTrpLysGluAlaMetSerAlaAspGlnAlaThrArglleLys	321
Q	2629	AAAAAGATGAAAAACTATTGGAGACAACTTCTAAACGCCAAGTTAATCACTCAACGTAAG	2688
ò	322	TyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArg	341
Op	2689	TTTGATAATTTAACGAAGCTGAACGTGGA	2718
ò	342 (	GlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArgAla	358
Dp	2719 (	GGTTTGAGTGAACTTGATAAAGCTGGTTTTATCAAACGCCAATTGGTTGAACTCGCCAA	2778
٥y	359 1	PheAlaAspTrpIlePheAlaAspTrpIle	368
qq	2779	ATCACTAAGCATGTGGCACAAATTTTGGATAGTCGCATGAATACTAAATACGATGAAAAT	2838
ογ	368		368
QQ	2839 (	GATAAACTTATTCGAGAGGTTAAAGTGATTACCTTAAAATCTAAATTAGTTTCTGACTTC	2898
οy	368		368
Dp	2899 (	CGAAAAGATTTCCAATTCTATAAAGTACGTGAGATTAACAATTACCATGATGCCATGAT	2958
ογ	368		368
QQ	2959 (	GCGTATCTAAATGCCGTCGTTGGAACTGCTTTGATTAAGAAATATCCAAAACTTGAATCG	3018
ò	369	SerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyr	383
qa	3019 (		3078
δ	384	LysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGly	402 ·

qq	3079	CAAGAAATAGGCAAAGGAACGCAAAATATTCTTTTACTCTAATATCATGAACTTCTTC 3138
Qy	403	aThrAsn
QQ	3139	
Qy	421	PAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLe 441
Dp	3198	GGAGAAATTGTCTGGGATAAAGGGCGAGATTT
οy	441	uAspArgLysValLeuProAlaMetLeuAspIleValArgArgArg 456
QQ	3246	Ħ
Οý	457	
Dp	3306	AGGCGGATTCTCCAAGGAGTCAATTTACCAAAAAGAAATTCGGACAAGCTT 3357
Οy	465	ePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPheVa 485
qq	3358	
Qy	485	AspLysSerValValProTyrSerAspLysPh
Op	3400	rccaacgeragcrrar
Qy	200	MetLeuLysSer
Dp	3459	GTTAAAGAGTTACTAGGGATCACAAT'
Οy	508	leGluLysA
QQ	3519	TITI CTTTGAAAAAAATCCGATTGACTTTTAGAAGCTAAAGGATATAAGGAAGTTAAAAAAGA 3578
δ	516	
Dp	3579	ŢŢ
Oy	536	aMetalaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGl 556
Db	3601	AGTTAGAAAACGTCGTAAACGGATGCTGGCTAGTGCCGGAG
Qy	556	uMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMe 573
Db	3657	AGCTGGCTCTGCCAAGCAAATATGTGAAT
ογ	573	
Dp	3717	GTCATTATGAAAAGTTGAAGGGTAGTCCAGAAGATAACGAACAAAAACAATTGT
ολ	588	TyrAsnTyrHisThrThrGlyLysGlyValLeuGlu
qq	3774	- AAGCATTATTTAGATGAGATTATTGAGCAAATCA
Qy	809	uPheAlaValGin612
Op	3825	IIII::: ::: ATTTTCTAAGCGTGTTATTTTAGCAGATGCCAATTTAGATAAAGTTCTTAGTGCATATAA 3884
οy	613	leLeuAspLeuPh
Dp	3885	CAAACATAGAGACAAACCAATACGTGAACAAGCAGAAAATATTATTTAT
Qy	621	rLysAsnTyrGlyAr 626
QQ	3945	CCCGCTGCTTTTAAATATTTTGATACAACAATTGATCGTAAAC
م م	626	gTyralaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsnAsnAsplleThrGly 645
RESULT AAX9175	LT 3 1754	

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260 nGlyTyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTy
                   825 CACGIACGGAGGACAAT
                                                                             oArglleGluValArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34388 to AAX94883 AAX91802 to AAX91989 represent PCR primers used in the 1solation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArg-ProAl 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCTATTT--------CCCTTTTCCAACAAATACTCTTCCGGTATATTGATGCC 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 aGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGl
                                                                           gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                   Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                          Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2853 BP; 736 A; 685 C; 691 G; 741 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2853
105
66
202
124
23
                                                          Porphorymonas gingivalis protein PG67 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                  Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 244-245; 588pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-008-355-2 (1-712) x AAX91754 (1-2853)
                                                                                                                                                                                                                                                                                                                 Hocking DM,
Webb EA;
 BP
AAX91754 standard; DNA; 2853
                                                                                                                                                                                             97AU-0000839.
97AU-0001182.
98AU-0001546.
                                                                                                                                                                                                                                            98AU-0003128.
98AU-0003338.
98AU-0003654.
                                                                                                                                                                                                                          98AU-0002264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.00909
134.50
34.41%
21.13%
3.62%
                                                                                                                                                                  98WO-AU01023
                                                                                                                                                                                    98AU-0005028
                                                                                                                                                                                                                                     98AU-0002911
                                                                                                                                                                                                                                                                          98AU-0004917
                                      (first entry)
                                                                                                         Porphorymonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gingivitis.
                                                                                                                                                                                                                                                                                                                 Barr IG,
Rothel LJ,
                                                                                     antigenic;
                                                                                                                                                                                                                                                                                                                                             WPI; 1999-385613/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY34536
                                                                                                                                                                                                                                                                                             (CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                            Porphorymonas
                                                                                                                          WO9929870-A1.
                                                                                                                                                                                                                         10-MAR-1998;
09-APR-1998;
23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                      25-AUG-1999
                                                                                                                                                                 10-DEC-1998;
                                                                                                                                                                                                                                                                          29-JUL-1998;
                                                                                                                                             17-JUN-1999
                                                                                                                                                                                             10-DEC-1997
31-DEC-1997
                                                                                                                                                                                                                                                       05-MAY-1998;
                                                                                                                                                                                                                  30-JAN-1998
                                                                                                                                                                                                                                                                 22-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                     gingivitis
                                                                                                                                                                                                                                                                                                                 Agius CT,
                 AAX91754
                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                            Ross BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- TTATCTACCACATTGTAGGGTATGTTCAAGCC 1724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACAGCAAGACCACCAGTCTGAATATCCGATGGACACACAGTCAGGATCCGAAGGCCAA 1106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValValArgPheAl 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTy 581
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                                                                           -ValGluAspArgIleGluAsnGluAsnAsnPr
                                                                                                                                                                                                                                                                                                                                   ----TTGGCATTGCGTGGGGAATCTTTTCCAAAGGGTCATGGGGCATTTCAGCCCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                  314 aAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATATAAGAAGAGTATAAGTACAACGGCTCGTTC-----GAAGCCAATTAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---CTGGTATCGAAGTCCGGCGACAAATACGTGCCCGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1212 AAGTTCGGCCGTGAGCTATTCGCGCAAGTTTCCGGGTACTCCTTTTTCGATTACGGGTAG
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                                                                                                                                                                                                                                                   ----IleLysGlnGlyIleTrpLysGluAlaMetSerAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 sAsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 aGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCT-------TTGCAAACGTTGTCGGCCAATGTCAATTTTGCCACCGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuProAl
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                                                                                                                                                          TTTGAGGAATGGTGGATATTTTTGCCTTCAGCGACTATATCGAT----
-CGCTATGGATTT-
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                                                                           rLeuThrSerTrpGly----
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Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                            ------TITICCTICGGAGGCAATCICATIATGATCCGICATCG 1772
                                                                                                                                                                                                                                                                     1833 TIGGGAGCTICTIGAGCATACGGATCAGAACGCCAAGCTGCATACGCTGCTCTACTCTCC 1892
                                                                                                                                             1773 CTTCACGCCCACTGTCAGTTTCTCCTATATGCCGGACTTCACGAAACGCCGATATGGCTT 1832
                                                                                                                                                                                                            640
                                                                                                                                                                                                         626 gTyrAla------GluAsnGlyGlnLeuHisIleAlaPheLeuSerAs
                                                                                        ----PheArgThrLysAsnTyrGlyAr
                                                                                                                                                                                                                                                                                                                                 640 n-----AsnAspIleThrGly------GlyAsnSerGlySerProValPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                    1893 TTATTTCGAGCAGATATTCGGTGCTCCCTCCATGGGCAATGCAGGATCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 pLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis protein PG67 ORF encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 153-154; 588pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hocking DM,
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX91621 standard; DNA; 2859 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97AU-0001182.
98AU-0001546.
98AU-0002264.
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98AU-0003338.
98AU-0003654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-385613/32
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 692 G; 742 T; 0 other;
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                                                                      Matches:
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Sequence 2859 BP; 738 A; 687
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                                                              1515 CGTACCGATCAGTTTGACTGTCCCTTTGTTGGATTATCAATCTGACTATGGGGGGTTAA 1574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae DNA for cellular proliferation protein #218
                     1455 AGAGAAAGATTTGCTCCAGAGCAATCTCGTGCGCGATTGGAAGAATGGTATGCGTCATTC
                                                                                                                                                                         rGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLySGlyValLeuGluLy
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tAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLysSe
                                                                                                                                                                                                                                                              ------PheArgThrLysAsnTyrGlyAr
                                          rValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGl
                                                                                    544 uLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyr-----ProGlyAr
                                                                                                                              gAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTy
                                                                                                                                                                                                                   601 sGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu-----
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                                                                                                                                                   1635 ATTCCTGCCTTCGGACACGACCTATAAATTCCGCAGACTGTAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL, Zyskind JW,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS55647 standard; DNA; 2652 BP.
                                                                                                                                                                                                                                                              200005-206848P-
200005-207727P-
200005-242578P-
200005-253625P-
200105-269308P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                          626 gTyrAla----
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Yamamoto RT,
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27-NOV-2000;
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26-MAY-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential cannot be themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus facefalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WipO at the printed probablished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 736 A; 609 C; 618 G; 689 T; 0 other;
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Mismatches:
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                                                                                           Claim 27; Seq ID No 9284; 511pp; English.
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338 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg 357 :::::                 :::   359 ACTCTTGACGAAGGTTTGTCA	Leul Leul HII: AACTG	895 AACGACGAACTATGAACGACTTGTTTTTCAGGCATG	315   AspalametalaasnalaTyralaIleGluLysGlyLysargLeuPhePheAlaGlyLeu   554
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Db     895       Qy     496       Db     946       Qy     516       Db     991       Qy     532       Qy     532       Db     1051	Qy     535       Db     1111       Qy     555       Db     1144       Qy     586       Qy     586       Qy     606       Qy     606       Db     1300

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283 SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 TGGGATACA---ACTTTGCAAGATATTATCATCCGTCAAAAACGCATGCAAGGTTTTGAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeu---Thr 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes the isolation of a novel Streptococcus pneumoniae vals protein. The new polypeptide and antagonist are useful for the treatment of an individual with abnormal vals protein levels, by administering vals to individuals requiring vals polypeptide, and administering the antagonist to individuals requiring inhibition of vals polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vals polypeptide and polynucleotide - useful for treatment of conditions associated with abnormal vals protein levels
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Matches:
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                                                                                                                          S. pneumoniae vals coding region DNA.
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  BP
                                                                                                                                                                      SS.
                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
AAX57027 standard; DNA; 2652
                                                                                                                                                                   vals; treatment; antagonist;
                                                                                                                                                                                                                                                                                                                                   97JP-0321886.
                                                                                                                                                                                                                                                                                                                                                                            97JP-0321886.
                                                                               (first entry)
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P-PSDB; AAY08339.
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Local Similarity:
Match:
                                                                                                                                                                                                            Streptococcus
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                                                                               19-JUL-1999
                                                                                                                                                                                                                                                                                          27-APR-1999
                                        AAX57027;
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9 RESULT

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318 378	337 .	357	373 534	388 594	396 654	414 684	434	448	455 834	475 894	495 945	515 990	531 1050	534	554	565 1203	585
303IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr	319 ArgileLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerile 3 	338 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAlaGluGluArg 3 :::::         :::	358 AlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGly 3	374 Asp	389 AlaAsnArgGluMetThrTyrLeu	397SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 4	415 AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 4	435 LysAspTyrLeuProSerLeuAspArgLysValLeuProAla 4	449 MetLeuaspIlevalargarg 4 ::	456 ArgileProAlaAspLysLeuProAspIlePheLysAsnValileAspLysLysPheLys 4	476 GlyaspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 4	496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys : ::	516 AsproalavalGluLeuSerLysServallleAlaAlaAlaArgAla	532Ileginala : :: 1051 GITGIGGITGAACCTCGCITGICTAATGGITCGTCAAGATGGACAATTGGCTAAG		555 ArgGluMetTyrProGlyArgAlaLeuProSer	566 AspalaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp
Qy Dp	Qy	δ. qa	Qy	Qy	Qy Db	Qy	Qy Db	Qy	Qy Dp	Oy Dp	Qy	Qy	Qy Dp	Qy Dp	Qy Db	Qy	Qy Dp

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This DNA encodes a S. pneumoniae valS polypeptide (EC 6.1.1.9), a member of the valy1 tRNA synthetase family. The polypeptide can be expressed recombinantly by transforming host cells with vectors comprising the valS gene. ValS polypeptides and polynotelectides are useful for diagnosing diseases due to an infection of an organism and also the stage and type of the infection. The polypeptides are also used for screening for their modulators which can be used in the treatment of diseases. Diseases diagnosed, prevented or treated include otitis media, conjunctivitis, pneumonia, bacteremia, sinusitis, pleural empyema, endocarditis and especially meningitis. ValS polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
                 Valyl tRNA synthetase; valS; otitis media; conjunctivitis; pneumonia; bacteremia; sinusitis; pleural empyema; endocarditis; meningitis; bacterial adhesion; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LysAspValArgMetValPheAlaPro 203
586 GlyAlaTrpTyrAsnTyrHisThrThrGlyLySGlyValLeuGluLysGlnAspProLys 605
                                                                                                                                                                                                                                                                      S. pneumoniae valyl tRNA synthetase (ValS) polypeptide encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus pneumoniae valyl tRNA synthetase (vals) gene and protein, useful for screening for antibacterial compounds, for prevention and treatment of Streptococci infections e.g. meningitis and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2652 BP; 733 A; 612 C; 621.G; 686 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                 1300 GGTGACGGATGGACTCAGGACGACGACGTCTTGGAT 1335
                                                               606 SerAspGluPheAlaValGlnGluAsnIleLeuAsp 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 6-9; 35pp; English.
                                                                                                                                                                    AAX32814 standard; DNA; 2652 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                    25-JUN-1999 (first entry)
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32.818
20.708
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                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-231674/20.
P-PSDB; AAY06828.
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Best Local Similarity:
Query Match:
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16	GATGTTTTCAAGCCTTCAGGCGATCAAAAGGCTAAGCCTTATTCAATCGTTATTCCACCA 135		
204	ProSerServalGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr 223      ::	δλ	51( 99)
224	GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer 24	Qy	532
163 244	. GGTCACGCT 171 LysAspAsnLysProTyrLysPheAlaAlaValSerMetGlnGlyTyrLys 263	Qy	53:
172	TGGGATACAACTTTGCAAGATATTATCATCCGTCAAAAACGCATGCAAGGTT	ò	555
264	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr 282     :::     ACCCTTGGGTTCCTGGGATGGACCACGCAGGGATTGCCACT 270	r da	114
283	SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly	8	1207
271	CAGGCTAAGG	3 8	1207
303		d d	1246
319	ArgileLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIle 337	Qy	1300
338	GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg	RESU AAA1	1LT 8
439	:::::       ::: ACTCTTGACGAAGGTTTGTCAAAAGTGTTTCGTAAG 474	O X X	AAA
358	AlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGly 373	X P X X	AAA 15-
374	AspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAlaLys 388	DE DNA XX XX (YA 1) KW (Aruc	Val dru
389		X X X X X X X X X X X X X X X X X X X	anț Str
397	SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn       :::       ACTCGTCCTGAGACCATGTTTGGGGACGTT	FT FT	Key CDS
415 685	AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434     :::           ::  GGGTTGCGGTCAACCCAGAAGACCGGGGTAC 717	FX PN XX	086
435	Lysasp	PD XX PF XX	18-7
449		PR PR XX	18-7 17-0 18-7
456 835	ArgileProAlaAspLysLeuProAspilePheLysAsnValileAspLysLysPheLys 475	PA XX PI	(SM) Brov
476 895	GlyaspThrLysLysTyralaaspPheValPheAspLysSerValValProTyrSerAsp 495	DR DR XX	WPI; P-PS
496	LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys 515 :::	Td TX	comp

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/*tag= a
/product= "Streptococcus pneumoniae valyl tRNA synthetase
(vals)"
                                                                                                                                                                                                                                                                    91 GGTGCCCTCGTCAAAATCGAAAAACGTGTCCACAGTTGGTCACAGGTACAGGT 1050
                                                                                                                                                                                       51 GTTGTGGTTGAACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AAGGCAGTCGTTGCTAAGTTGGAAGAATC 990
                                            16 AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla------ 531
                                                                                                                                          32 ------IleGlnAla 534
                                                                                                                                                                                                                                        35 AspalaMetalaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeu 554
                                                                                                                                                                                                                                                                                                                                  55 ArgGluMetTyrProGlyArgAlaLeuProSer------565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A encoding Streptococcus pneumoniae valyl tRNA synthetase (valS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vel valS polypeptides of valyl tRNA synthetase family useful for sating otitis media, conjunctivitis, pneumonia and bacteremia nprises a specified amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyl tRNA synthetase; valS; inhibitor; stringent response;
ug screening; antibacterial; antibiotic; genetic immunisation;
tibody; bacterial infection; meningitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06 SerAspGluPheAlaValGlnGluAsnIleLeuAsp 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       own JR, Lawlor EJ, Wang M, Jaworski DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reptococcus pneumoniae strain 0100993.
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1..1652
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97US-0844064.
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  16 CGTTTTGAAGCTCGT----
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PSDB; AAY90514.
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-OCT-1997;
-APR-1997;
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This sequence represents DNA encoding Streptococcus pneumoniae valy1 tRNA synthetase (vals, NCIMB Deposit No. 40794). Streptococci are the cause of swrand diseases, including otitis media, conjunctivitis, pneumonia, bacteraemia, sinusitis, pleural empyema, endocarditis and especially meningitis. The frequency of S. pneumoniae infections has risen dramatically over the past 20 years, probably due to the emergence of multiply antibiotic resistant strains and an increasing population of immunocompromised people. ValS represents a target for new antibacterial capents. Inhibition of tRNA synthetases such as vals leads to a reduction in the levels of charged tRNA, which triggers a cascade of responses (known as the stringent response) resulting in a state or dormancy in the bacteriam vals, its variants and fragments, anti-vals antibadies, vals inhibitors and nucleotides encoding vals mationed as meningitis.

Companded to the compounds for inhibitory activity. Vals may also be useful as an antigen for vaccination of a host to produce specific antibodies which protect against bacterial invasion into damaged tissues. Such antibodies could, for example, prevent the adherence of bacteria to wounds. Nucleotides encoding vals may be used as capents, particularly for genetic immunisation.
Claim 13; Columns 7-10; 21pp; English.
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other;	2652 106 62 166 178 25
21 G; 686 T; 0	Length: Matches: Conservative: Mismatches: Indels: Gaps:
733 A; 612 C; 62	0.0223 30.00 32.81% 20.70% 3.50%
AA Sequence 2652 BP; 733 A; 612 C; 621 G; 686 T; 0 other;	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:

	203	223 162	243	263	282 270	302	318 378	337	357
	Pheala      TATTCC	OArgHisThr     CACCTT	oAlaGluTyrSer ::::::	AGLYTY     :: AGGTTT	rLeu ::: 3ATTGC	JValAr :::: CCTTGG	oglnála : II ATATGC	sAsnSe: : rGAGCG	aGluGl:      GTTCG
2652 106 62 166 178 25	AspvalPhe	ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr     ::  CGAAACGTTACAGGTAAACTTCACCTT	GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer      GGT	LysaspasnLysProTyrLysProValTyrPhealaalaValSerMetGlnGlyTyrLys 	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr 	SerTrpGlyValGluAspArgIleGluAsnGluAsnAspArgIleGluValArgGly	IlélysGlnGlylleTrpLysGlualaMetSerAlaAspGlnAlaThr GAGTCTTTCTTGACGAAAGTCTGGGAATGGAAAGACGAATATGCCACT	ArglleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIle          :::    :::  ACTATCAAGGAACAATGGGGGAAGATGGGGGTCTCTGTAGACTATTCTGTGAGGGTTTC	GlyMetasnargGlyLeualaargLeuaspValIleGlyArgLysargalaGluGluarg :::::          :: aCTCTTGACGAAGGTTTGTCAAAAGCTGTTCGTAAG
:: .: .: .:	spvalAr TTATTC	snTrpMe	spAsnAr	lavalse AAAAACG	erThras FGGACCA	snProAr       TTCCC	LaMetSe	laAsnTy :::   rAGACT <i>P</i>	LyArgLy
Length: Matches: Conservative Mismatches: Indels: Gaps:	Lysas     CTAAGCC	hraspas	lyalaAs	heAlaA] rccGrc	roglyse        CTGGGA	luAsnAs     AGGGCA7	ysGluA]   :::  AGAC	InserA     rcrcrg	alileG]
Len Matr Con Miss Inda Gap		lyAspT]	yrAlaG	alTyrP :: TTATCA	lyPheP   GGCTTC	luAsnG   GTGGTG	leTrpL	yrAlaG TGGGGC	euAspV
0.0223 130.00 32.818 20.708 3.508 x AAA14369	GCGATC	heGlyG TT	rgvalT	ysProv :: AAGATA	hrileG   :::  CCCTTT	rgileG   :::  GCTTGC	lnGlyI	erLysT      GCAAGA	laArgL :: CA
	CTTCAG	ProSerSerValGlyLysPheGl     :::  CAAACGTTACAGGTAAACTT	/alPheA	roTyri : ACTTTGC	laMetT	llaspa   :::  saggago	iléLysG        CGAAAG	AlaS	SlyLeuA       :  GTTTGT
:: .ty: .arity: (1-712)	Phe      TCAAGO	Servald      STTACAG	GlyAspPheServalPh      GT	AsnLysi ACA <i>p</i>	AspTyr#	Slyvald 	rrcrrg	Lystyr#      AAGGAAC	AsnArg( ::: GACGAA(
ores lari imil	AspvalPhe-            GATGTTTTCA	ProSer:    :::  CCAAAC	GlyAspi       GGT	Lysasp     TGGGAT	AlaAsp	SerTrp( CAGGÇT)	GAGTCT	Argile         ACTATC	338 GlyMetAsnArgGlyLeuAlaArgL  :::::       ::: 439 ACTCTTGACGAAGGTTTGTCA
Alignment Scoree Pred. No.: Score: Percent Similar. Best Local Simi. Query Match: DB: US-10-008-355-2	192	204	224	244	264	283	303	319	338
Alignn Pred. Score: Percer Best I Query DB:	Qy Db	Oy Dp	Qy Dp	Qy	Qy Dp	Qy	Qy Dp	Qy	QY

358 AlaPheAlaAspTrpIleArgLys------AsnGlyLysSerAlaValTyrGly 373

δ

qa	::: 475 GTCTTTGTGGACCTTTACAAGAAAGGCTGGATCTACCGTGGTGGAGTTTATCATCAACTGG 534	
Qy	374 AspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAlaLys 388	
Qy	389 AlaAsnArgGluMetThrTyrLeu 11	
Qy	397SerGluThrLeuPheGlyGlyThrGluValValArgPheÄlaGlnPheAlaAsn 41        ::        655 ACTCGTCCTGAGACCATGTTTGGGGACGTT	
ΟY	laLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysT   :::          :::	
QQ	685 G	
Qy	435 LysaspTyrLeuProSerLeuAspargLysValLeuProAla 448	
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r S	4/6 GIYASPITNTLYSLYSTYTALAASPENGVALPNEASDLYSSSTVALVALPIOTYTSSETASP 495	
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δλ	516 AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla 531	
qq	991 GGTGCCCTCGTCAAAATCGAAAAAGGTGTCCACAGTGTTGGTCACTCAGAGCGTACAGGT 105	0
Qγ	532IleGlnAla 534	
QQ	1051 GTTGTGGTTGAACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 111	0
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QQ	1111 AACGCCATTGCCAACCAAGACACAGGGCAAG	m
oy :	555 ArgGluMetTyrProGlyArgAlaLeuProSer565	
qq	1144 GTCGAATTCTACCCACCTCGTTTCAACGATACCTTCCTTC	m
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2 (	ביין מעניין	
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qq	1300 GGTGACGGATGGACTCAG	
RESI ABK! ID XX AC	RESULT 9 ABK52414 XX ABK52414 standard; DNA; 2652 BP. XX AC ABK52414;	
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271 CAGGCTAAGGTAGAGGAGCGCTTGCGTGAGGGCATTTCCCGCTATGACCTTGGTCGT 330
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                                                                                                                                                                                                                                                                                                        The invention describes an isolated valS polynucleotide encoding a mature polypeptide the same as that expressed by a valS gene contained in a deposited strain of Streptococcus pneumoniae, a complementary sequence or a polynucleotide containing at least 15 continuous bases of the polynucleotide. The antibody to the encoded protein is used for the treatment of microbial infection. This sequence encodes valS derived from
                                                                                                                                                                                                                                                         for producing a valS polypeptide, used disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGATACA---ACTTTGCAAGATATTATCATCCGTCAAAAACGCATGCAAGGTTTTGAT
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Conservative:
Mismatches:
                                     ValS; microbial infection; antibacterial; gene;
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                                                                            Location/Qualifiers
1..2651
/*tag= a
/product= "ValS"
                                                                                                                                                                                                                                                        vel valS polynucleotide useful the treatment of valS-related
                                                                                                                                                                                                                                                                                      Claim 4; Fig 1-3; 24pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2652 BP; 733 A; 612 C;
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P-PSDB; AAU97883.
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Best Local Similarity:
Query Match:
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                  DNA encoding
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14-AUG-2002
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                                                                                                                                                                                                                                 379 ACTATCAAGGAACAATGGGGCAAGATGGGGCTCTCTGTAGACTATTCTCGTGAGCGTTTC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaPheAlaAspTrpIleArgLys-----AsnGlyLysSerAlaValTyrGly 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SerGluThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       835 CACGATCCAAATGACTTCTTGGTTGGCCAACGTCATAACTTGCCACAAGTCAAGGTCATG 894
                                                                                                                                                     ArgileLysTyrAla --- SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIle 337
--IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr
                                                                        331 GAGTCTTTCTTGACGAAAGTCTGGGAATGGAAAGAC------GAATATGCCACT
                                                                                                                                                                                                                                                                                                          GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTTGTGGACCTTTACAAGAAAGGCTGGATCTACCGTGGTGAGTTTATCATCAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTTCTACCACATGAATTACATGCTGGAAGATGGTTCACGCGTCCTTGAAGTTGCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 ArgileProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            895 AACGACGACCGAACCATGAATGACTTGGCCTTTGAATTTTCAGGCATG-----GAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     946 CGTPTTGAAGCTCGT------AAGGCAGTCGTTGCTAAGTTGGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IleGlnAla
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SerAspGluPheAlaValGlnGluAsnIleLeuAsp

q

BP.

AAV52160 standard; DNA; 6004

(first entry)

23-OCT-1998

AAV52160;

Streptococcus pneumoniae; computer readable medium;

Streptococcus pneumoniae.

WO9818931-A2

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TAAGGTCTTTGTGAACCTTTACAAGAAAGGCTGGATCTATCGTGGTGAGTTTATCATCAA 3701
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                                                                                                                                                                                                                                                                                               4315 AAAATAAATACGAATTTGTCTGCAGAAGAAGCTGCTAAGCAAATTCAAAATAAAATA 4256
                                                                                                                                                                                                                                                                                                                                                                                                                    4255 AACAAAATAGAGAAAGGACACACACATGTCTAAAGAACTTTCACCTAAATACAATCCAGC 4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1063 CGCTTGGGATACG---ACTTTGCAGGATATCATCCGTCAAAAACGCATGCAAGGCTT 4007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3904 TCGTGAGTCTTTCTTGACGAAGGTCTGGGAATĠGAAGAC------GAATATGC 3857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTACCATCAAGGAACAATGGGGCAAGATGGGGCTTTCTGTAGACTATTCTGGGGGG 3797
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                                                                                                                                                                                                                                       131 LysileValLysValThrAspLysValGluGlyGlnLeuLysGlyIleThrAspGluMet 150
                                                                                                                                                                                                                                                                                                                                                          151 GluArgLeu-ArgLysAlaGlnGluValCysGlnGluLeuAlaLysLysGluAsnAlaAs 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aThrArgIleLysTyrAla---SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSe 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GluGlyAlaLysAlaAsnArgGluMe 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pGluAsnGlnLeuCysIleValGluProPheTyrSerAsnAsnGluTyrPheLeuIleVa
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3640 AGGTGCCTTCTACCACATGAATTACATGCTGGAAGATGGTTCACGCGCCCTTGAAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 aProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHi
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   116
77
194
187
26
                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4195 CGAGGTTGAGGCTGGTCGTTACCAAAAATGG-------
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|TACAACTCGTCCTGAGACTATGTTTGGGGACGTT-----
   Matches:
                                                                                                                     Gaps:
                                                                                                                                                                             US-10-008-355-2 (1-712) x AAV52160 (1-6004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 lTyrAspValPhe------
129.00
33.62%
20.21%
3.47%
                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4072 CCTTGGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1006 TGAT---
                                                                                         Query Match:
                                                             Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV5524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequence at least 95% dentical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. AAV5524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating members of the molecule and properly and produced from an organism, amplifying nucleic acid molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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                                                                                   1246 CCTGCCTGGTACAAT ----GCTGATGGTGAAATGTATGTCGGCGAAGAAGCTCCAGAA 1299
                           586 GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules whose nucleotide sequence is homologous to amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. pneumoniae; genome; diagnosis; ass
vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical compositions and vaccines for S. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fannon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **Streptococcus pneumoniae genome fragment SEQ ID NO:27
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                                                                                                                                                                                                     1300 GGTGACGGATGGACTCAGGACGAAGACGTCTTGGAT 1335
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Dougherty

Dillon PJ,

Choi GH, Rosen CA;

Barash SC, Kunsch CA,

WPI; 1998-272225/24.

(HUMA-) HUMAN GENOME SCI INC

97WO-US19588. 960s-0029960

30-OCT-1997; 31-OCT-1996;

07-MAY-1998

Claim 1; Page 305-309; 1409pp; English.

pneumoniae

Length:

0.0831

Alignment Scores:

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0y 433 sty 0b 3546 0y 433 sty 0b 3517 CTA 0y 447 OAI 0y 454 9AI 0y 454 9AI 0y 454 9AI 0y 454 9AI 0y 454 9AI 0y 533 nAI 0b 3340 CAI 0y 533 nAI 0b 3348 AAI 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584 NAS 0y 584	:::           ::: -GCGGTTGCGGTTAATCCAGAA	STyrLysAsp	oAlaMetLeuAsp	GARGARGIIeProAlaAspLysLeuProAspIlePheLysAsnValIIeAspLysLysPh 474		rAspLysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGl 514                     -  -  -	uLysAspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla 531 	533	aggigicgtagtigagccacgctigictactcaatggticgtcaagatggaccaattggc 3125	nAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGl 553 :::   :::         TAAGAAGGCGATTAGGAGAAGAGAGAGAGAAGAAGAAGAAGAAGAAGAA	565	ATGGATGGAAAATGT 30	ASPAGANTATOTOTOGACATATOGACACATATOGACACATATOTOGACACACACACACACACACACACACACACACACACACAC	nAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspPr 604 	oLysSerAspGluPhealaValGlnGluAsnIleLeuAsp 617  :::     :::	standard; DNA; 2652 BP. ; 002 (first entry)	s pneumoniae DNA for ce	e; ds; prokaryotic cellular proliferation gene; ic; antibacterial; drug design.	eptococcus pneumoniae.	955-A2.	001.	001; 2001WO-US09180. ·
	;		447 OAlaMetLeuAsp   :::     3460 AATCGTTGGAGAT	454 gArgArgllePr     3400 TGCCCACGATCC	474 eLysGlyAspTb     340 CATGAACGACGA	494 rAspLysPheHi    ::    288 -GATCGTTTTGA			3184 AGGTGTCGTAGT					584 nAspGlyAlaTr     1111 989 AATCCCTGCCTG	604 oLysSerAspGl  :::     935 AGAAGGTGACGG		tococcus	ense; d iotic;	eptococcus pne	170955-A	SEP-2001.	R-2001;

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aurens, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The convention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer 243
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                                                                                                                                                                  Carr GJ;
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                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                  Trawick JD,
                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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105
64
165
178
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                            Claim 27; Seq ID No 9586; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-255625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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127.00
33.018
20.518
3.418
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Xu HH;
                                                                                                                             (ELIT-) ELITRA PHARM INC
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P-PSDB; AAU38090.
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Best Local Similarity:
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Yamamoto RT,
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notion relates to a protein (ABP25413-ABP30895) from group B coccus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS occus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS occus pyogenes), comprising one of 5483 sequences (S1), given in sification. The proteins have antibacterial and antiinflammatory (1), nucleic acids encoding (I), ABN66044-ABN71526 and lements for timent or prevention of infection or disease caused by cocus bacteria, particularly S. agalactiae and S. pyrogenes. acids encoding (I) are used to detect Streptococcus in a smaple. (I) is used to determine whether a compound binds to composition comprising (I) or a nucleic acid encoding (I), may be a vaccine or diagnostic composition. The disease caused by occus that is prevented or treated may be meningitis. Nucleic ording (I) may be used to recombinantly produce (I) and may be gene therapy. Antibodies to (I) are used for affinity gene therapy, immunoassays, and distinguishing/identifying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s; GAS; GBS; group B streptococcus; Streptococcus agalactiae; ptococcus; Streptococcus pyogenes; antibacterial; gene; tory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      occus protein for the treatment or prevention of infection saused by Streptococcus bacteria, such as meningitis, and ig a compound that binds to the protein -
                                                                                                           |||||||||
|GGTACAAT-----GCTGATGGTGAATGTATGTCGGCGAAGAAGCTCCAGAA 1299
   ----- 1245
                                                                   rpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys 605
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2000GB-0028727.
2001GB-0005640.
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126.50 Similarity: 33.29% cal Similarity: 19.81% itch: 3.40% 24 08-355-2 (1-712) x ABN681	AsnGlnGluAsnLe     :::    AATCCAGATAATGA TyrSerPheAspLy	AGAGAAATGATTAA	GlylleT    A	Ile	AspTyrLeuargAspGlyPheValSerArgThrMetGlyGluGluLeuProlleProG 	3=5	3∷8	IleThraspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGl           ::: :::::        AAAATTGTTGATGAGCTTAAAGTCATGGGATACGAACCTGAACAAATTGTGGTTGA	LeualaLysLysGluasnalaaspGluasnGln- :::[   :::	AAACTTCTTGATGATGGCGTT	ProP : GAAT	AACGGAAGAGATATGTATACAGGGGAAGCTCTAGATATTGACAATTTAAGTCAATATGAT		AspThrAspAsnTrpMetTrpProArgHi        ::: GATAATCGTGTT	AlaGlyAlaAspAsn :::         rCATCTGCTAAAAT	ASDLYSPrOTyr      ::: rgtaaagtrttctg	
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2710 AATTTGACTAAGGCAGAGGCGGGAGGCCTAACTTCCGATGATAAGGCAAGATTTATCCAA 2769 2770 CGTCAGTTGGTTGAGCACGACAAATTACCAAGCATGTTGCCCGTATCTTGGATGAAGC 2829 :::|||::: 2890 AAGTCAAATTTGGTTTCAAATTTCCGAAAGAATTTGGATTCTATAAAATTCGTGAAGTT 2949 ::: |||| 2950 AACAATTATCACCATGCACATGCTTATGCTAATGCAGTAGTTGCTAAAGCTATTCTA 3009 3010 ACCAAATATCCTCAGTTA----- 3039 2830 TTTAATAATGAGCTTGATAGTAAAGGTAGAAGGATCCGCAAAGTTAAAATTGTAACCTTG 2889 ||| :::||| 3433 TTAGTTGTAGCTGATATCAAAAAGGGTAAAAGCACAAAAAACTAAAAACAGTTACGGAACTT 3492 3493 ITAGGAATTACCATCATGGAGAGGTCCAGATTT------GAGAAAAATCCATCA 3540 ------CCAAAATATAATAGTTAC 3072 3133 AAAACTAAGGTAACTTTAGCGGATGGAACCGTTGTTGTAAAA------GAT 3177 3541 GCTTTCCTTGAATCAAAGGCTATTTA------AATATTAGGGCTGATAAACTA 3588 290 IleGluAsnGluAsnAsnPro--------ArgIleGluValArgGlyIle 303 LysglnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThrArgIleLysTyrAla 323 324 SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArgGlyLeu 343 344 AlaArgLeuAspValIleGlyArgLySArgAlaGluGluArgAlaPheAlaAspTrpIle 363 364 ArgLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyr 383 384 LysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGlu------ 398 LysaspTyrLeuProSerLeuAspArgLysValLeu----ProAlaMetLeuAspIle 452 AlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGly----- 476 477 ---AspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495 538 Ala------AsnAlaTyrAlaIleGluLysGlyLysArgLeuPheAla 552 -----ThrLeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsn 414 415 AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434 519 ValGluLeu---SerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMet 537 553 GlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThr---- 570 273 PheProGlySerThrAspArgTyrLeuThrSerTrpGly------ValGluAspArg LysPheHisAlaMetLeuLysSer-----453 ValArgArgArgIlePro-----3040 435 304 399 459 496 504 δλ g qq ò g δ QQ δ g ò q δy QQ οy Dp QQ g ò ò δλ QQ οy δý Dp ŏ QQ ò Ω δ qq ò

Db 3649 AGTGCTGGTGAATTACAAAAGGTAATGAGCTTACCAACACACATTATGAAGTTC 3708  3709 TTATACTTGCAAGTCGTTGAATGGTCAAACGCGTTACCAACACAACGAGGGGTTGAGAG 3765  Db 3709 TTATACCTTGCAAGTCGTTATAATGAGTCAAAACGAGGGGTTGAGAG 3765  3709 TTATACCTTGCAAGTCGTTATAATGAGTCAAAACGAGGGGTTGAGTAATTAAT	•	14-APR-1998; 98US-0059584.  (CONN-) CONNAUGHT LAB LTD.  Myers LE, Schryvers AB, Harkness RE, Loosmore SM, Du R, Yang Y; Klein MH;  WPI; 1999-620376/53.  P-PSDB; AAV43380.	Nucleic acid encoding transferrin binding protein 2 of Moraxella catarrhalis, useful for diagnostics, immunization and recombinant protein production -  Claim 2; Fig 6; 114pp; English.  This sequence encodes the Moraxella catarrhalis strain LESI transferrin binding protein (Tbp2) of the invention. This sequence is also referred to as the TbpB gene. The TbpB gene is used to produce recombinant Tbp2; for identification or diagnosis of Moraxella, or for cloning related for identification asserved.
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Moraxella infections, e.g. otitis media. The Tbp2 proteins are useful as antigens, either in vaccines (including components of conjugate vaccines that contain antigens from other bacteria or from tumours, in which case they elicit production of antitumour antibodies that may be coupled to chemotherapeutic agents or biologically active agents) or to raise antibodies (for use as diagnostic reagents and for treating Moraxella infections), also for detecting Moraxella antibodies.
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2065 GGGTCATTTACACACGATACCGAT 2088

1165 GOTGGCAGGGGCAGGGGCAGGGGAAGGGAAAGGAAGGAAGGA	1105 366	ACAGCTGTAACCGCCAAAGAGCGTTATAAAATAGAAGCTGATATCCACGGCAACCGGTTC 1164 AsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGlu 385
GIAILLysalaasnargGluMetThrTyr'-LeuSerGluThrLeuPheGIyGIyThr GRCGCAAACCCCAACCCCTTTACCAGGAGCTACAAACAGGAGGAAACGGAACCGAACCCAACAAACGGAACCCCTTTACCAGGAGAACAACAACAACAACAACAACAACAACACAACA	65	
GluvalvalArgPhealaGlnPhealaAnnalaLeualaThrkanProAspalaHisala 424  TATGGACCAAAGCCGACGACGTAAATTCTTAACCCATTACTTTTTTTT	86 98	GlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThr :::1
G1y11eteulysSerleunAsphaplysTyrlysAspTyrLeuProSerLeunAspArglys 444	05	GluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAla :::             :: :: TATGGACCAAAAGGCGAGGAGCTGGCAGGTAAATTCTTAACCGATGACAACAACTTTT
GGGGTCTTTGGTGCTAAACGAGATAAAGTAGAAAAACCGAAGCCATCTTAGATGCTAT 137 ValleuProAlaMetLeuAspIleValargArgArgIleProAlaAspLysLeuProAsp 464 GCATT	25	ဟ
ValleuProAlaMetLeuAspilevalArgArgileProAlaAspLysLeuProAsp 464  CCACTTTTTATATATATAATACAATAAGCACCATTCACCCCATTACCAAAAACATGGAT 144	18	
IlepheLysAsnValIIeAspLysLysPheLysGlyAspThrLysLysTyrAlaAsp 483   CATTAATAATAATACAAATAAGCAACCACATTCACCCCATTTACCAAAAAACACTGGTT 144	45	ValLeuProAlaMetLeuAspIleValArgArgIleProAlaAspLysLeuProAsp         GCACTT
"PhevalPheaspLysservalvalProTyrSerAspLysPheHisalametLeuLys 502	165	483
ACTTGGCAATGCCAAAAAGTTGGTTTTACCGTCATTAATTTGGTGTCTACC 150 SerMetAsplysGluLyshellelgluLyshspproalavalGluLeuser 522 GATGCCACCAAAAAGTTCACCAAAAATTCACCAAAGAC	184	502
SerMetAsplysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer 522  GATGCCACCAAAAATTCACCAAAAATTCACCAAAAACCCAAAAAA	147	150
GATGCCACCAAAATCAATTCACCAAAAATTCACCAAAGAC	503	
LysSerVallleAlaAlaAlaArgAlaIleGInAlaAspAlaMethlaAsnAlaTyrala 542	507	
IleGluLysGlyLysargLeuPhePhealaglyLeuargGluMetTyrProGly 560   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   III   IIII   III   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII	523	542
ATCGTCAAAACCTATGCCAAAAACTTTGAATACCTAAAATTTGGTGAGCTTAGTGTGGGT 166 ATGALa	543	
Argala	909	AACCTATGGCAAAAACTTTGAATACCTAAAATTTGGTGAGCTTAGTGTGGGT 166
SerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr	561	
CCAACCACAGGCAAAGCCAAATATCTGGGGTAGGTAGGTA	577	593
ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGluGlu	726	CCAACCACAGGCAAAGCCAAATATCTGGGAACTGGGTAGGATACATCACAGGGGGGGC 178
ASDILELEUASPLEUPHEATGRUCCCARGATION  ASDILLELEUASPLEUPHEATGTHTLYSASNTYTGIYATGTYTAIGGUASNGIYGINLEU  SERIAL	594	
TTTGACATTGACTTTGAGAAAATCAGTTAAAGGCAAACTGACCACCAGGCGCGCACA HISILeAlaPheLeuSerAsnAsnAsnAspileThrGly	2 7	
HisilealapheLeuSerAsnAspileThrGly	325	
GATCCTGTCTTAACATCCAAAGGTGAAATTGCAGGCAATGGCTGGACAĞGCAAAGGCAGGCAAGGCA	34	64
ACCACCAAAGCGGACGCTACAAGATACATTCTAGCAGTACAGCAATCCATC PheAspLysasnGlyArgLeulleGlyLeualaPheAspGlyAsnTrpGlualaMetSer :::1   :::1   :::1   GTCATCGAAATGCCGAAGTTACTGGGGGCTTTTATGGTCCAATGCAAACGAGATGGGG	385	
ACCACCAAAGCGGACGCAGGAGGCTACAAGATAGATTCTAGCAGTACAGGCAATTCTAGCAGTACAGGCAATTCTAGCAGTACAGGCAATTCTAGCAGTACAGGAGTACAGGTAGTAGATTCTAGCAGTACAGTAGTAGTAGTAGTAGTAGAAATGCAAATGCAAATGCAAATGCAAATGCAAATGGGGGGTTTTATGGTCCAAATGCAAAGGAGATGGG	346	
PheAspLysAsnGlyArgLeulleGlyLeuAlapheAspGlyAsnTrpGluAlaMetSer :::	145	
GlyspileGluProAsp 680	53	
	173	

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The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1735 ACTGCAGGACTCAAAGGCATGGGTAAATTCGGTAAGTTG-------GCTAGCGGT 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| :::||| ||| |||
1675 GGCGGAGTTGTATTGCCTGGGGBAAAGGAAAAGGBAAGTTAAACTTTTCAGCAAAGCT 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 ------LysGlyMetTrpLeuLeuAsnGluLeuAsnGlnGluAsnLeuAspArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 MetargGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysProSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                       Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and pathogenicity of Listeria (potential therapeutic agents), all treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4716 BP; 1750 A; 734 C; 1110 G; 1122 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAsp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4716
138
104
308
187
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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                                                                                                                                                                                                                                     Listería innocua DNA sequence #1034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; SEQ ID 2408; 180pp; French.
                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                               ABQ69595 standard; DNA; 4716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2001; 2001WO-FR03061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000FR-0012697
                                                                                                                                                                  29-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.253
122.50
32.84%
18.72%
3.29%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-Listeria vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-332479/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F, Glaser P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                       Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200228891-A2.
                                                                                                                                                                                                                                                                                                                                           infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2002.
                                                                                                  ABQ69595;
ABQ69595
                                                                                                  X D X D X X D X X D X D X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D 
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۵	1783	GTAGGTGTTTTAGGTGTAGGATTAAGCGCTACTGAGTTGATTGGTATGAACAAAATAAT 1842		
<u> </u>	62			
Q	1843	GCAGGTGAAAAAACTGGTGGCTTTGGTGGTTCTTTAGGTGGTATGGCTGGTGGT 1896		
<u>~</u>	82	GlyLeuIlePheThrAsnHisHisCysGlyTyrGlyAla94		
۵	1897	GCTGCAATAGGA		
¥	95			
۵	1957	GCTTTTGCTGGAACTGCATTAGGTAAAGAATTAGGGAAATATGTTCAAAAAGAAGGACCA 2016		
λ	101			
۵	2017		_	
Σ	120	ProlleProGlyLeuSerValLySTyrLeuArgLyS1leValLys 134		
۵	2077			
¥	135	36		
ā	2137	ATTAAAGCAGTTGGAGACACGCATAAAACTGTTTGGAATGCTTCAAAATCAATAGTCGCC 2196		
×	137	AspLysValGluGlyGlnLeuLysGlyIleThrAspGluMetGluArgLeuArg 154		
ā	2197			
×	155		-	
ā	2242	TCTGCTAAAGCAATGAACGAGTATTTACGAAATGAGCAGAAATGCAAGATAGTCGAGTC 2301		
۲ <u>۶</u>	175			
۵	2302	GAAATCATGGTATCTGGTCGTATTACTGAAAAGAACTCGAA		
<u>&gt;</u> -	188	LeulleValTyrAspValPheLysAspValArgMetValPheAlaProProSerSerVal		
ð	2353			
<u>≻</u>	208	GlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSer 227		
ð	2410			
λ	228			
ą	2455	GTTTCTAAAGATACAGCTAGCGCAAAGAAACAC		
<u>≯</u>	244	LysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLys 263		
ð	2515			
Ϋ́	264	AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThrSer 283		
ą	2574	2574		
<u>~</u>	284	TrpGlyValGluAspArgIleGluAsnGluAsnAspProArgIleGluValArgGlyIle 303		
۵	2575	GGGCAAGAAGAGATTACACGAAATGCTGAAAATAGAATTAATGCT		
<u>≻</u>	304			
ā	2623	AAACAGAAAGCTAGCAAAGAGAAACGGAAATTAACAAAAGATGAAGAAAAAAAA		
۸	322	TyralaSerLysTyralaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMetAsnArg 341		
۵	2682	2682		
λī	342	GlyLeuAlaArgLeuAspVallleGlyArgLySArgAlaGluGluArgAlaPhe 359	•	
ā	2683		_	

OY	60 AlaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAspV
qq	2734 GAAAAAGAAGTTAGAAAGATTGAA 2757
Qy	80 GluLysalaTyrLysGluGlyalaLysalaAsnArgGluMetThrTyrLeuSerGluThr 399
qq	2758 GAAAAGCAAAGGAAAGCTGCTATTGCACTCACTGCTTCAGCTAAAGAACAAAAATA 2817
δλ	400 LeuPheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThr 418 :::
QQ	Ϋ́
Qy	419AsnProAspAlaHisAlaGlyileLeuLysSerLeuAspAspLysTyrLys 435
QQ	CATCCGTAAAGAAGCTAATAA
ΟŊ	436 AspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArg .455
QQ	
ΟŊ	456 ArgileProAlaAspLysLeuProAspIlePheLysAsnVallleAspLysLysPheLys 475
QQ	1
QY	476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495
QQ	3034 AACGGCGTAGTTAAAGAAGCGGAGAAGATGCACGATAATGTAGTGCGAGAAGCTCAGCAA 3093
Qy	496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlalleGluLys 515
qq	4 CAAGCAAAAGGACATTTAAGAGAAGTAGAAATTGGGAAACTGGTGAAACATTAAATAAG 31
Οy	516 AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAsp 535
qq	TTAACAGTATAAAAGATGCA 32
δλ	536 AlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArg 555
qq	CTGCGACAGTTAATATTTCAGTGGAATGAAA 32
Qy	56 GluMetTyrProGlyArgAl
q	-GCGTTGAGAGTATTTGATAGTTTTAAGACAAACTTGTATAAAGTCATTAAT 33
δy	576 GlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThr 593
q	GTAATTACCGGAGTCAATAAAGTACTATCGTTC
Qy	594ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 612
qq	ATAGGTTCAAGT
Qy	613 GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGln 632
qq	3412 GABABCHGTTTATCTGCBABGGATABGBABACGTATCATTCTBCBTCCCABTCAGGBABAT 3471
QY	leAlaPheLeuSerAsnAsnAspIleThrGly
qq	ATGGCTGGT
Qy	649 GlySerProValPheAspLysAsnGlyArgLeuIleGly 661
qq	32 GGTTTCGAGATTGCATATAACAAGAACTCAGCACAAGCGAGAATTCTAGGG 35
RESU ABQ6 ID	JLT 15 57873 ABQ67873 standar
Y S X	ABQ67873;
XX	29-AUG-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                                                (ABO67188-ABO71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1857
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LysGlyMetTrpLeuLeuAsnGluLeuAsnGlnGluAsnLeuAspArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 GlyLeuIlePheThrAsnHisHisCysGlyTyrGlyAla----------
                        food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4731 BP; 1752 A; 735 C; 1117 G; 1127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       present invention relates to nucleic acid sequences
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 Listeria innocua DNA sequence #675.
                                                                                                                                                                                                                                                                                                               Claim 7; SEQ ID 686; 180pp; French.
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32.84%
18.72%
3.29%
                      Antibacterial; Listeria;
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Best Local Similarity:
                                                          Listeria innocua
                                                                                  WO200228891-A2
                                    infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2152 ATTAAAGCAGTTGGAGACACGCATAAAACTGTTTGGAATGCTTCAAAATCAATAGTCGCC 2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asp-----LysValGluGlyGlnLeuLysGlyIleThrAspGluMetGluArgLeuArg 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThrSer 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 TrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGlyIle 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLysAlaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThr 399
...----IleGlnSerGlnSerThr 100
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                                                                 1972 GCTTTTGCTGGAACTGCATTAGGTAAAGAATTAGGGAAATATGTTCAAAAAGAAGGACCA
                                                                                                                                      101 ValAspHisAspTyrLeuArgAspGlyPheValSerArgThr---MetGlyGluGluLeu
                                                                                                                                                                                  155 LysAlaGlnGluValCysGlnGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeu
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3427 GAAAACAGTITATCTGCAAAGGATAAGAAAACGTATCATCTACATCCCAATCAGAAAT 3486
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3280 GATACA---GCGTTGAGAGTATTTGATGATTTTAAGACAAACTTGTATAAAGTCATTAAT 3336
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893 GTTAAAAATTCCGCAAAAGCTAGAGATGCATCCGTAAAAGAAGCTAATAAAGAGTATAAA 2952
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                                                                                                                        436 AspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArg 455
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                                                  419 ------AsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyrLys
                                                                                                                                             496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLys
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Sequence 11, Appli Sequence 139, App Sequence 27, Appli Sequence 79, Appli Sequence 79, Appli Sequence 70, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 142, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

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GenCore version 5.1.4_p5_4578  Copyright (c) 1993 - 2003 Compugen Ltd.  OM protein - nucleic search, using frame_plus_p2n model  Run on: May 23, 2003, 09:42:03; Search time 60.7132 Seconds  (without alignments) 3596.482 Million cell updates/sec Title: US-10-008-355-2 Perfect score: 3719 Sequence: 1 MQMKLKSILLGAALLLGASGLFMIDKWGQCPRLIQELKLI 712 Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5 Ygapop 10.0, Ygapext 0.5 Fyapop 10.0, Ygapext 7.0 Pelop 6.0, Fgapext 7.0 Delop 6.0, Delacx 7.0	Searched: 441362 seqs, 153338381 residues  Total number of hits satisfying chosen parameters: 882724  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%  Maximum Match 100%  Listing first 45 summaries	Command line parameters:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SUMMARIES  SEQUENCE 726, App Sequence 726, App Sequence 1045, App Sequence 107, App Sequence 107, App Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl 11, 110, 3, 0, 2319, 4, US-09-134-078-134, Sequence 114, Appl 11, 110, 3, 0, 2319, 4, US-09-134-078-14, Sequence 114, Appl 11, 110, 3, 0, 2319, 4, US-09-134-078-14, Sequence 114, Appl 11, 110, 3, 0, 2319, 4, US-09-134-078-14, Sequence 115, Appl 11, 110, 3, 0, 2319, 4, US-09-134-001C-195, Appl 12, Appl 12, Appl 13, DESCRIPTION SEQUENCE 114, Appl 13, DESCRIPTION SEQUENCE 114, Appl 13, DESCRIPTION SEQUENCE 114, Appl 13, DESCRIPTION SEQUENCE 115, Appl 13, DESCRIPTION SEQUENCE 115, Appl 13, DESCRIPTION SEQUENCE 114, Appl 14, DESCRIPTION SEQUENCE 115, Appl 15, Appl 15, DESCRIPTION SEQUENCE 115, Appl 1

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Matches:
Conservative:
Mismatches:
Indels:
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             27340-20021.00
                                                                                                                                                                               Gaps:
                                                                                                       ORGANISM: PORYPHYROMONAS GINGIVALIS
NAME: MODICOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-494-0792
TELEX: 706141
                                            726:
                                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: UNKNOWN
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                                         INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1...1974
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Sequence 382, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
1317
168
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172
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 10-DEC-1998
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT: INFORMATION:
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TELEPHONE: 650-813-5600
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LOCATION: 1...1317
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 3
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Query Match:
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STRANDEDNESS:
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TELEFAX: 6
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                                                      16 CAGATGAAAGAGCGCGGCCTTAAGATGAAGAATACGACCTTTATAATCCCAACGGCACA
   ArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysPro
                                                                                                                                               SerIleAlaAsnAlaValValIlePheGlyGlyGlyCysThrGlyIleThrValSerAsp
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US-10-008-355-2 (1-712) x US-09-221-017B-382 (1-1317)

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US-09-221-017B-1045
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                                                                                        ---LysAspTyrLeuProSerLeu
                                                                      411 GlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeu
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                         442 AspArgLysValLeuProAlaMetLeuAspIleValArgArgArgIlePro 458
395 TyrLeuSerGluThrLeuPheGlyGlyThrGluValValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFERATING SYSTEM: Windows
SOFTWARE: FESESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILLING DATE: 23-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,430
ER: 27340-20021.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 31-DEC-1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
PPLICATION DATA:
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
FILING DATE: 10-DEC-1998
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                      Sequence 1045, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO: 1045:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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E: DNA (genomic)
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REGISTRATION NUMBER: 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650-494-0792
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EDNESS: double
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                                                                                                                                          431 AspAspLysTyr-
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ZIP: 94304-1018
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GluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLysSerValIle 526
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                                                                                                                                                                                                                                                                                                                                                                                         66 GACGAATACCGCAAACTCTACAACGAACTTCGTCCCTATGACGATCCTATTCTAAGGGCA 125
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                                                                                                                                                                                                                                                                            GAAAAGCTTGCC------GAAGATCCTATGGTACTCTTCGCCTCTTCGTTTTC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
STREET: 755 PAGE MILL ROAD
                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                         US-10-008-355-2 (1-712) x US-09-221-017B-1045 (1-2384)
                      Length:
Matches:
                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        706 IleGlnGluLeuLysLeuIle 712
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                      2.82e-38
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61.84%
43.48%
11.87%
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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Alignment Scores:
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APPLICANT: Brown, James
       Patent No. 5849555
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ArgMetArgGluLeuGlyPheThrLeuProLeuAspSerLeuTyrSerPheAspLysPro 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetGlnMetLysLeuLysSerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGly 20
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22
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Matches:
Conservative:
Mismatches:
Indels:
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                                     OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                NAME: MODEOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC 1997
FILING DATE: 31-DEC 1997
PRIOR APPLICATION NUMBER: PP156
FILING DATE: 30-JAN 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC7AU98/01023
FILING DATE: 10-DEC-1998
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                      APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08953492
                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.28e-20
265.50
96.83%
93.65%
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 561 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1...561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
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544 TCCATGGCA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-221-017B-12
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US-08-953-492-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
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---LysAspValArgMetValPheAlaPro 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CACCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 ProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 GlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgFroAlaGluTyrSer 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 GGT------CACGCT 171
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106
62
166
178
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
Indels:
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                                                              TITLE OF INVENTION: NOVEL valS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
SAITHKLING Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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APPLICANT: Jaworski, Deborah
APPLICANT: Lawlor, Elizabeth
APPLICANT: Wang, Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA
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TYPE: nucleic acid
STRANDEDNESS: single
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32.81%
20.70%
3.50%
                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
TELEX:
                                                                                                                                                                 CITY: King of Prussia STATE: PA
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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		264 AlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr 282 229	Db 1144 GTCGAATTCTACCCACTCGTTTCAACGATACCTTCCAATGGAAAATGTCCAC 1203  Qy 566 AspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp 585
· · · · · · · · · · · · · · · · · · ·		LysaspTyrLeuProSerLeuAspargLysValLeuProAla	PRIOR APPLICATION DATA:  APPLICATION NUMBER:  FILING DATE:  ATTORNEY/AGENT INFORMATION:  NAME: Brookes, A. Ander:  REGISTRATION NUMBER: 36,373  REFERENCE/DOCKET NUMBER: PB340P1  TELEPHONE: (301) 309-8504  TELEPHONE: (301) 309-8512  INFORMATION FOR SEQ ID NO: 27:  SEQUENCE CHARACTERISTICS:  LENGTH: 6004 base pairs  TYPE: nucleic acid  STRANBEDNESS: double  COS-08-06-127-27
435   LyaAspTyrLeuProSerLeuAspArgLysValLeuProAla 448	. 40 60 60 60 60 60 60 60 60 60 60 60 60 60	496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaileGluLys 515  316 CGTTTTGAAGCTCGTAAGCAGTCGTTGCTAAGTTGGAAGAATC 990  516 ASPProAlaValGluLeuSerLysSerValileAlaAlaAlaArgAla 531  11:::::	C
1	a % a %	1051 GTTGTGGTTGACCTCGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110 535 ASPALAMETALAASNALBTYTALBILGGLULYSGLYLYSATGLEUPhePheAlaGLYLeu 554 :::   ::        1111 AACGCCATTGCCAACCAAGACACAGAGCAAGCAAGCAAGC	OS-10-008-353-2 (1-/12) X US-U8-961-32/-2/ (1-6004) OY 131 LySILeValLySValThrAspLySValGluGlyGlnLeuLySGlyIleThrAspGluMet 150

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pneumoniae Polynucleotides and Sequences
rrGlySerIleLysGlyTyrGluProGlnAsp 585
:|||
|GGGTCAC------CAAATC 1245
                                         yLysGlyValLeuGluLysGlnAspProLys 605
|::: ::::: |||:::
:rGAAATGTATGTCGGCGAAGAAGCTCCAGAA 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysGlnGluLeuAlaLysLysGluAsnAlaAs 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6004
116
77
194
187
26
                                                                                                                                                                                                                                                                                                          ch, 1.4Mb storage
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                     leLeuAsp 617
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TCTTGGAT 1335
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                                                                                                                                                                                                                                  ss, Inc.
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Ov 474 eLysGlyAspThrE	3340	494	3288	m	532	3184	DD 3124 TAAGAACGCCATTG	Qy 553 yLeuArgGluMetT   11     Db 3087GTCGAATTCT	Qy 566AspAlaÀsnP	Oy 584 nAspGlyAlaTrpT		7	RESULT / NS-09-059-584-52 / Sequence 52, Applicati / Patent No. 6440701	GENERAL INFORMATION: HOPPLICANT: Myers, APPLICANT: SChryve APPLICANT: Harknes	; APPLICANT: LOOSMOR ; APPLICANT: Du, Run APPLICANT: Yang, Y APPLICANT: Klein, Y	EEES	G ta G	; ZIP: MSG 1R7 ; COMPUTER READABLE F: MEDIUM TYPE: IBM PC ; COMPUTER: IBM PC	) OPERATING SYSTEM:  SOFTWARE: PATENT CURRENT APPLICATION APPLICATION NUMBE	; FILING DATE: 14- ; PRIOR APPLICATION: ; APPLICATION NUMBE	; FILING DATE: 03- ; CLASSIFICATION: ; ATTORNEY/AGENT INFO ; NAME: Stewart, M
4255 AACAAAATAGAGAAAGGACACACACATGTCTAAAGAACTTTCACCTAAATACAATCCAGC 4196	170 pGluAsnGlnLeuCysIleValGluProPheTyrSerAsnAsnGluTyrPheLe	190 lTyrAspValPhe		202 aProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHi 222        :::           4099 ACCACCAAAGTAACTTAGGAAACTT	222 sThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTy 242	4072 CCTTGGTCA 4064	242 rSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTy 262 ::::				3904 TCGTGAGTCTTTCTTGACGAGGTCTGGGAATGGAAGAC	317 aThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSe 336 	336 rIleGlyMetasnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGl 356 	356 uArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTy 372   ::         :: ::       378   3760 TAAGGTCTTTGTGAACCTTTACAAGAAAGGCTGGATCTATCGTGGTGGTTATCATCAA 3701	372 rGlyAsp 384 	385	393 tThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValValValArgPheAlaGlnPheAl 413 	413 aASNAlaLeuAlaThrASnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLy 433 	433 STYTLysAspTyrLeuProSerLeuAspargLysValLeuPr 447 :	447 oAlaMetLeuasp	
g	oy G	ò	Dp	QY Db	Qγ	qq	QY Db	Qy	Oy do	oy Oy	QQ	Qy Dp	OY Db	Qy	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	QY	Oy Db

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ValGluLeuSerLysSerVallleAlaAlaAlaArgAla----- 531
||||::::: ||  ||  ||   |::
|GCCAAAATCGAAAACGTGTCCACAGTGTTGGTCACTCAGAACGTAC 3185
                                                                                                                                                                                                          GAGCCACGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGC 3125
                                                                                                                                                                                                                                                              AlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGl 553
                                                          AlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGl 514
                                                                                                                                                                                  -----11eGl 533
                                                                                                                                                                                                                                                                                                        TyrProGlyArgAlaLeuProSer------565
                                                                                                                                                                                                                                                                                                                                                                 PheThrMetArgMetSerTyrGlySerIleLy$GlyTyrGluProGl 584
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Yan-Ping
N Michel H
Transferrin Receptor Genes of Moraxella
ES: 60
DRESS: no
& MCBurney
& MCBurney
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Floppy disk
4 PC compatible
FER: PC-DOS/MS-DOS
FERI Release #1.0, Version #1.30
TION DATA:
MHBR: US/O9/059,584
14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::
TGGACTCAGGACGAAGACGTCTTGGAT 2896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheAlaValGlnGluAsnIleLeuAsp 617
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3ER: US 08/778,570
3-JAN-1997
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vers, Anthony B
mess, Robin E
ore, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ion US/09059584
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Michael I
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LeuProlleProGlyLeuSerValLysTyrLeuArgLysIleValLysValThrAspLys 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProPheTyrSerAsnAsnGluTyrPheLeuIleVal-----TyrAspValPheLys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspValArgMetValPheAlaProProSerSerValGlyLysPheGlyGlyAspThrAsp 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGlyAla 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: ::|||
760 ACCGACCACAAAAAAAACCAATTATGGTGGCTATGTATTATAAAGGC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703 ---AACCGTGATCTAGAATATGTCAAGTCTGGTTTTAACTATCTTTCTGGATATACCGCC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ala-----TyrLysAla 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ile---LysGlnGlyIleTrpLysGluAlaMetSerAlaAspGln---AlaThrArgIle 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 TTTGAAGCACAAAAAGGCGGTATTGAAAATAACACAAAGACTGACACAAAGATTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 ValCysGlnGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 AGCGAAACCGCCAAAGAGCTA-----CCACAAACAAGGTGCAAAATATAAAGGTTAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACTTTATGACAGATGCCACACTTGATAACAAATACACG------GATTTGCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspAsnArgProAlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspaspTyralaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThrSerTrp
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-008-355-2 (1-712) x US-09-059-584-52 (1-2142)
                                                                                                                                                                                                                                                                                      Length:
REGISTRATION NUMBER: 21038-REFERENCE/DOCKET NUMBER: 1038-TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155 TELEPAX: (416) 595-1163 TELEFAX: (416) 595-1163 SEQUENCE CHARACTERISTICS: LENGTH: 2142 base pairs TYPE: nucleic acid caranbedness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpLysAsnSerIleGly-----
                                                                                                                                                                                                                                                                               0.00141
123.50
32.178
19.90%
3.328
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                           US-09-059-584-52
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9
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1387 ACATITIAATAATACAAATAAAGCAACCACATICACCCATITIACCAAAAAACAACTGGAT 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1549 AAGCCAACTTCTGCCACAAAAAAGCGGGGGAGACT---TTGATGGTGAATGATGAAGTT 1605
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.666 GATAGCCATAGCGTCTTTTTACAAGGCGAACGCACCGCTACCACAGGCGAGAAAGCCGTA 1725
                                                                                                                                                                               1165 CGTGGCAGTGCC-----GAA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAACCACAGGCAAAGCCAAATATCTGGGGAACTGGGTAGGATACATCACAGGAGCGGGC 1785
1045 GATGTTAATTTTGCTGATAAAAAATTAAAGGCAAACTTATCAGTAATCAGTTATCAGGC 1104
                                                                                      1105 ACAGCTGTAACCGCCAAAGAGCGTTATAAATAGAAGCTGATATCCACGGCAACCGCTTC 1164
                                                                                                                                                                                                                                                                          1258 TATGGACCAAAAGGCGAGGAGCTGGCAGGTAAATTCTTAACCGATGACAACAAACTCTTT 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGTCTTTGGTGCTAAACGAGATAAAGTAGAAAAAACCGAAGCCATCTTAGATGCCTAT 1377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 IleGluLys-----GlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGly 560
                                                                                                                                                                                                                               GlyAlaLysAlaAsnArgGluMetThrTyr---LeuSerGluThrLeuPheGlyGlyThr 404
                                                                                                                                                                                                                                                                                                                          405 GluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAla 424
                                                                                                                                                                                                                                                                                                                                                                                                                     GlylleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLys 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 ValLeuProAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAsp 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 IlePheLysAsnValIleAsp---LysLysPheLysGlyAspThrLysLysTyrAlaAsp 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PheValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLys 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561 ArgAla------LeuProSerAspAlaAsnPheThrMetArgMetSerTyrGly 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGlu 613
                                             LeuAspValIleGlyArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLys
                                                                                                                                    AsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysSerValIleAlaAlaAlaArgAlaTleGlnAlaAspAlaMetAlaAsnAlaTyrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 HisIleAlaPheLeuSerAsnAsnAspIleThrGly--------------
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Oy 673 GlyaspileGluPheGluProAsp 680		119 uProlleProGly
Db 2065 GGGTCATTTACACACATACCGAT 2088	qq	
RESULT 8	٥y	131
. 5-00-75-024-1. ; Sequence 1, Application US/08793824 · Datont No Equipment	qa	2001 CCGTGGCAGCTTGGAGCGCGTGATT
GENERAL INFORMATION:	QY	132
	qa	2061 ACACACGCCACGTGATGCCAATTAT
	ογ	138
	qa	2121 TGTTTTGGCTAATATCATCAGCAAGG
; ADDRESSEE: Griffith Hack 6 Co	QY	149 uMetGluArgLeuArgLysAlaGlnG
CITY: No. 5981838th Sydney	qa	2181 TATGGATGAGCTCAAACAGGCCTTC
	Qy	166 sGluAsnAlaAspGluAsnGlnLeuC
COMPUTER READABLE	qa	1::: 2241 AAAGTACACCCAGTACAATATCCCA(
	Qy	186 rPheLeuIleValTyrAsp
SOFTWARE: Patentin	qa	2301 TATCACTCGTGTTTACTACGGGGAC
# APPLICATION NUMBER: US/08/793,824	Oy	204 oSer
	ΩD	2361 ATCACCGTACTATAATGCCATCGAT
APPLICATION NUM	QY	206
TELECOMMUNICATION	qa	2421 TGGTCAAGACATGAAGGTTACTAAG
	QY	207 IGLYLYSPheGLYGLYASpThrAsp
NI	qa	2481 TGGTAAGGGGGCAGAAGAGCC
CECUTAL CHARACTERS; LENGTH: 4453 base pairs . TYPE: nucleic acid	Qy	221 gHisThrGlyAspPheSerVal
	qq	2537 GAATGCTGGTCCTTACAGCCAACCG
MOLECULE TYPE: DNA (genomic): HYPOTHFTICAL: NO	QY	239ProAlaGluTyrSerLysAs
ANTI-SENSE: NO	QQ	2597 TAGTCAATATGGGAGCTGCCCACAA
ORGANISM: S	Qy	257
lianment Sco	QQ	2657 CGACAGGTCTTGCGACCTACCTCAA
0.0423 Length: 115.00 Matches:	Qy	257 alSerMetGlnGlyTy
t Similarity: 34.10% Conservative: ocal Similarity: 20.56% Mismatches	qa	2717 CGGACAATCAAGGGAACTTGACCTT
3.09%	Qy	272 lyPheProGlySerThrAspArgTy
-10-008-355-2 (1-712) x US-08-793-824-1 (1-4853)	qa	2777 AAGTTTCAGGTTA
` ⊟	QY	292 snGluAsnAsnProArgIleGluVa
1776 GGTGGAATGTGGATCTCTTGCAGATTGCTTCTGATACTTCAAGGAAAATA	q <sub>Q</sub>	
Oy 85 PheThrAsnHisHisCysGlyTyr-GlyAlalleGlnSerGlnSe 99	δλ	
Db 1836 CCGTGTCGCAGATAATGAAGCAAATGCCATTGCTCATTGTCAATCCTTGAAGCTTGGTC 1895	qa i	CATCAGCAGCTCTTGATTCACA
Qy 99 rThrValAspHisAspTyrLeuArgAspGlyPheValSerArgThrMetGlyGluGluLe 119 	da cz	320 IELYSTYTALASSELVYSTYF 1:
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δy	119	ProGly
qq	4.1	
Qy	131	131
qq	2001	CCGTGGCAGCTTGGAGCGCGTGATTACTAACTCTTTAACAATCGTTCAAGTGAGCAGAA 2060
QY	132	
qq	2061	acacacgccacgtgatgccaattatattttcgtgcgagcccatgatagtgaagtgcaagc 2120
δy	138	
QQ	2121	TGTTTTGGCTAATATCATCAGCAAGCAGATTAATCCAAAAACAGATGGTTFCACCTTCAC 2180
QY	an a	uMetGluArgLeuArgLysAlaGlnGluValCysGlnGluLeuAlaLysLy 166
qq .	2181	ratggatgagctcaaacaggccttcgaaatctacaatgcggacatcgcgaaggctgataa 2240
Οy	166	sGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyrSerAsnAsnGluTy 186
QQ	2241	AAAGTACACCCAGTACAATATCCCAGCTGCCTATGCCACAATGTTGACCAACAAGGATAG 2300
Οy	186	rPheLeulleValTyrAspValPheLySAspValArgMetValPheAlaProPr 204
QQ	2301	IATCACTCGTGTTTACTACGGGGACCTCTTTACCGACGATGGCCAATACATGGCTGAAAA 2360
Qy		OSer
Dp	2361	III ATCACCGTACTATAATGCCATCGATGCCCTGCTCCGTGCTCGCATCAAATATGTAGCAGG 2420
δλ	206	Serva 207
QQ	2421	Ĕ
Qy	207	lGlyLysPheGlyGlyAspThrAspAsnTrpMetTrp
QQ	2481	
QY	221	9HisThrGlyAspPheSerValPheArg-ValTyrAlaGlyAlaAspAsnArg 238
QQ	2537 (	GAATGCTGGTCCTTACAGCCAACCGTCCAGATATGAAGTTGGGAGCTAATGATGTCGG 2596
QY	239	ProAlaGluTyrSerLysAspAsnLysProTyrLysProVàlTyrPheAlaAla- 256
QQ	2597	TAGTCAATATGGGAGCTGCCCACAAAATCAGGCTTACCGTCCATTGCTTCTCAGCAAAT 2656
Qy	257	V 257
Dp	2657	CGACAGGTCTTGCGACCTACCTCAAGGATTCTGATGTACCAGCTGGATTGGTTCGCTATA 2716
Oy	257	alSerMetGlnGlyTyrLysAlaAspAspTyrAlaMetThrIleG 272
qq	2717	CGGACAATCAAGGGAACTTGACCTTCACGGCAGATGATATTGCTGGTCATTCAACCGTTG 2776
Qy	272	Ţ.
QQ	2777	AAGTITCAGGTTAATITGGCAGTITGGGTGCCAGTGGGTGCCTCAGAAA 2824
QY	292	snGluAsnAsnProArglleGluValArgGlyIleLysGlnGlyIleTrpLysG 310
qq	2825	ACCAAGATGCCCGAACCAAGGCTTCGAGCACCAAGAAGGGTGAGCAGGTCTTTGAAT 2881
Oy	310	lualametSeralaaspGlnalaThrang
QQ	2882	.::
δŏ	320	leLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysA 335 
QQ	2942	TTAAGACACCAAGTCAGTACACCAACGTGTTATTGCTCAAAATGCCAAACTCTTCAAA- 3000

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LeuArgAspGlyPheValSerArgThr 114
|||||||
CCTGCGCGATGGTTGCTCGCGCGT--- 4023615
                                                                                                                                                                                                                                                                                                                                                                                    VallysTyrLeuArgLysIleValLys 134
||| :::::||| :::
CGTCGCGTTTATCCGCAACGTGACCGAC 4023579
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CGCCACGGGCATATCACCCAGATGATC 4023420
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IleThrAspGluMetGluArgLeuArg 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysGluAsnAlaAspGluAsnGlnLeu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /alTyrAlaGlyAlaAspAsnArgPro 239
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RAIN ANALYSIS IN MYCOBACTERIUM
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	Db 4022669GGGGCCTTGCGAAGCGCTACCGCGATTCGGCGATGATGGQG CGTTGCGAAGCGTACCGCGATTCATGTGTGTGTGTGTGTG
259	402
274ProGlySerThrAspArgTyrLeuThrSerTrpGlyValGlu-AspArgIleGl 291	4022594
291 uAsnGluAsnAsnProArg1leGluValArgGlyIleLySGlnGlyIleTrpLySGluAl 311	Oy 619 -PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGInLeuHisIleAl 
m 13	Qy 638 uSerAsnAspIleThrGlyGlyAsnSerGlySerProValPheAs
402310	Oy 656 nGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGl
345 gLeuAspValIleGlyArgLysArgAlaGluGluArgAlaPheAl 360 :::	Qy 675 eGluPheGluProAspLeuGlnArg 683 :::         .
360 aSeralaValry 372 	RESULT 10 US-08-961-527-134 ; Sequence 134, Application US/08961527 ; Patent No. 6420135
372 rGlyAspValLeuSer	; GENERAL INFORMATION: ; APPLICANT: Charles Kunsch ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotid ; NUMBER OF SEQUENCES: 391
383 rLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGl 403   1   1   1   1   1   1   1   1   1	CORRESPONDENCE ADDRESS:  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
403 yThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHi 423	STATE: Maryland COUNTRY: USA TIP: 20850
4022877	<b>555</b>
4022876 4022844 4022876	
:: GTGGGCGCCGTCTGCCCCGG	FILING DATE: CLASSIFICATION: 424 FIRIDA APPLICATION DATA:
407 and property of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file of the file o	* APFLICATION NUMBER:
yrAlaAspPheValPheAspLysSerValValProTyrSerAspLysPheHisAl 4	; NAME: Brookes, A. Anders ; REGISTRATION NUMBER: 31,373 ; REFERENCE/DOCKET NUMBER: PB340P1
4022/78	; TELECOMMUNICATION: ; TELEPHONE: (301) 309-8504 ; TELEPAX: (301) 309-8512 ; INFORMATION FOR SEQ ID NO: 134:
uSerLysSerValIleAlaAlaAlaArgAlaIleG ::::	: LENGTH: 1265 base pairs : TYPE: nucleic acid : STRANDEDNESS: double : TOPOLOGY: linear
539 nAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPr 559 :::	Length:
559 oGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579	Score: 110.50 Matches: 132 Percent Similarity: 35.47% Conservative: 100 Best Local Similarity: 20.18% Mismatches: 246

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eAspLysAs 656
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|CCGAC---- 4022439
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GTGGTGACAC 4022398
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                                                                                                               4022490
                                                                         CCAGGCTGA 4022536
                                    4022595
-GGCATCCT 4022623
                                                      AspLeu-- 618
                                                                                            AlaPheLe 638
                   GlyvalLe 599
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Sun May 25 15:40:29 2003

		141	867	161	921	181	981	201	993	221	1029	. 539	1062	251	1122	269	1179	289	1233	298	1293	318	1350	331	1410	351	1467	371	1521	390	1581	410	
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176 30	-12665)	svalThrAspL		gLysAlaGlnG:	.GAACG	uCysIleValG	ACTGATGATGG	eLysAspValA		rAspAsnTrpM	ATCTTCT	yAlaAspAsnA	ACTA		AGAAAAGGTAG	rLysAlaAspA	AAAAGAAGAAGA	rSerTrpGlyV	ACTTGAAATTG	-AsnGluAsnA	GAAAGCTAACG	aMetSerAlaA	GAGTAAACAAG	-TyrAlaSerLysTyrAlaGlnSerAlaAsn	AGAAGAAGCTA	.aArgLeuAspV  :::	AAAACGAGGAG	gLysAsnGlyL	-GCGAAGTCTTCAGATTCTAGCGTA	rLysGluGlyA	AAAAAAGGTAG	yThrGluValV	
Indels: . Gaps:	7	Ly	 SAGCTATGCAAA	tGluArgLeuAr	SAACAACATTAA	pGluAsnGlnLe	CCAACTACAGAT	lTyrAspValPh		eGlyGlyAspTh	TGAAAAGGACTC	gValTyrAlaGl		OTyrLysPro	SACAGAACCAGG	rMetGlnGlyTy	AGCCAAGGATCA	pArgTyrLeuTh	CAAAACGCTTGA		ACTAGTAAAAGT	eTrpLysGluAl	AGCGGAAGTTG?	TyrAlaSe	TGAAGAAGCAGA	nArgGlyLeuAl	AAAGGGGCGGG	aAspTrpIleAr 	rgargc	uLysAlaTy 	CTGAAACCAGA	rLeuPheGlyGl	
2.978	x US-08-961-	Ileval		ThrAspGluMet	GTTAACGAGTTC	GluAsnAlaAsp :::	ACCTCAGAAAG(	PheLeuIleVa		ValGlyLysPhe	GTGTCTAAGTT	SerValPheArg		AspAsnLysPro	CCAAACAAGCC	ValTyrPheAlaAlaVaiSerMetGlnGlyTyrLysAlaAspAspTyrAlaMet	  GCTGAGAAAAA	GlySerThrAsp	ACCATT		GCGGAGCTTGA	LysGlnGlyIle	AAGCAAGCAGA		AAGACAGATCG	·IleGlyMetAsr 	GGTAAACC	ArgAlaPheAla :::	AAAAAAGAAAA	SerSerLeuGl	CCAAGCCCATC	TeuSerGluTh:	
CI 4	-2 (1-712)	sTyrLeuArgLys	:::   :::::	GlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGln	TACTGTAGCTCTA	GluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr	aaaatagttgaatcaacctcagaaagccaactacagatactgatgatggagagtcgatca	SerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPhe :::	AAAGTAGATGAA	AlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProAr		HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgPro	TCAAGTTCAGACTCTTCC	AlaGluTyrSerLysAspAsnLysProTyrLysPro	AGATACAGCGAAG	:	AAGAAGGTTGAAGAAGAAAAAAAGCCAAGGATCAAAAAGAAGAAGAAGGATCGTCGT-	ThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArg	:	IleGlu	GTGGAAGTTAAAAAAGCGGAGCTTGAACTAGTAAAAGTGAAAGGTAACGAACCTCGAGAC	GluValArgGlyIleLySGlnGlyIleTrpLySGluAlaMetSerAlaAspGlnAlaThr	GAGCAAAAAATTAAGCAAGCAGAAGCGGAAGTTGAGAGTAAACAAGCTGAGGCTACA	ArgileLys	AGGTTAAAAAAAATCAAGACAGATCGTGAAGAAGAGCAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	TyrTrpLysAsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArg	TGCTAAAGAGCAA	LysArgAlaGluGluhrgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaVal	AGCAACACCTGAT	TyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAlaLysAlaAsn	GGTGAAGAAACTCTTCCAAGCCCATCCTGAAACCAGAAAAAAAA	ArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValValArgPheAla ::::::::::::::::::::::::::::::::::::	
Match:	-008-355	127 LY	808 GA	142 G1	868 AT		922 AA	182 Se	982 AA	202 Al	466	222 Hi	1030 TC	240 AL	1063 TC	252	1123 AA	270 Th	1180	290 Il	1234 GT	299 G1	1294 GA	319 Ar	1351 AG		1411 GA				1522 GG	391 Ar	
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2263 TACTATCTAAACGCTAATGGTTCAATGGCAACAGGATGGCTCCAAAACAATGGTTCATGG 2322
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                                        1702 AAAAAAGCGGAGCTTGAACTAGTAAAAGAGGAAGCTAAGGAA-----CCTCGAAACGAG 1755
                                                                                                                                                                                                            1816 ----------GAAAAATCAAGACAGATCGTAAAAAGCAGAA 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 ArgGluMetTyrProGlyArg....-AlaLeuProSerAspAlaAsnPheThr 570
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423 HisAlaGlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAsp 442
                                                                                   443 ArgLysValLeuProAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeu 462
                                                                                                                                                                      463 ProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyrAla 482
                                                                                                                                                                                                                                                         483 AspPheValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLys 502
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                                                                                                                                                                                                                                                                                                                                                                                                                               523 LysSerValIleAla-------AlaAlaArgAlaIleGlnAlaAspAlaMet 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 TyrHisThrThrGlyLys-----GlyValLeuGluLysGlnAspProLysSerAsp 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538 AlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhe-----PheAlaGlyLeu
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TILLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09134078 Patent No. 6368844 GENERAL INFORMATION:
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; ADDRESSEE: Gray Cary Ware & Freidenrich LLP : STREET: 4365 Executive Drive. Suite 1600	Oy	182 rAsnAsnGluTyrPheLeuIleV
CITY: San Diego	qu	450 CGATGGAGAGCTCGGAGCCG
COUNTRY	Qy	202 aProProSerSer
COMPUTER	qα	507 CCCGTTTCTAAGTGGGTAAAGG
COMPUTER:	ó	216
	qa	567 CCAGGTTGTGAACATGGAATACA
APPLICATION FILING DATE	δλ	225 pPheSerValPheArgValT
	qa	627 TCTCGACGGAGTGTTCTACCTCT
APPLICATION N	Qy	244 sAspAsnLysProTyrLysProV
	qa	672 GATCAGAACAACCGTCGATCCT-
AT	QY	264 aAspAspTyrAlaMetThrIleG
REGISTRATION UNBER: 38,3	qa	717 CAACCAAGAGAGCGCCGTTGTGA
; TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	Qy	284 pGlyValGluAspArgIleGluA
TELEFAX: 8	qa	768 GGAAA
SEQUENCE CHARACTERISTICS:	Qy	304 sGlnGlyileTrpLysGluAlaM
່ບ	qa	:
TOPOLOGY: linear	Qy	320 eLysTyrAlaSerLysTyrA
MOLECULE TYPE FEATURE:	qa	:    864 AAAAAACAAAGGCCTCTATCTCG
NAME/KEY LOCATION	Qy	aArg
US-U9-134-078-14	q <sub>0</sub>	:        :::
ent Scores: 0.0475 Length:	Qy	359 eAlaAspTrp
110.00 Matches: 33.12% Conservative:	qq	::: 984 CTTTGATTTCTACAGGCGACG
LY: 19:738 2.968 4	ογ	373
-10-008-355-2 (1-712) x HS-09-134-078-14 (1-2319)	qq	1043 GTTACGATCCTTACCTGTTCATG
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/* INTELL FALSE FOR THE THE THE THE THE THE THE THE THE THE	qa	1103 CACACACGAGAATCAGAGAAGTC
laspHisaspTvrLeuargaspGlvPheVa	Qy	402 yGlyThrGluvalv
228 GAAAAAGAAAGTCTTCAAGGTTACTGTTGAC	QQ	1163 GTGTGATTATGGACATGGTGTTC
GlvLeuSer	Qy	419 nProAspAlaHisAlaGlyIleL
262	qa	1223 ATCAGACGGTGCCGTACTACTTC
136VallveTvrLendrdIveTleVallweValThraenIveValCiveI	Qy	434
309 CATAGACGTACCTACGTCAGAATCGTCCTTTCTGAATCCCTGAAGAAGACCT	qa	1283 GCGGATGTGGTAACGTCATCGCA
142 nLeuLysGlylleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGl	Qy	442 pArgLysValLeuProAlaMetL
	qa	
Oy 162 uLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyrSe 182	oy e	462 euProAspIlePheLysAsnVal :::::
Db 429 G	- A	

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GGAACTCGATAAAGATTT-CGAGAAGTACTACAACTGGG 1042
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rgrggaactcggtgttacacacgttcatatacttccttr 983
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                                                                      -----ValGlyLysPheGlyGlyAspThrAsp---- 215
                                                                                           -----AsnTrpMetTrpProArgHisThr---GlyAs 225
                                                                                                                                                                            AAGGGAAACGGGGTCTGGGAAGCGGTTGTTGAAGGCGA 626
                                                                                                                                                                                                                  TyralaGlyAlaAspAsnArgProAlaGluTyrSerLy 244
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183 AsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPheAla 202
                                                    ThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyr 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly 302
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IMMUNOGLOBULIN BINDING PROTEINS DERIVED FROM L PROTEIN AND THEIR USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /codon_start= 103
OTHER INFORMATION: /product= "immature protein L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OD: experimental /codon_start= 280 /product= "mature protein L" /evidence= EXPERIMENTAL
                                                                                     ANDKESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Peptostreptococcus asaccharolyticus
STRAIN: 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
LOCATION: 280.:3183
LOCATION: S00.:3183
OTHER INFORMATION: /codon_start= 280
OTHER INFORMATION: /product= "mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-008-355-2 (1-712) x US-08-446-137B-1 (1-3279)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIETCATION: 314
ATTONNEY, AGGENT INFORMATION:
NAME: MCMASIERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMNUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3279 base pairs
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: Laurence, Oliver S. APPLICANT: Duggleby, Clive J. TITLE OF INVENTION: IMMUNGGLOB! TITLE OF INVENTION: FROM L PRO'N UMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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20.59%
2.96%
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208..279
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STRANDEDNESS: double
                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and I
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                               STATE: Washington
COUNTRY: USA
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LOCATION: 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                       98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-446-137B-1
                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958 AAATACAAAGGGATGGATAGATTTGATTGTAGAAATCAGCTTGTTAAAGACTTAAAAGAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1078 GGTGCAATAGTAGAACCTTATTTGTCTACACAATGGTTTGTAAAAATGAAACCTTTGGCA 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1302 TGAAGTCTTTGTTGGTGAAGAAGCACCTGAAGACATCGAGAATTGGATACAAGATGAGA 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1422 TACAAATGCTGATGTTTTAAACGTTATTATCCGACAAATGCATTAGTTACTGGTTATGA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614 nIleLeuAspLeuPheArgThrLys-AsnTyrGlyArgTyrAlaGlu---AsnGlyGlnL 633
                                                                                                                                                                                                                                                                                                                                                                      880 TITGAAATIGGICAAAGACATCAATIAGAAAATATIATAGTCATGGATGAATATGGTAAG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595 yLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln---GluAs 614
                                                                                              425 GlylleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLys 444
                                                                                                                                                                           445 ValLeuProAlaMetLeuAspIleValArgArgArgIlePro-----AlaAspLysLeu 462
                                                                                                                                                                                                    465
                                                                                                                                                                                                                                                                                                                                        466 ------AspLysLysPheLysAsnValIle-----AspLysLysPheLys 475
                                                                                                                                                                                                                                                                                                                                                                                                                      476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                              940 ATGAACGATAAA-----GCTGAT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 LysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIle---Glu 514
                405 GluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAla 424
                                                                                                                         820 GTTGATATTGAATTTGGTTCAGGAGCAATGAAAGTTACTCCGGCACATGATCCTAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515 LysAspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 rGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542 -----AlaIleGlu------LysGlyLysArgLeuPheAlaGlyLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 GluMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMet-ArgMetSerTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1482 TATCATTTTCTTCTGGGTAGCCCGTATGATTTTCCAAGGATTAGAATTTACTG 1534
                                                          -------GCTATTGTTGTAAATCCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 hrGlyGlyAsnSerGlySerProVal---PheAspLysAsnGlyArgLeuIle 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 AspalaMetAlaAsnAlaTyr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   633 euHisIleAlaPheLeuSerAsnAsnAspIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08446137B Patent No. 6162903
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Atkinson, Anthony
Murphy, Jonathan I
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APPLICANT:
APPLICANT:
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۸.	29	TrpLeuLeuAsnGluLeuAsnGlnGluAsnLeuAspArgMetArgGluLeuGlyPheThr 48	
Ω	1861		
<u>ہ</u> م	1921	LeuProLeuAspSerLeuTyrSerPheAspLysProSerIleAlaAsnAlaValValIle 68	
>-	69	AsnHis 88	
Q	1963		
>-	88	HisCysGlyTyrGlyAlaIleGlnSerGlnSerThrValAspHisAspTyrLeuArgAsp 108	
۵	2002	CACGCTGGATTAAAAGAT 2034	
۲. ۰	109	GlyPheValSerArgThrMetGlyGluGluLeuProlleProGlyLeuSerValLysTyr 128	
, a	2095	LEUALGLYSILEVALLYSVAITINFASDLYSVAIGIUGLYGIN	
ı >	145	GlylleThrAspGluMetGluAraLeuArgLysAlaGluGluValCysGln	•
۹	2155	ATTGAAGTTGCAGAGGAAGAACCAGGTGAAGACACTCCAGAAGTTCAAGAAGGTTAC 2214	
>-	162		
۵	2215		
λ.	176	IleValGluProPheTyrSerAsnAsnGluTyrPheLeuIle189	
۵	2272		
>	190	ValTyrAspValPheLysAspValArgMetValPheAlaProProSerSerValGly 208	
Ω	2311		
. >-	209	LysPheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSer 227	
Q	2371		
>-	228	ValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLys 247	
q	2425	GCAATCAAAGAATTAAAAGAAGCAGGAATCAGTTCTGAC 2463	
>-	248	ProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyr 267	
Q	2464		
>	268	AlaMetThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGlu 287	
۵	2482		
>-	288	Asparg11eGluAsnGlu	
Q	2512	GCGTTAAAGAACGAAATCTTAAAAGCACACGCTGAAAACCAGGCGAAAACCCAGGA 2568	
>-	298	IleGluVal 310	
Δ	2569	ATCACAATTGATGATGGTTATTAAAGAATGCTAAAGAGCTGCAATCAAGAATTAAAA 2628	
>-	311	AlaMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGln 328	
Q	2629	GAAGCAGGAATCACTGTATTCAACTTAATCAACAAAAACAAAAAACAGTAGAA 2688	
>-	329	329 SerAlaAsnTyrTrpLysAsnSerIle	
Q	2689	GGCGTAGAATCATTAAAGAACGAAATCTTAAAAGCACACGCTGAAAAACCAGGCGAAAAC 2748	

```
RESULT 14
US-08-961-527-139/c

### Sequence 139, Application US/08961527

### Sequence 139, Application US/08961527

### Sequence 139, Application US/08961527

### Sequence 139, Application US/08961527

### Sequence 139, Application US/08961527

### TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

### TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

### CORRESPONDENCE ADDRESS:

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### CORRESPONDEN
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                                                                                              --ACAATTGAT 2766
                                                                                                                                                                                                                                       2902 TTAAAGGCTCATAAAAAGATGAAGAACCAGGTAAAAAACCAGGTGAAGACAAAAACCA 2961
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                                                                                                                                                                                   361 AspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGlu 380
                                                                                                                                                                                                                                                                                                                                                                  381 LysAlaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeu 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheGlyGlyThrGluValValArgPheAlaGlnPheAlaAsnAlaLeu------ 416
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341 ArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArgAlaPheAla 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 -----AlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 LysAspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArg 454
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COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP VECTRA 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NATA:
CLASSIFICATION A24
PRIOR APPLICATION A24
PRIOR APPLICATION A34.
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brookes, A. Anders
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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                         2749 CCAGGAATC-----
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	TELECOI TELECOI TELEI TELEI INFORMAT: SEQUENC LENGT TYPE TYPE TYPE TYPE TOPOI	RENCE/DOCKE MUNICATION PHONE: (30 PHONE: (301) CON FOR SEC CE CHARACTE FH: 15363 In nucleic VDEDNESS: COGY: line	139:	P1			
Alignm Pred. Score: Percer Best I Query	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match:	ores: larity: imilarity:	1.14 109.00 29.03% 17.39% 4	Length: Matches: Conservative: Mismatches: Indels: Gaps:	15363 124 222 284 30		
JS-10	10-008-	355-2 (1-712)	x US-08-961-527	-139 (1-15363)			
ογ	210	PheGlyGlyAsp:::    	TGTGGGTTGGGGGAA	Thraspas     ::  AACAGCAACCGCTTC	PheGlyGlyAsp	221 10524	
2y Db	222 10523	HisThrGlyAspP} :: GACAACGCTGGCTF	HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAsp- 	TyrAlaGlyAlaAs  :::         cTGGACAGGTACGA	AsnArgPro         ATATTGGTGAACCT	239	
ά	240	AlaGluTyrSerLysAspAsnLys	;	-ProTyrLysProValTyrPheAlaAl	aValSer	258	
g	10463	ACACCATGGCACA	:::      CCAAAATCAAACTCC	  TGTTAAGAGCTCTTA		10404	
Oy Dp	259	MetGlnGlyTyrL)     ACAGCCGGCATTCC	/sAlaAspAspTyrAl    ::: :AAAACATGACTTCTA	.aMetThrIleGlyPh ::: .TCTCTACCAAAGCCA	MetGlnGlyTyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAsp 	278 10344	
ογ	279	Arg ::: AAGAAACCGATGG7	ArgTyrLeuThrSerTrpGlyValGluAsparg ::: AAGAAACCGATGGTACACCTTCTTCCTCACTGGAACTGGGAAACAAAGAATTAGCAT	-TyrLeuThrSerTrpGlyValGluAspArg 	; 8	289	
οy	290				nPro	296	
Op	10283	AAAGTAGCTGACTC	CAGAAGGTAAGATTCC	AGTTCGTGCTTATTC	AAAGTAGCTGACTCAGAAGGTAAGATTCCAGTTCGTGCTTATTCGAATGCTTCTAGTGTA	10224	
ογ	297 10223	ArgileGluValAı ::: :: GAATTGTTCTTGA	ArgileGluValArgGlyIleLysGlnGlyIle :: ::	.yile  ::: ;rcttaAGACTTTCAP	ArgileGluValArgGlyIleLysGlnGlyIle	307 10164	
ογ	308				ρ	309	
QQ	10163	GATGGGCGGACTT	ACCAAGAAGGTGCAAA	NTGCTAATGAACTTT	TT	10104	
οy	310		GluAlaMe	GluAlaMetSerAlaAspGlnAla-	[a	317	
Dp	10103	GCCTATCAACCAG	::     : STACCTTGGAAGCAAT	TGCTCGTGATGAATC	GCCTATCAACCAGGTACCTTGGAAGCAATTGCTCGTGATGAAGTTGCTGGTGATCTGGCAAGGAAATTGCT	10044	
ΟŻ	318	ThrArgileLy	-ThrArgileLysTyrAlaSerLys			325	
Dρ	10043	CGAGATAAGATTAC	GACTGCTGGTAAGCC	AGCGGCAGTTCGTC1	CGAGATAAGATTACGACTGCTGGTAAGCCAGCGGCAGTTCGTCTTATTAAGGAAGACCAT	9984	
οy	326			TyrAlaG	-TyrAlaGlnSerAlaAsnTyrTrp	333	
g	9983	GCGATTGCAGCAGA	<b>YTGGAAAAGACTTGAC</b>	TTACATCTACTATG	GCGATTGCAGCAGAATGGAAAAGACTTGACTTACATCTÀCTATGAAATTGTTGACAGCCAG	9924	
δ	334	LysAsnSerIleG	LysAsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGly	euAlaArgLeuAspVa	alilegly	350	
g	9923	GGGAATGTGGTTCC	CAACTGCTAATAATĊT	GGTTCGCTTCCAATT	GCATGGCCAAGGTCAA	9864	
οχ	351		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ArgLysArgAl	-ArgLysArgAlaGluGluArgAlaPhe	359	

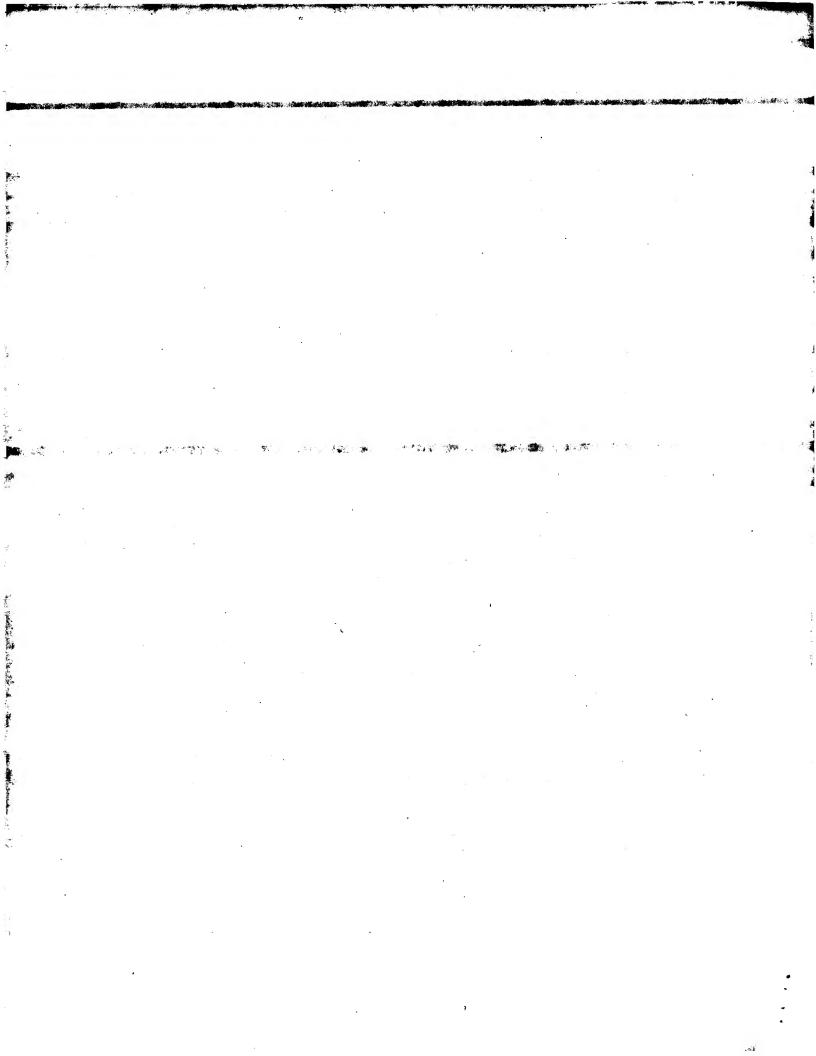
a a	DD 9863 CTGGTCGGTGTAGATAACGGAGAACAAGCCAGCCGT	AACGCTATAAGGCGCAAGCAGAT 9804
٥y	360 AlaAspTrpileArgLysAsnGlyLy	
QQ	9803 GGTTCTTGGATTCGTAAAGCATTAATGGTA	AAGGTGTTGCCATTGTCAAATCAACTGAA 9744
ōλ	370A1	alLeuSerSerLeuGluLysAla 382
qq	9743 CAAGCAGGAAATTCACCCTGAC	TGCCCACTCTGATCTTGAATCGAACCAAGTCACT 9684
δŏ	38	erGluThrLeuPheGly 402
qq ^0	9683 GTCTTTACTGGTAAGAAGAAGACGACAAGA(A)	1 1
g 연		ACCACT 95
οy	Oy 407 ValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHiSAlaGlyIl	snProAspAlaHisAlaGlyIle 426
QQ	9581 GTTCCGTTT	. ₹
٥y	427	yrLysAspTyr 43
qq	9521 GATGTGAGCAAGCCTGGTATT	,
ολ	438 LeuProSerLeuAspArgLys	ValLeuProAlaMetLeuAspIleValArgArgArgIle 457
qq	9464 GAAGCTCGTGTAGAAGTGATT	TACCAGTIGIGAAACGTATTGCT 9405
Qy	458 ProAlaAspLysLeuProAspIlePheLysAsnV	/alileAspLysLysPheLysGlyAsp 477
qq	9404	TTŢĠ
Οy	Qy 478 ThrLysLysTyrAlaAspPheValPheAspLysSerValVal	alValProTyrSerAspLys 496
qa	9344 GTTGAAGAGTATGAA	AGATTGCCGAAGAAGATAAAGCT 9294
Qγ	ζу 497	
qq	Db 9293 AAGTTAGCAATTCCAGGTTCTCGTATTCAAGCGACCGGTTATTAGAAGGTC	GTTATTTAGAAGGTCAACCAATT 9234
δλ	Qy 498 HisalaMetLeuLysSerMetAspLysGluLysPhealaLysAlalleG	luLy
qq	9233	
Qy	518	526
qq	9182 ACTGTAACGGTTGGTGG	NCTAGTCAAAAACCAATGCAATAC 9123
Qy	Qy 527	AlaAla 528
qq	Db 9122 CGCACTCTTGCTTATGGAGCTAAGTTGCCAGAAGTCACAGCAAGTGCT	CAGCAAGTGCTAAAAATGCAGCT 9063
Οy	529 Ala	539
qa	9062 GTTACAG	ATGCGTGCGAGCATCTTTATTCAG 9006
Qy	540	_
QQ	9005 CCTAAAGAIGGIGGCCCTCTTCAAACCTAIGCAATT	CAATTCCTTGAAGAAGCGCCAAAA 8946
Οy	549 LeuPhePheAlaGlyLeuAr	gGluMetTyrProGlyArgAlaLeuProSerAsp 566
QQ	8945 ATTGCTCACTTGAGCTTG	SACAGICICAAAGAAGACCAAACT 8889
Οy	567 AlaAsnPheThrWetArgMetSerTyrGlySerIl	eLysGlyTyrGluProGlnAspGly 586
qa	8888 GTCAAATTGTCGGTTCGAGCT	CAAGATGGA 8853
Ολ	587 AlaTrp	TyrAsnTyrHisThrThrGlyLysGlyValLeu 599
QΩ	8852 ACGCAAGCTGTATTACCAGC	:::    :::     CTACAAGTGGTGAAGGG 8799

Oy Oy	600 GluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPhe 619  8798
Oy Dp	AlaPheLeuSerAsnAsp1leThrGlyGlyAsnSerGlySerProValPheAspLys :::    :::   :::
Qy Dp	656 AsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIle 675 :::    ::: 8651AATGTAGTGACAGATTTG 8634
Qy Dp	676 GluPheGluProAspLeuGlnArgThrIleSerValAsp 688 
RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-	15 103- ence nnt Nnt LICA LICA LICA LE CO LE CO LE CO LE CO LE CO LE CO LICA NEW TWAN
10 - FI	TIPE. DNA PREATURE: OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, L, c or g
Aligni Pred. Score Percel Best Query DB:	Alignment Scores: 7.14e+03 Length: 4403765  Pred. No.: 7.14e+03 Length: 4403765  Score: 109.00 Matches: 136  Score: 29.34 Conservative: 60  Best Local Similarity: 20.364 Mismatches: 189  Query Match: 2.934 Indels: 34  BBs: Conservative: 60  A Gaps: 60
US-10	0-008-355-2 (1-712) x US-09-103-840A-2 (1-4403765)
Oy Db 4	75 GlylleThrValSerAspGlnGlyLeullePheThrAsnHisHisCysGlyTyrGlyAla 94
Oy Db 4	95 IleGinSerGinSerThrValAspHisAspTyrLeuArgAspGlyPheValSerArgThr 114 :::::
Oy Db 4	115 MetGlyGluGluLeuProlleProGlyLeuSerValLysTyrLeuArgLysIleValLys 134 115 MetGlyGluGluLeuProlleProGlyLeuSerValLysTyrLeuArgLysIleValLys 134 1015695
0y 0b 4	135 ValThrAspLysValGluGlyGlnLeuLysGlyIleThrAspGluMetGluArgLeuArg 154 :::       :: 4015659 ATCGAAGACAAGATC

οy	155 LysalaGlnGluValCysGlnGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeu 174
QQ	4015644
QY	175 CyslleValGluProPheTyrSerAsnAsnGluTyrPheLeuIleVal 190
QY	191 TyraspvalPheLysaspvalargMetValPheAlaProProSerSerValGlyLysPhe 210
QV	211 GlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPhe 229 4015533
Qγ	230
QQ	4015500 GAGATGATCGAGCCCTGATCCAGGCCGCCACGCTGATACCGGTGGCGTGAC 4015447
QY Db	240 AlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSer 258 111111111111111111111111111111111111
o Y	259MetGlnGlyTyrLysalaAspAspTyrAlaMetThrIleGlyPhe 273 3::    ::
67	274ProGlySerThrAspArgTyrLeuThrSerTrpGlyValGlu-AspArgIleGl 291
Dp	4015362 GCTGCCGGCAAGCGGGACCAGCGCGACTTCACTTGTGGAAGGGCGAAAAGCCGGGTG 4015305
QY Db	291 uAsnGluAsnAsnProArg1leGluValArgGlyIleLysGlnGlyIleTrpLysGluAl 311
δ, d	311 aMetSerAlaAspGlnAlaThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAs 331
δλ	331 nTyrTrp
qq	
Oy Dp	345 gLeu
. Qy	360 aSeralaValTy 372
οy	372 rGlyAspValLeuSer
QQ	4015066 GGCCACGTGTTGTCCATGCCGGCGATGTTGCAGCGGGTGCGGCTGAGCTGCGTTA 4015007
Qy	383 rLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGl 403   1
Οy	403 yThrGluValValArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHi 423
· Dp	4014958 4014958
ογ	423 sAlaGlyIleLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspAr 443
යි	7
oy Op	443 gLysvalLeuProAlaMetLeuAspIleValArgArgArgIle
Οy	479

		<pre>Qy 656 nGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGl 676</pre>	Db 4014570GCCGACGAGATCCGGGGTCGGCTGAAGAGGCGGCATCGAGGTCACCGAC 4014520	4014859 499 4014859 519 4014824 539 4014787 559 4014751 579 4014571 638 4014520 676	Db 4014871 CGATCCGACCCA.  9y 479 sLysTyralaAspPheValPheAspLysSerValValPrOTyrSerAspLysPheHisAl  Db 4014859
Db 4014570GCCGACGAGTCCGGGGTCGGCTGAAGAGCGGCATCGAGGTCACCACA 4014520  Qy 656 nGlyArgLeulleGlyLeualaPheAspGlyAsnTrpGlualaMetSerGlyAspIleGl 676  Db 4014519	Db 4014570GCGGACGAGATCCGGGGTCGGCTGAAGAGCGGCTCGAGGTCACGAC 4014520  Qy 656 nGlyargLeulleGlyLeualaPheAspGlyAsnTrpGlualaMetSerGlyAspIleGl 676	Db 4014570GCGACGAGATCGGGGTGGGCTGAAGAGGGGGGGCTCGAGGTCACGAG 4014520		656	638 uSerAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLySAs
638 uSerAsn 4014570GC 656 nGlyArg 4014519	Oy 638 uSerAsnAsnAsplleThrGlyGlyAsnSerGlySerProValPheAspLysAs 656	Oy 638 uSerAsnAsnAsp1leThrGlyGlyAsnSerGlySerProvalPheAspLysAs 656 i::::	Oy 638 uSerAsnAspleThrGlyGlyAsnSerGlySerProValPheAspLysAs 656	4014571	> 4014616 ACTACAGAATCGGGAAAAAGGCCCGCGAGCAGCGCGCAACTGGGCGCCTC
Db 4014616 ACTACAGAATCGGGAAAAGGCCCGGGAGCAGCGGCGCTC	Db 4014616 ACTACAGAATCGGGAAAAGGCCCGCGAGCAGCGCGCTC	Db 4014616 ACTACAGAATCGGGAAAAGGCCCGGGGGGGGGCCCC	Db 4014616 ACTACAGAATCGGGAAAAGGCCGCGGGGAGCGCGCGCTC 4014571  Oy 638 uSerAsnAsnAsnAsplleThrGlyGlyAsnScrProvalPheAspLysAs 656	638	619 -PheArgThrLysAsnTyrGlyArgTyrAlagluAsnGlyGlnLeuHisIleAlaPheLe
0y 619 -PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLe 638  11	Oy 619 -PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLe 638	Oy 619 -PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHislleAlaPheLe 638  1:::::::::::::::::::::::::::::::::::	Oy 619 -PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHislleAlaPheLe 638  1:	4014617	4014675 -GAATCCCGAGACGAAACCTCGGCAGCGCTGGCCGCCGTCGATGTGCTGGTCCAGGCTGA
Db 4014675 -GAATCCCGGAGACGAAACTCGGCAGCGCTGGCCGCTCGATCCTGGTCCAGGCTGA 4014617  Qy 619 -PheArgThrLysAsnTyrGlyAAgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLe 638  iii	Db 4014675 -GAATCCCGAGACGAAACCTCGGCAGCCCGCCGTCGATCTCCTCTCTCT	Db 4014675 -GAATCCCGAGACGAAACTCGGCAGCGCTGGCCGCTCGATCCTGGTCCAGGCTGA 4014617  Qy 619 -PheArgThrLysAsnTyrGlyAagTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLe 638  Db 4014516 ACTACAGAATCGGGAAAAGGCCGGGGGGCACACTGGGCGCTC	Db 4014675 -GAATCCCGAGACGAAACCTCGGCAGCCCTGGCCCGTCGATCTCTGTCCAGGCTGA 4014617  Qy 619 -PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLe 638  Db 4014616 ACTACAGAATCGGCAAAAGCCCGCGAGCAGCGCAACTGGCGCTC 4014571  Qy 638 uSerAsnAsnAsplleThrGlyGlyAsnSerGlySerProValPheAspLySAs 656	618	599 uGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu
Oy 599 uGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu- 618	Oy 599 uGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu- 618	Oy 599 uGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu 618	Oy 539 uGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu- 618	4014676	9 4014703 GGGCTGTGACCGCTCGACCAGCGCTGG
Db 4014703 GGCTGTGACCGCTCGACCAGCGCTGG	Db 4014703 GGCTGTGACCGCCTCGACCAGCGCTGG	Db 4014703 dGGCTGTGACCGCTCGACCAGCGCTGG	Db 4014703 ddccrdcrdcdccrdcdccrdcdccrdcdcrddd	599	579 sGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLe
0y 579 sGlyTyrGlubroGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLe 599	Oy 579 SGLYTYGLUPrOGINASPGLYALATrpTyrAsnTyrHisThrThrGlyLysGLyValle 599	0y 579 sGlyTyrGluProGlnAspClyAlaTrpTyrAsnTyrHisThrTdlyLysGlyValLe 599	Oy 579 SGLYTYGLUPrOGINASPCLYALATrpTyrAssnTyrHisThrThrGlyLysGLyValle 599	4014704	4014750GGGGCCTTGCGAAGCGCTAGCGCGATTCGGGCGATGATGGGCATCCT
Db 4014750GGGGCCTTGCGAGGCCTAGCGGCCGATTCGGGCGATGATGGGGATCCT 4014704  Qy 579 sGlyTyrGlubroGlnAspGlyAlaTrTyrAsnTyrHisThrThrGlyLysGlyValle 599  Db 4014703 GGGCTGTGACCGGCTGGCCGCTGG	Db 4014750GGGGCCTTGCGAAGCGCTATCGGGCGATCGTATGGGGTCCT 4014704  Qy 579 sGlyTyrGlubroclnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValle 599	Db 4014750GGGGCCTTGCGAAGCGCTACGGGCGATCCTGGCATCCT 4014704  Qy 579 sGlyTytGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLe 599  Db 4014703 GGGCTGTGACCGGCTGGCCTGGCTGGTGTGTGTGTGTGTG	Db 4014750GGGGCCTTGCGAGGCGATTCGGGCGATGATGGGGTCCT 4014704  Qy 579 SGlyTyrGlubrodlnAspGlyAlartpTyrAsnTyrHisThrThrGlyLysGlyValle 599  Db 4014703 GGGCTGTGACCGGCTGGCTGGCTGG	579	559 oGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy
0y 559 oGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579	0y 559 oGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579	0y 559 oGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579	Oy 559 oGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579	4014751	GAAGGCAACCGGGCACTCGATGCCGGGACCACGAC
Db 4014786	Db 4014786	Db 4014786	Db 4014786	559	
0y 539 nalaTyralaileGluLysGlyLysArgLeuPhephealaGlyLeuArgGluWetTyrPr 559  1111111111111111111111111111111111	0y 539 nalaryralailedluLysGlyLysArgLeuPhephealaGlyLeuArgGluWetTyrPr 559  11111	09 539 nalaTyralaileGluLysGlyLysArgLeuPhephealaGlyLeuArgGluMetTyrPr 559  :::	09 539 nalaTyralaileGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPr 559  :::	4014787	
Db 4014823 TCCGATCCCGACCCGAATTCACCACCTCCGGGCG	bb 4014823 TCCGATGCCGCTGCCGAATTCACCACGTGCGGCG	Db 4014823 TCCGATCCCGACCGAATTCACCACGTGCGGCG	Db 4014823 TCCGATCCGCTCGCGGATTCACCACGTGGGGCG	539	, 519 IGluLeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAs
0y 519 IGIULGUSERIYSSERVAILIEANAANAARANAANAARANAARANAARANAARANAARAN	0y 519 IGIULGUSERLYSSERVAILIEANAANAARANAANAARANAARANAARASANAARAS 539   ::::::	9y 519 IGIULeuSerLysSerValilealaAlaAlaArgAlaIleGINAlaAspAlaMetAlaAs 539	0y 519 IGIULEUSETLYSSErValIlealaAlaAlaArgAlaIleGINAlaAspAlaMetAlaAs 539	4014824	> 4014858
bb 4014858	bb 4014858	Db 4014858	Db 4014858	519	
Qy         499 aMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlava 519           Db 4014858         ::::     ::::::                Db 4014858         ::::      :::              Qy         519 IGluLeuSerLysSerValITeAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAs 539           Db 4014823         :::::	0y 499 ametLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaVa 519 4014858	Qy         499 aMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlava 519           Bb 4014858         :::      :::    :::               Ch 4014858         :::       :::               Ch 4014858	0y 499 ametLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlava 519  :::     ::: ::    ::     ::      ::	4014859	
Db 4014859	Db 4014859	Db 4014859	Db 4014859	499	
QY         479 SLySTyralaAspPheValPheAspLySSerValValProTyrSerAspLySPheHisal 499           Db         4014859           CY         499 aMetLeuLySSerMetAspLySGluLysPhaalaLysAlaIIeGluLysAspProAlaVa 519           CY         499 aMetLeuLySSerMetAspLySGluLysPhaalaLysAlaIIeGluLysAspProAlaVa 519           CY         519 IGULeuSerLySSerValILEAlaAlaAlaArgAlaIIeGluLysAspProAlaAs 539           CY         519 IGULeuSerLySSerValILEAlaARGALARGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	479 SLySTyralaAspPheValPheAspLysSerValValProTyrSerAspLysPheHisAl 499 bb 4014859	479 SLySTyralaAspPheValPheAspLysSerValValProTyrSerAspLysPheHisAl 499  499 AMELEULYSSERMELASPLYSGIULLysPheAlaLysAlaIleGluLysAspProAlaVa 519  519 1GluLeuSerLysSerWetAspLysGluLLysPheAlaLysAlaIleGluLysAspProAlaVa 519  519 1GluLeuSerLysSerValIleAlaAlaArgAlaIleGluLysAspProAlaVa 539  519 1GluLeuSerLysSerValIIleAlaAlaArgAlaIleGluLysAspProAlaNa 539  519 1GluLeuSerLysSerValIILeAlaAlaArgAlaIleGluLysAspProAlaNa 539  519 1GluLeuSerLysSerValIILeAlaAlaArgAlaIleGluLysAspProAlaNa 539  519 1GluLeuSerLysSerValIILeAlaAlaArgAlaIleGluLysAspAlaMetAlaAs 539  529 1GluLeuSerLysSerValIILeAlaAlaArgAlaArgAlaIleGluArgGluMetTyrPr 559  529 0GlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579  529 0GlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579  529 0GlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLy 579  529 0GlyArgAlaLeuProGlAASPGCGCATGGGCGCATGAGGCC	0y         479 sLysTyralaaspPheValPheAspLysSerValValProTyrSerAspLysPheHisal 499           0b         4014859         4014859         4014859           0b         4014859         4014859         4014859           0b         4014859         4014824         4014824           0b         4014858         4014824         4014824           0c         4014821         4014824         4014824           0c         4014823         4014824         4014824           0c         4014823         4014824         4014787           0c         4014823         4014787         4014787           0c         4014823         4014787         4014787           0c         4014823         4014787         4014787           0c         4014823         4014787         4014787           0c         4014786         4014787         4014787           0c         4014786         4014787         4014751           0c         4014786         4014776         4014776           0c         4014786         4014776         4014776           0c         4014786         4014776         4014776           0c         4014786         4014776         4014	4014859	

Search completed: May 23, 2003, 13:33:17 Job time: 4891.71 secs



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Sequence 171, App
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Sequence 197, App
Sequence 11, Appl
Sequence 14, Appl
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APPLICANT: Botempa, Jan S

APPLICANT: Banbula, Agnieszka

TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use

FILE REFERENCE: 23.00440101

CURRENT APPLICATION NUMBER: US/10/008,355

CURRENT APPLICATION NUMBER: US 60/246,827

PRIOR APPLICATION NUMBER: US 60/246,827

PRIOR APPLICATION NUMBER: US 60/246,827

NUMBER OF SEQ ID NOS: 26

SOFTWARRE: Patentin version 3.0

SEQ ID NO 1

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Patent No. US20020164759A1
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qq	721 GAMTACAGCAAGGACAATAAACCCTATAAGCCCGTTTACTTCGCTGCCGTATCCATGCAA 780	
oy Op	261 GlytyrLysAlaAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyr 280	, da
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٥٨	01 ArgGlyIleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThrArgIle 32	Oy . 10
QQ	1 CGCGGTATCAAGCAAGGCATCTGGAAGGAAGCCATGAGCGCAGATCAGGCTACCCGTATC 96	Οy
y e	321 LysTyrAlaSerLysTyrAlaGInSerAlaAsnTyrTrpLysAsnSerIleGIyMetAsn 340	Dp 3
c vo	41 ArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArgAlaPheAla 360	ογ

LysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLys AAGCTCCCCGATATATTCAAGAATGTAATCGACAAGAAATTCAAAGGCGACACGAAGAAG GlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAsp AspTrp11eArgLysAsnGlyLysSerAlaValTyrGlyAspValLeuSerSerLeuGlu LysalaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeu LeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGlu LeuSerLysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAla ThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsn AsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIle GlnCysProArgLeuIleGlnGluLeuLysLeuIle 712 

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991 GGTGCCCTTGTCAAAATCGAAAAGGTGTCCACAGTGTTGGTCACTCAGAACGTACAGGT 1050
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                                                                                                                                                                                         331 GAGTCTTTCTTGACGAAAGTCTGGGAATGGAAAGAC-------GAATATGCCACT 378
                                                                                                                                                                                                                                                                                           379 ACCATCAAGGAACAATGGGGCAAGATGGGGCTCTCTGTAGACTATTCTCGTGAGCGTTTC 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGACTTGATTGGTAAAAACGTCATCCTTCCA---ATCGCTAATAAACTCATCCCAATC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IleValArgArg 455
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GTTGGAGATGACGCAGGATCCTGAGTTTGGTACTGGTGTGGTGAAAATCACACCTGCC 834
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                                                                                                                                                                                                                                            ArgileLysTyrAla --- SerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIle 337
                                                                                                                                                                                                                                                                                                                                         338 GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg 357
                                                                                                                                                                                                                                                                                                                                                                                                                                      358 AlaPheAlaAspTrpIleArgLys------AsnGlyLysSerAlaValTyrGly 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595 GCCTTCTACCACATGAATTACATGCTGGAAGATGGTTCACGCGCCCTTGAAGTTGCTACA 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434
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  --ACCCTTTGGCTTCCTGGGATGGACCACGCAGGGATTGCCACT 270
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                                                  283 SerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGly
                                                                                                                                               -----IleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGlnAlaThr
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|GCGATTGCGGTTAATCCAGAA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGTTTTCAAGCCTTCAGGCGATCAAAAGGCTTAAGTTTTCAATCGTTATTCCACCA 135
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRASTSEQ FOR WINDOWS VERSION 4.0
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2101 CAGTGCCCCGTCTCATCCAAGAGCTGAAGTTGATC 2136
                                                                                            Sequence 9284, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W
                                                                                                                                                                     APPLICANT: Haselbeck, Robert
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33.20%
20.70%
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Query Match:
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US-09-815-242-9284
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Oy 586 GlyAlaTrpTyrasnTyrHisThrThrGlyLysGlyNDb 1246 CCTGCTTGGTACAATGCTGATGGTACAATGLY 606 SerAspGluPheAlaValGInGluAsnIleLeuAspUb 1300 GGTGACGATGGACTCAGGACGACGACGACGACGACGATGGATG	1TyrHisThrThrG1  GCTGATG	GlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLys	uf.veGlnAenDrof.ve	605	-
1246 606 1300 1300 5017 3 -09-815- Sequence Patent N SEMPLICA APPLICA	-				
1300 SULT 3 -09-815- Sequence Patent N SENERAL APPLICA APPLICA	\ValGlnGluAsnIl	srgaaargrargrege leLeuasp 617	GGAAGAAGCTCCAGAA	1299	
RESULT 3 1S-09-815-242-9586 Sequence 9586, Applicat Patent No. US200206156 GENERAL INFORMATION: APPLICANT: Haselbeck, APPLICANT: Ohlsen, Ke APPLICANT: Cyskind, 1					
GENERAL INFORMATION: APPLICANT: Haselbeck, APPLICANT: Ohlsen, Ka	ton US/0981524	13			
	Robert				
	robert hri L. Judith W.				•
APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert	John D. ht J. Robert T.				
Xu, H. HC NVENTION: I	ication yotes	of Essential Genes	les in		
FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242	N.011A WBER: US/09/81	15,242		٠	•
CURRENT FILING DATE: 200 PRIOR APPLICATION NUMBER: PPIOP ETITING DATE: 2000-0	: 2001-03-21 UMBER: 60/191,078	m			
APPLICATION N	2000-03-21 UMBER: 60/206,848 2000-05-23	m			
APPLICATION N	2000 03 23 UMBER: 60/207,727 2000-05-26				
. <b>z</b> .	2000 03 20 UMBER: 60/242,578 2000-10-23	m			
APPLICATION N	2000 10 23 UMBER: 60/253,625	10			
APPLICATION N	2000 11-27 UMBER: 60/257,931 2000-12-22	_			
APPLICATION N FILING DATE:	2000 12 22 UMBER: 60/269,308 2001-02-16	m			
R OF	14110 Windows Version	0			
SEQ ID NO 9586 LENGTH: 2652		•			
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FEATURE: NAME/KEY: CDS					
US-09-815-242-9586	<u>.</u>				
ent Scores: No.:	.000784	Length:	2652		
larity: imilarity:	127.00 33.01% 20.51%	Matches: Conservative: Mismatches:	105 64 165		-
	3.418	Indels: Gaps:	178 25		
US-10-008-355-2 (1-712) x	x US-09-815-242-9586	2-9586 (1-2652)			
Oy 192 AspValPhe 	TCAGGGGATCAAAA	LysAspValAr     AGGCTAAGGCTTAATTG	AspValPhe	203	
204	Lysphedlydlyds	pThrAspAsnTroMe	ProSerSerValG1vLvsPheG1vG1vAspThrAspAsnTrpMetTrpProAraH1sThr	22.3	

γο	224	GlyaspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSer 243 
٥y	44	SASPASnLySPrOTyrLySProValTyrPheAlaAlaValSerMetGlnGlyTyrLyS 26
Dp	172	
. <b>Q</b> y	264	aAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThr 28
qa	229	ACCCTTTGGCTTCCAGGTATGGACCACGCTGGTATT
Qy	283	/a]
qa	271	reaccracercer 3
Qy	303	Ø
QΩ	331	GAATATGCCACT 3
οy	6	pLysAsnSerIle 3
qq	379	AAGGAACAATGGGGCAAGATGGGGCTT
Qy	338	GlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLysArgAlaGluGluArg 357
q <sub>Q</sub>	439	AAAGCTGTTCGTAAG 4
δy	358	AsnGlyLysSerAlaValTyrGly 3
Dρ	475	CTTTGTGGACCTTTACAAGAAGGCTGGATCTATCGTGGTGAGTTTATCATCAACTGG 5
δò	74	p
gg	535	LCAGCAGCTCGCACAGCCCTTTCTGATATTGAGGTGATTCACAAGGATGTAGAAGGT
Qy	85	
q	262	CTAC
Οy	395	eAlaGlnPheAlaA
qq	655	ACTCGTCCTGAGACTATGTTTGGGGACGTT
٥y	415	i AlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 434
qq	685	
Óγ	435	euP:
qq	718	TTC
δλ	449	MetLeuasp
qq	775	GTIGGAGATGAGCACGCAGATCCTGAGTTTGGTACTGGTGGTGGTAAATCACACCTGCC 834
QY	456	ArgileProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLys 475
qq	835	ω
Óγ	476	ProTyrSerAsp 49
qq	S	AACGACGGACTATGAATGACTTGCCTTTGAATTTTCAGGCATGGAT 945
Qy	496	AlaileGluLys 51
qq	946	
Qγ	516	AspProAlaValGluLeuSerLysSerValIleAlaAlaAlaArgAla 531
QQ	991	GGTGCCCTTGTCAAAATCGAAAAACGTGTCCATTCAGTCGGTCACTCAGAACGGACAGGT 1050

δλ	532	IleglnAla 534	
qq	1051 GTCGTAC	GTCGTAGTTGAGCCACGCTTGTCTACTCAATGGTTCGTCAAGATGGACCAATTGGCTAAG 1110	
Qy	535 Aspalah :::   : 1111 AACGCCA	AspalametalaasnalaTyralaileGluLysGlyLysargLeuPhePheAlaGlyLeu 554 :::   :::            AAGGCCATTGCCAAGAACAAGAGACAAG	
ΟΥ	555 ArgGluN      114 GTCGAA1	ArgglumetTyrProglyArgalaLeuProSer	
oy Op	566 Aspala   11   1204 GACTGGG	AspalaasnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAsp 585	
Qy	586 GlyAla1             1246 CCTGCCT	GlyalaTrpTyrasnTyrHisThrThrGlyLysGlyValLeuGluLysGlnaspProLys 605                  	
Qy Db	606 SerAsp(      1300 GGTGACC		
RESULT US-10- Sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont	143. 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USZ0030072771A1  APPLICANT NO. USZ0030072771A1  APPLICANT ROSP, MIKE  APPLICANT ROSP, MIKE  APPLICANT ROSP, MIKE  APPLICANT SORGYCA, DAVID E  APPLICANT SURKHARY, KELLY  APPLICANT SURKHARY, KELLY  APPLICANT SURKHARY, KELLY  APPLICANT SURKHARY, MIKE  APPLICANT SURKHARY, MIKE  APPLICANT SURKHARY, MIKE  APPLICANT SURVEYTON SORGY SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SORGY SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TITLE OF INVENTION SURVEY  TYPE: DAY  TYPE: DAY  ORGANISM: PACACINE REPRODUCTIVE AND RESPIRATORY SYNDROME VITUS  TYPE: DAY  ORGANISM: POTCHIN FOR THE SURVEY  TYPE: DAY  ORGANISM: POTCHIN FOR THE SURVEY  TYPE: DAY  TYPE: DAY  ORGANISM: POTCHIN FOR THE SURVEY  TYPE: DAY  ORGANISM: SORGEN  THE SURVEY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DAY  TYPE: DA	•
d y	10035 TCTAATO	TCTAATGTGTTGCGCAGCAGGTTCATCATCATCGCCCGCGTGCTGGGAAA 10085	
qq .	10086 ACATACT		
qq	10146 ACCATG	10146 ACCATGCTCGATATGATTAGGGCTTTGGGGACGTGCCGGTTCAACGTCCCAGCAGGTACG 10205	

ΟŅ	54	LeuTyrSerPheAspLysProSerIleAlaAsnAlaValValIlePheGlyGly 71
QQ	10206	
Qy	72	GlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis 88
QQ	10266	TGGTGTCCTGGCAAGAATTCCTTCCTGGATGAAGCAGCGTATTGTAATCACCTTGATGTC 10325
Qy	88	88
QQ	10326	TTGAGGCTTCTTAGCAAAACTACCCTCACCTGTCTGGGAGATTTCAAACAACTCCACCCA 10385
Qy	88	
qq	10386	GIGGGITITGATICTCATIGCTATGITITIGACATCATGCCTCAACTGAAGACC 10445
Οý	100	ThrValAspHisAspTyrLeuArgAspGly 109
QQ	10446	ATCTGGAGATTTGGACAGAATATCTGTGAGGCCATTCAGCCAGATTACAGGGACAAA 10502
Qy	110	Pro
QQ	10503	CTTGTATCCATGGTCAACACCAACCCGTGTAACCTACGTG 10541
δλ	130	ArgLysIleValLysValThrAspLysValGluGly 141
qа	10542	
Qy	142	LeuLys
qa	10602	GCCATCACAATTGACTCCAGTCAAGGCGCCACATTTGATGTGTTACACTG 10652
Οy	162	GluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr 181
Db	10653	CACTAAAGATTCACTCAACA
Οy	182	SerAsnAsnGluTyrPhcLeuIleValTyrAspValPhcLysAspValArgMetValPhe 201
QQ	10704	ACCAGGGCAAGACTGTTTTTTTTTTTTTTTTTTTTTTTT
Qy	202	AlaProProSerSerValGlyLysFheGlyGlyAspThr 214
QΩ	10764	GATCTTCTGCGAAAGGCACACCCGTCAACCTCGCTGTGCACCGTGACGAG 10814
Qy	215	AspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGly 234
Dp	10815	CAGCTGATCGTGCTAGATAGAAATAACAAAGAATGCACGGTTGCTCAGGCTCTAGGCAAT 10874
οy	235	luTyrSer
qq	10875	GGGGATAAATTCAGGGCCACAGACAAGCGCGTTGTAGATTCTCTCCGCGCC 10925
Oy	255	lyTyrLysAla
QQ	10926	ATTIGIGCAGATCTGGAAGGGTCGAGGCTCCCCAAGGTCGCACACACA
QY	273	PheproGlySerThrAspArgTyrLeuThrSer283
QQ	10986	  TTTATTTCTCGCCTGATTTGACACAGTTTGCTAAACTCCCGGTAGAACTTGCA 11039
QY	284	eGluAsnGluAsnAsn
qq	11040	:::         TGGTGACAACCAGAACAATGA
ΟÝ	302	luAlaMetSerA
QQ	11079	GCCAGACCGGTTGGTTGC
ΟY	321	STyr.
5	111121	

Db 12116 CCAACTTTTCGTGGATGCTTTC 12137

367 yLysSerAlaValTyrGlyAspValLeuS 11301 GAGCGAGAAATTGCTG 387 aLysAlaAsnArgGluMetThrTyrLeuS	yLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl 387	
	418	
418 rASnProAspalaHisAlaGlyIleLeuLysSerLeuAspAspLysTyr 	rAsnProAspalaHisAlaGlyIleLeuLysSerLeuAspaspLysTyr 434 :::!	•
435 -LysAspTyrLeuProSerLeuAspAr :::         11501 CGAAGCTTACCTCCACCCAGAGACCCCAGTC	-LysAspTyrLeuProSerLeuAspArgLysValLeuProalaMetLeuAspIleVa 453 :::          CGAAGCTTACCTCCACCCAGGCCCAGTGCTGGAAAATGATGTTGGACTTTCAA 11560	
453 largargileProalaaspLysLeuProaspllePheLysasnValileAspLysLy	NASPI1ePheLysasnValileaspLysLy 473 ::: SACGGCCTATTTCAACTTGAAGGCCGCCA 11620	
473 SPheLysGlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValPr 	AspPheValPheAspLysSerValValPr 492 	
492 oTyrSerAspLysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAl   1::: 11669 TGTTAACTCTAC	SerMetAspLysGluLysPheAlaLysAl 512 TCTAC 11680	
512 alleGluLysAspProAlaValGluLeuSerLysSerVallleAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaA	JeuSerLysSerValilealaalaar 530 	
530 galaileGinalaAspalaMetAlaAsnalaTyrAlaileGiuLysGlyLysArgLeuPh	<pre>yralalleGluLysGlyLysArgLeuPh 550  </pre>	
550 ePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAs 	roGlyArgAlaLeuProSerAspAlaAs 568         :: ::      ::GGGTACAAAATCCTGGCGTGGCGGGA 11854	
568 nPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGl	erileLysGlyTyrGluProGlnAspGl 586     ::     ACACCTGGGGGTTTGAATCGGATAC 11911	
586 yalaTrpTyrasnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSe	1.yvalLeuGluLysGlnAspProLysSe 606 	
606 rAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyAr 	spLeuPheArgThrLysAsnTyrGlyAr 626 :::	
626 gTyralaGluAsnGlyGlnLeuHisIle	CCGGGCCCTGTCATTGAACCAACTTAGG 12064	
637 eLeuSerAsnAsnAspileThrGlyGlyAsnSerGlySerProValPheAspLysAsnGl 	yAsnSerGlySerProValPheAspLysAsnGl 657 	
657 yArgLeulleGlyLeuAlaPhe 664		

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APPLICANT: LAGER, KELLY
APPLICANT: LAGER, KELLY
APPLICANT: GAGER, KELLY
APPLICANT: GORCYCA, DAVID E
APPLICANT: GORCYCA, DAVID E
TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VACCINE,
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
TITLE OF INVENTION: BASED ON ISOLATE JA-142
FILE REFERENCE: 27093
CURRENT APPLICATION NUMBER: US/10/143,186
CURRENT APPLICATION NUMBER: US/09/461,879
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-14-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: BATENTIN VET: 2.1
SED ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10086 ACATACTGGCTCCTTCAACAGGTCATGGTGATGTCATTTACACGCCAACTCACCAG 10145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10146 ACCATGCTCGATATGATTAGGGCTTTTGGGGACGTGCCGGTTCAACGTCCCAGCAGGAGGTAGG 10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10206 ACGCTGCAATTCCCTGCCCTCCCGTACCGCCCTTGGGTTCGCATCCTAGCCGGCGGT 10265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10386 GTGGGTTTTGATTCTCATTGCTATGTTTTTGACATCCTGCACACTCAACTGAAGACC 10445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10326 TTGAGGCTTCTTAGCAAAACTACCCTCACCTGTCTGGGAGATTTCAAACAACTCCACCCA 10385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAspLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----36 July 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 GluAsnLeuAspArgMetArgGluLeuGly-----PheThrLeuProLeuAspSer 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 LeuTyrSerPheAspLysProSerIleAlaAsn-----AlaValValIlePheGlyGly 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 GlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 -------HisCysGlyTyrGlyAlaIleGlnSerGlnSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; ORGANISM: Porcine reproductive and respiratory syndrome virus US-10-143-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                       ; Sequence 2, Application US/10143186
; Publication No. US20030072771A1
; GENERAL INFORMATION:
                                                                                 APPLICANT: MENGELING, WILLIAMS L. APPLICANT: VORWALD, ANN APPLICANT: LAGER, KELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.155
116.50
33.128
20.438
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
US-10-143-186-2
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129   ::::    Db 11441 AGCCCCGGAAAGC	2y 435 -LysAspTyrLeu 141 ::        Db 11501 CGAAGCTTACCTCCA	Qy 453 Db 11561	473		0y 512 Db 11681	Qy 530 Db 11741	QY 550 Db 11795	272 Qy 568 nPheThrMet Db 11855 GTCTCGCTTGACGF	Qy Db 11	606 11963	626 12005	334 627 eLeuSerAsnAsnAs Db 12065 CCTGAATTGAAATG1180	350 657 yArgLeuIleGlyLe 1::    Db 12116 CCAACTTTTGTGG	367 RESULT 6 US-09-925-301-170 ; Sequence 170, Applicat: ; Patent No. US2002005230	387 ; GENERAL INFORMATION: 387 ; APPLICANT: ROSEN et al. ; TITLE OF INVENTION: N. 11347 ; FILE REFERENCE: PA106	407 ; CURRENT APPLICATION NI ; CURRENT FILING DATE: ; PRIOR APPLICATION NUM 11380 ; PRIOR FILING DATE: 200	418 ; PRIOR APPLICATION NUM
PheValSerArgThrMetGlyGluGluLeuProlleProGlyLeuSerValLysTyrLeu	ArgLyslleValLysVal	GlnLeuLysGly1leThrAspGluMetGluArgLeuArgLysAlaGluValCysGln	GluLeualaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr 	SerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPhe ::: ::: ::: ::: ::: ::: :::	AlaProProSerSerValGlyLySPheGlyGlyAspThr	AspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPheArgValTyrAlaGly 234 :::           :::	AlaAspAsnArgProAlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPhe	AlaalaValSerMetGlnGlyTyrLysalaAspAspTyrAlaMetThrIleGly	PheProGlySerThrAspArgTyrLeuThrSer	TrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArg	GlylleLysGlnGlylleTrpLysGluAlaMetSerAlaAspGln-AlaThrArglleLy	STYIALaSerLysTyralaGlnSerAlaAsnTyrTrpLys		YARGLYSARGAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl	YLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl ::::::	aLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVa	
10503	10562	142	162	182	202	215	235	255	273	284	302	321	335	350	367	387	407
δy d	8	6 y	QV	QY Db	O.y Db	o P	QY Db	Qy	G Gy	Qy Db	Oy Dp	ογ Op	Qy	Qy Dp	Qy	Oy Dp	QY Db

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||| ::: ||| CCTGCCTTGCCACAGAAGAGTTGTCGGGTCCAC 11740
ATGGTCTGGAAGGACAAGACGCCTATTTCAACTTGAAGGCCGCCA 11620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCCAGTGAGGTACAAACACACTGGGGGTTTGAA---TCGGATAC 11911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGAGTICACCGGAAACGGT-----GAGGACTGGGAGGATTACAA 11962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3CGCGCCAG-------AAAGGGAAAATTTATAAGGC 12004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAGGTTTCATTTTCCCCCGGGCCCTGTCATTGAACCAACTTTAGG 12064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATG------GGGTCCATGCAAAGCCTCTTTGACAAAATTG 12115
                                                                                                                                                                                                                                                           ||||||| ::::::
AGCTTGCAAGCTATGCCTCGTACATC-----CGAGTTCC 11668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSe 606
                                                                                                                                                                                                                                                                                                                                                                                                   ProAlaVal-----GluLeuSerLysSerValIleAlaAlaAr 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ArgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGl 586
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                                                         ---ProSerLeuAspArgLysValLeuProAlaMetLeuAspIleVa 453
                                                                                                                                              roalaaspLysLeuProaspIlePheLysasnValIleaspLysLy 473
                                                                                                                                                                                                                                AspThrLysLysTyrAlaAspPheValPheAspLysSerValValPr 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspalametalaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPh 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AlaPh 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGl 657
                                                                                                                                                                                                                                                                                                                     PheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAl 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyGlnLeuHisIle------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
N NUMBER: US/09/925,301
E: 2001-08-10
2000-03-08
NUMBER: PCT/US00/05882
2000-03-08
NUMBER: 60/124,270
1999-03-12
S: 1694
Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tion US/09925301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yLeualaPhe 664
|||||||
GGATGCTTTC 12137
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us-10-008-355-2.p2n.rnpb

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; TYPE: DNA ; ORGANISM: Homo sapiens	qa	494 AAGAATCGCCAAGTCAMCCATGCTCGA
FEATURE: NAME/KEY: misc	Qy	313 SerAlaAspGlnAlaThrArgIleLysTyrAl
LOCATION: (1) COUNTRY INFORMATION: Decise) S + C	QQ	542ACAACGCTGCCTCGAGT
Older Information: H equals a, L, g, OI NAME/KEY: Hisc_feature	Qy	333 TrpLysAsnSerIleGlyMetAsnArgGlyLe
CTHERMATION: n equals a,t,g, or c	qq	587 ATGGAGAAATGTTGGGA
	Oy 4	
	Q V	023 CAGGTOTTTGAGCGCTGGAI 373 GlyAspValLeuSerSerLeuGluLysAlaTy
US-04-923-301-1/0	qq	:::       671 CACTCCTACATCAACTTTGAGCTGAGATP
. 0.0203 Length: 116.00 Matches:	QY	393 MetThrTyrLeuSerGluThrLeuPheGlyGl
nt Similarity: 33.80% Consentive: Local Similarity: 19.06% Mismatches:	qq	719 CGCACCATTATGAGCGAKTTGTCCTCGTGCA
3.128	Qy	
(1-3598)	qq	GCCGCTTTGAAGAAAA
Oy 90 CysGlyTyrGlyAlaileGlnSerGlnSerThrValAspHisAspTyrLeuArgAspGly 109	δλ dd	418
Db 39 TGTGGTTTCGGTGAG	} &	
Oy 110 PheValSerArgThrMetGlyGluGluLeu	PP QD	
v	δλ	451 AspileValArgArgArgileProAlaAspLy
121 CCACCGG-GCCGGGAAGCAGCGATTCCCAAAGTGGCCAAGGTGAAAAAAAGCCCCG	QQ	953 GACAGAATTTCNAAACAAGA.
141 GlyGlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCys	Qy Dp	469 ValileAspLysLysPheLysGlyAspThrLy:::::::          :::1001 ATCTTTGAGAAGAAGTTTGGTGATAGGCC
185	ò	489 SerValValProTyrSerAspLvsPheHisAl
Oy 161 GInGluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIle 176  Db 239 CTTGAGCTTCTTCCACCTCAACAGAAGATCACAGAGAAGAAGAAGAATAA 292	qq	
α	상	508 LysPheAlaLysAlaIleGluLysAspProAl ::: :::         1118 GATTACTTTCCTTTGGTAGAAGTGACGCAGA
Db 293Adigattataaactaaggaaaaggaagactttgaaga 331	3 8	
Oy 197 ValargmetValPheAlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsn 216	S S	
217 TroMetTroproA	δλ	548 ArgLeuPhePheAlaGlyLeuArgGluMetTy
365 TGGATAAAATACGCACAATGG	qq	1217 CACTGGAAGCGTACATTTP
3 AlaGlyAlaAspAsnArgProAlaGluTyrSerLysAspAsnLysProTyrLysProVal	QY	568 AsnPheThrMetArgMetSerTyrGlySerIl
Db 386	qa ,	
253 TyrPheAlaAlaValSerMetGlnGlyTyrLysAlaAspAspTyrAlaMetThrIleGly 2	oy da	588 TrpTyrAsnTyrHisThrThrGLyLySGLyVa                 1241 TGGATCAACTATGCACTCTATGAAGAA
4.25 TACGAGCGTGCTTTAGATGTAGACTAC	Qy	608 GluPheAlaValGlnGluAsnIleLeuAspLe
Oy 273 PhebroGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArgIleGluAsn 292	qq	:::     :::    1295 AGACGTGTATCAAGCCTCTTTGGAACT
293 GluAsnAsnProArglleGluValArgGlyIleLysGlnGlyIleTrpLysGluAlaMet :::	RESULT US-09-	RESULT 7 US-09-815-242-6368 ; Sequence 6368, Application US/09815242
	)	reservation constructed to the policy by

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TATGAAAGGCCATTGCCAATGTCCCACCCATTCAGGAGAAGAGG 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------CTT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| |||||| :::
TTT---GGTGATAGGCGGGGTATTGAAGATATCATTGTGAGCAAA 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARGAAGAGGTGAAGGCGAATCCACAATTATGATGCATGCTTT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| :::|||
|FGAAGCGCTACATTTAT-----1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: [||||| :: TCTATGAAGAA-----TTGGAGGCAAAGGATCCTGAGAGGACA 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheLysGlyAspThrLysLysTyrAlaAspPheValPheAspLys 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAspLysPheHisAlaMetLeuLysSerMetAspLys---Glu 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleGluLysAspProAlaValGluLeuSerLysSerValIleAla 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnalaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLys 547
                                                                                                         ACAACGCTGCCTCGAGTTAATCAGTTCTGGTACAAGTACACGTAC 586
                                                                                                                                                               31yMetAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLys 352
                                                                                                                                                                                                                                                                                                                                                                                                                          ::: |||
AACTTTGAGCTGAGATACAAAGAG------GTGGATCGGGCC 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ThrAsnProAspAlaHisAlaGlyIle---LeuLysSerLeu 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeu 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::::::
3AGT'IT-----GAAAGGGTACGAGTGATTTACAAGTATGCCCTG 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgileProAlaAspLysLeuProAspIlePheLysAsn----- 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAla 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetSerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAla 587
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AMCCATGCTCGA------AATATCTGGGACCGGGCCATA 541
                                                      ThrArgIleLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyr 332
                                                                                                                                                                                                                      -----AACGTTGCCGGTGCCCGG 622
                                                                                                                                                                                                                                                                            AlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyr 372
                                                                                                                                                                                                                                                                                                                                  -----TGGATGGAGTGGCAGCCTGAGGAGCAAGCCTGG 670
                                                                                                                                                                                                                                                                                                                                                                                        SerLeuGluLysAlaTyrLysGluGlyAlaLysAlaAsnArgGlu 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluThrLeuPheGlyGlyThrGluVal------ValArgPhe 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACATGCTTATTTTGCCCATGCACGGAAAGTGTATGAGAGGCT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3ATGAACATATGGATGAGCACCTTTATGTTGCCTTTGCCAAGTTT 898
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::: ||||:::||| :::
GCCTCT---TTGGAACTAATTCCTCACAAAAGTTC 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaLeuAla-----
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US2002006156 FORMATION:		260 GlnGlyTyrLy
APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.	qu	195 TCAGCGCATGC
APPLICANT: Zyskind, Judith W.		OS THE TABLE
	do do	
	Z-O V	
ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes	QQ	111 315 CGCCGCGAAG
FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242	Q.	312 MetSerAlaAs
RICE APPLICATION NUMBER: 60/191,078	qq	375 TACCCGTCAGA
RIOR APPLICATION UNDBER: 60/206,848	QY	331 nTyrTrpLysA
RIOR FILING DAIE: COUP-US-23 RIOR APPLICATION NUMBER: 60/207,727	qa	411 CTGGGAGCGTG
RIOR APPLICATION UNMBER: 60/242,578	97	351 gLysArgAlaG
RIOR APPLICATION NUMBER: 60/253,625	qa	111 459 GAAAGAAGTTT
RICK FILING MATE: 2000-11-2/ TOR APPLICATION NUMBER: 60/257,931	Oy	371 lTyrGlyAsp
PRIOR FILTING DAIR: 2000-12 22 PRIOR APPLICATION NUMBER: 60/269,308	qa	519 AAACTGGGATC
NUMBER OF SEQ ID NOS: 14110	QY	386
. Fastsby for windows version 6368	qa	579 GAAAGGITCGA
	QY	392 uMetThrTyrL
	qa .	639 TAAAGATTATC
. NATION (1)(2856)	: Oy	406 lvalArgPheA
	qu	699 A
	ΛO	426 eLeuLysSerL
t Similarity: 30.56% Conservative:	qu —	715
. 3.058 3.058 10	- Oy	446 uProAlaMetI
1-815-242-6368 (1-2856)	<b>q</b> d	
150 MetGluAraLenAraIvsAlaGlnGluValCvsGlnGluLenAlaIvs 165	δō	464 pilePheLysA
CACTGGGAAAAG	qa	
166LysGluAsnAlaAspGluAsnGlnLeuCysIleValGluPro 179	QV OY	
	<b>대</b>	864
180 PheTyrSerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMet 199	ΟŊ	479
120 120	අ <u>ධ</u>	924 TGAAAGCGCCC
200 ValPheAlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrp 219	QY	495 pLysPheHisA
	qa	978 CGAAATCCCTG
220 ProArgHisThrGlvAspPheSerValPheArgValTvrAlaGlvAlaAspAsnArgPro 239	, ,	515 sAspProAlaV
::        ::	qa	7
240 AlaGluTyrSerLysAspAsnLysProTyrLysProValTyrPheAlaAlaValSerWet 259	Q9	531
	qa —	1062 GGAAGAATTA

QY	260	lyPheProGlySerThrAspArg 27
qq	195	ATGCAGGGCAAAAACACCCTGTGGCAGGTCGGTACTGACÇACGCCGGGATCG
Qy	280	TyrLeuThrSerTrpGlyValGluAspArgIleGluAsnGluAsnAsnProArgile 298
QQ	255	CCAGATGGTCGTTGAGCGCAAGATTGCCGCAGAAGAAGGTAAAACCCGTCACGACT
ΟŊ	299	GluValArgGlyIJeLysGlnGlyIJeTrpLysGluAla 311
QQ	315	CGGCCGCGAAGCTTTCATCGACAAATCTGGGAATGGAAAGCGGAATCTGGCGGCACCAT 374
QY	312	Tyr
QQ	375	
Qy	331	nTyrTrpLysAsnSerIleGlyMetAsnArgGlyLeuAlaArgLeuAspValIleGlyAr 351
QQ	411	CTGGGAGCGTGAACGCTTCACCATGGACGAGGCCTGTCCAATGCGGT 458
δλ	351	gLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGlyLysSerAlaVa 371
QΩ	459	GAAAGAAGITTICGTICGICIGITATAAAGACCIGAITIACCGIGGCAACGCCIGGI 518
Oy	371	TyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGlu 385
QΩ	519	CGAAACTGCGCACC
QY	386	GlyAlaLysAlaAsnArgGl 392
op qu	579	GAAAGGITCGAIGIGGCACAICCGCIAICCGCIGGCIGACGAGGAAACCGCAGACGG 638
QY	392	uMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGlvVa 406
qa .	639	TGGTCGCGACTACCCGTCCAGAAACCCTGCTGGGCGATACTGGCG
Qγ	406	alArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHi
Dp	669	
Qy	426	eLeuLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLe 446
qa	715	
Qy	446	uProAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAs 464
QQ	748	GTTAACCGTCGTATCGATCGTTGGCGACGAACACGCCG
QY	464	pilePheLysAsnVal469
qq	804	
Qγ	470	-IleAspLysLys
qq	864	agreggraaacercaceccrecceargarcaacarccreaccrrrgaceeccararcce 923
Qγ	479	SLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAs 495
qq	924	TGAAAGCGCCCAGGTGTTCGATACCAAAGGTAACGAATCTGACGTTTATTCCAG 977
Qy	495	IleGl
qq	978	CGAAATCCCTGCAGAGTTCCAGAAACTGGAGCGTTTTGCT 1017
Qy.	515	spProAlaValGluLeuSerLysSerVallleAlaAlaAlaArgAla
qq	1018	GCACGTAAAGCAGTC
Qy	531	531
QQ	1062	GGAAGAAATTAAACGGCACGACCTGACCGTTCCTTACGGCGACCGTGGCGGCGTAGTTAT 1121

Intlarity: 35.39% Conser 1 Similarity: 19.88% Mismat ch: 3.03% Indels Indels Green Mismat	US-10-008-355-2 (1-712) x US-08-781-986A-221 (1-10758)  Qy 246 AsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGly 261	341 AACAAGGACTACGAAGGTGCTTATTATCCAAGTGTAGAAAATTTCCAAGGTGCGAAAGAT	OY 262	QY 270 ThrileGlyPheProGlySerThrAspargTyrLeuThrSerTrp 284 :::	Qy 285	31	Oy 316 GlnalaThrargIleLysTyralaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsn 335 ::	Oy 336 SerIleGlyMetasnargGlyLeualaargLeuaspvalIleGlyArgLysArgalaGlu 355 :::	Qy 356 GluargalaPhealaAspTrpIleArgLysAsnGlyLysSerAlaValTyrGlyAspVal 375	Oy 376 LeuSerSerLeuGluLysalaTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyr 395 ::: ::::::	Oy 396 LeuserGluThrLeuPheGlyGlyThrGluValValValArgPheAlaGlnPheAlaAsnAla 415	Oy 416 LeualaThrAsnProAspalaHisalaGlyIleLeuLysSerLeuAspAspLysTyrLys 435 :::    :: :: ::     ::	Oy 436 AspTyrLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArg 455	Oy 456 ArgilebroalaaspLysLeuProaspilePheLysasnValileaspLysLysPheLys 475 11111 11111 11111 11111 11111 11111 1111	Oy 476 GlyAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAsp 495 Db 936 936	Qy 496 LysPheHisAlaMetLeuLysSerWetAspLysGluLysPheAlaLysAlaIleGluLys 515	Oy 516 ASPPROALAVAIGIULEUSERLYSSERVAILIEAlAALAALAALAALAGIAALA 534  Db 991 GGTTACCCTAGTGAAATCAATAGTTTTGTACCATTGGATAGCAGCCAAT 1047	535AspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAla             :::::
Oy 532	Db 1182 TGAAGCGGTTGACAACGCCGACATTCAGTTCGTACCGAAGCAGTACGAAACATGTACTT 1241  Ov 551 GAlaGlvLen	1242 CICCTGGATGCGCGATATTCAGGACTGTGTATCTCTCGTCAGTTGTGGTGGGGGTCACCG	Qy 562 aLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGl 582 :::    Db 1302 TATCCG1308	582 uProGlnAspGlyAlaTrpTyrAsn	591TyrHisThrThrGlyLysGlyValLeuGluLysGlnAspProLysSe 1356 CGAAGGAAAGAAATAATAATACTGGGGGGGGGGGGGGGG	606 rAspGluPheAlaValGlnGluAsnIlaLeuAsp 617 1408GAAGACGTTCTCGAT 1422	RESULT 8 US-08-781-986A-221	. 4	TYPENTION: Staphylococcus duteus Folynucleoliues and SEQUENCES: 5255 NDENCE ADDRESS: SEE: Human Genome Sciences, Inc.	CITY: Rockville STATE: Maryland ; COUNTRY: USA	8855		CLASSIFICATION: 435 ; PRIOR APPLICATION DATA: ; PAPLLICATION NUMBER:	HTORNEY/AGENT INFORMATION: NAME: Benson, Bob REGISTATION NUMBER: 30,446 PEFFERENCE/INCKET MIMMED: DB3/80D	22	; INFORMATION FOR SEQ ID NO: 221: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 10758 base pairs ; TYPE: nucleic acid	; STRANDEDNESS: GOUDLE ; TOPOLOGY: linear US-08-781-986A-221	Alignment Scores: 0.251 Length: 10758 Pred. No.: 12.50 Matches: 100

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1048 CCTAAGGACCTAAATGATTACAAATATGATCCTGAAAAAGCTAAAAAATCTTAGATAAG 1107
                                                   TTAGGTTATAAAGATAGAGATGGTGACGGATTTAGAGAAGATCCTAAAGGTAATAAATTT 1167
                                                                                                                    -----GAGATTAACTTT----AAACATAATTCAGGTTCTAATCCTACTTTTGAACCA 1215
                                                                                                                                                                            1216 AGAACTGCTGCGATA--------AAAGATTTCTGGGAAAAGTTGGC 1254
                                                                                                                                                                                                                                                                                                                                                     584 GlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGlnAsp 603
                                                                                                                                                                                                            604 ProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLysAsn 623
                                                                                                                                                                                                                                                                                                                                                                                          AsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIle
                                                                                    564 ProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluPro
                                                                                                                                                                                                                                                                      636 AlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLys
                            676 GluPheGluProAspLeuGlnArgThrIleSerValAspIleArgTyrValLeuPheMet
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver: 2.1
SENGTH: 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                        1255 TTGAAACAAATGTGAAGTTAGTAGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 197, Application US/09769787 Publication No. US20030091577A1 GAPPLICANT: Microbial Technics Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0365
110.50
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-769-787-197
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---LysValThrAspLysValGluGly 141

LysTyrLeuArgLysIleVal-

127

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1132 AAAAAAGCGGAGCTTGAACTAGTAAAAGAGGAAGCTAAGGAA-----CCTCGAAACGAG 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 TyrGlyAspValLeuSerSerLeuGlu---LysAlaTyrLysGluGlyAlaLysAlaAsn 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ACTAAACCGGAAGCT 492
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                                                                                                  ATTACTGTAGCTCTAGTTAACGAGTTGAACAACATTAAG-----AACGAGTATTTGAAT 351
                                                                                                                                         GluLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyr 181
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                                                          142 GlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGln 161
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                                                                                                                                                                                                                                                                                                               202 AlaProProSerSerValGlyLysPheGlyGlyAspThrAspAsnTrpMetTrpProArg 221
222 HisThrGlyAspPheSerValPheArgValTyrAlaGlyAlaAspAsnArgPro----
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Query Match:
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Patent No. US20020172690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AN INFECTIOUS CDNA CLONE OF NORTH AMERICAN FORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME (PRRS) VIRUS AND
TITLE OF INVENTION: USES THERROF
FILE REFERENCE: PC10.278A
CURRENT APPLICATION NUMBER: US/10/127,391
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US/99/470,661A
PRIOR FILING DATE: 1999-112-22
NUMBER OF SEQ ID NOS: 45
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1186 GAAAAAGTTAAGCAAGCAAAAGCGGAAGTTGAGAGTAAAAAAGCTGAGGCTACAAGGTTA 1245
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                                                                                            AspPheValPheAspLysSerValValProTyrSerAspLysPheHisAlaMetLeuLys
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA
OTHER INFORMATION: corresponding to No. US20020172690Alth American Porcine
OTHER INFORMATION: Reproductive And Respiratory Syndrome (PRRS) Virus
OTHER INFORMATION: Genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgLysIleValLysVal------ThrAspLysValGluGly 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGln 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SerIleLeuLeuGlyAlaAlaLeuLeuLeuGlyAlaSerGlyValAlaLysAlaAspLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GlyMetTrpLeuLeuAsnGluLeu----------------AsnGln 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAsnLeuAspArgMetArgGluLeuGly------PheThrLeuProLeuAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10127 ACCATGCTCGACATGATTAGGGCTTTGGGGGACGTGCCGGTTCAACGTCCCAGCAGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 LeuTyrSerPheAspLysProSerIleAlaAsn-----AlaValIlePheGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis-----
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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110.50
32.57%
20.03%
2.97%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
SOFTWARE: Patentin
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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		Ov 515 sAspProA
δ	202 AlaProProSerSerValGlyLysPheGlyGlyAspThr 214 `	3
QQ		Db 11671 GGACCCT
ó	7 215 ASPASnTrpMetTrpProArqHisThrGlyASpPheSerValPheArdValTvrAlaGly 234	Qy 533 nAlaAspA
Dp	10796	Db 11731 AGCTGACC
Οy	235 AlaAspAsnArgPro	553
qq	10856	1.1785 CGCTT
Qy	255 AlaAlaValSer	Qy 571 tA
ΟD	10907 ATTGTGCTGATCTGGAAGGTCGAGCTCCCCGCTCCCCAAGGTCGCACAACTTGGGA	11845
Óγ	273	58.9
qa	11967 TITTATITCTCACCTGATTTGACACAGTTTGCTAAACTCCCGGTAGACCTTGCA 11020	11899
δλ	7 284TrpGlyValGluAspArglleGluAsnGluAsnAsnProArglleGluValArg 301	Uy 609 eALAVALG
qq	11021 CCCCACTGGCCCGTGGTGACAACC	000
δλ	302 GlylleLysGlnGlyIleTrpLysGluAlaMetSerAlaAspGln-AlaThrArglleLy 321	0 0
QQ		ဗ္ဗ
ΟŊ	, 321 sTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLys334	Qy 638LeuS
QQ	11102 TATAGCCGTGCGTGCATTGGTGCCGCCTATATGGTGGGCCCCTCGGTGTTTCTAGGCACC	Db 12043 AGGCCTGA
ò	335AsnSer[]oG]vWetAsnAraG]vLenA]abra[onBenVa][]oG]	Qy 656 nGlyArgL
7 d	11162 CCTGGGGTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	Db 12094 TGGCCAGC
ł		RESULT 11
g Dp	11	Sequence 14, App
ò	370 aValTvrGlv&enValIenSerSerIenGlniveRlaTvrTvcGlnGlvBlaIveAlabe	GENERAL INFORM
g 8	11278 CAGGGAGCGAGAAGTTGCTGAGCCCTCCCACATGCCTTCATTGCGACGCGACGTCAAAGGC	TITLE OF
ò	390	CORRESPON
: a	11336ACACCGTTGGGGATGTCATCATCATCAAA	STRE
ó	408ArgPheAlaGlnPheAlaAshAlaLeuAlaThrAsnProAs	STAT
o qq	11371 ATACCTTCCGCGCTTCCCAAGGAATCAGTCGCGGTAGTCGGGGTTTCGAGCCCCGG	ZIP:
δý	421	, MEDI
QQ		; OPER
٥y٠	/. 437 rLeuProSerLeuAspArgLysValLeuProAlaMetLeuAspIleValArgArgAr 456	CURRENT A
Dp		FILI
٥y	/ 456 glleProAlaAspLysLeuProAspIlePheLysAsnValIleAspLysLysPheLysGl 476	PRIOR APP
QQ.	11551	; FILI
δý	476 yAspThrLysLysTyrAlaAspPheValPheAspLysSerValValProTyrSerAs 495	FILT STORY
qq	11611 GTATCAGCTTGCAAGCTACGTACATCCGTGTTCCTGTCAAC 11656	; FILI ; ATTORNEY/
δý	495 pLysPheHisAlaMetLeuLysSerMetAspLysGluLysPheAlaLysAlaIleGluLy 515	REGI
qq	) 11657TCCACGGTGTATCT 11670	TELECOMMU ; TELECOMMU : TELECOMMU :

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AGTTCACCGGAAACGGT------11929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACCAGCATGAAGTTTTATTTTCCCCCGGGCCCCGTCATTGAACCAACTTT 12042
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                                                                                                                                                                                                                                 TCGCAGTCACCCCTTAT----GATTACGGTGCTAAAATCATCTTGTCTAG 11784
                                                                                                                                                                                             --ArgGluMetTyrProGlyArgAlaLeuProSerAspÄlaAsnPheThrMe 571 '
|||||| |||||| :::: ::: |||
                                                                                                                                                                                                                                                                                           rgMetSerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTy 589
                                                                                                                                                                                                                                                                                                                                                                                           isThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPh 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGl 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAs 656
sAspProAlaVal----GluLeuSerLysSerValIleAlaAlaAlaAlaIleGl 533
                                                                                                laMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGl 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InLeuHisIleAlaPhe-----
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DF INVENTION: GLYCOSIDASE ENZYMES
OF SEQUENCES: 72
ODNBENCE ADDRESS: 7
DDRESSEE: Gray Cary Ware & Freidenrich LLP
FREET: 4365 Executive Drive, Suite 1600
TTT: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITY: USA

IP: 92121

ER READABLE FORM:

ER READABLE FORM:

EDIUM TYPE: Diskette

OMFUTER: IBM Compatible

PERTAING SYSTEM: Windows95

OFFWARE: FastSEQ for Windows Version 2.0

T APPLICATION UNMER: US/10/121,032

LASSIFICATION UNMER: US/10/121,032

LASSIFICATION NUMBER: US/09/134,078

ILING DATE: 13-AUG-1998

PELICATION NUMBER: US/99,026

ILING DATE: 10-OCT-1997

FILING DATE: 10-OCT-1997

FILING DATE: 10-OCT-1997

FILING DATE: OF-DEC-1996

FILING DATE: OF-DEC-1996

FILING DATE: OF-DEC-1996
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STRATION NUMBER: 38,347
STRATION NUMBER: 09010/024002
INICATION INFORMATION:
PHONE: 858/677-1456
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14

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162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-----ATCCTGGACGACTACTATA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 rAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPheAl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 CGATGGAGAG---CTCGGAGCCGTATATTCTCCCAGAGAGGACGATATTCAGAGTCTGGTC 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 CCAGGTTGTGAACATGGAATACAAGGGAAACGGGGTCTGGGAAGCGGTTGTTGAAGGCGA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 GATCAGAACCACCGTCGATCCT---TATTCGAAAGCGGTT------TACGCAAA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                          93 GlyAlaIleGlnSer---GlnSer-ThrValAspHisAspTyrLeuArgAspGlyPheVa 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 pPhe.--SerValPheArgValTyrAlaGlyAlaAspAsnArgProAlaGluTyrSerLy 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 TCTCGACGGAGTGTTCTACCTCTAT------CAGCTGGAAAACTACGGAAA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 sAspAsnLysProTyrLysProValTyrPheAlaAlaValSerMetGlnGlyTyrLysAl 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717 CAACCAAGAGGGGGCGCTTGTGAATCTTGCCAGGACAAACCCAGAA-----GGATG 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 aAspAspTyrAlaMetThrIleGlyPheProGlySerThrAspArgTyrLeuThrSerTr 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluValArgGlyIleLy 304
                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                             74 ThrGly---IleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 CATAGACGTGACGAACTACGTGAGAATCGTCCTTCTGAATCCCTGAAAGAAGAAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 nLeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 CAGAAAAGACGTGGAACTGATCATAGAAGGTTACAAACCGGCAAGAGTCATCATGATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 lSerArgThrMetGlyGluGluLeuProIleProGlyLeuSer--------
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                                                                                                                                                                                                                                      2319
155
105
268
258
42
                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                        NAME/KEY: Coding Sequence
LOCATION: 1...2316
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                     Gaps:
         INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGHH: 2319 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                           TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
TELEFAX: 858/677-1465
                                                                                                                                                                                                                                    0.0486
110.00
33.128
19.758
2.968
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Best Local Similarity:
                                                                                                                                                                                                                      Alignment Scores
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                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                        Pred. No.:
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Db	768	
Qy	304	
QQ	804	: :: ::: ::: ::: ::: ::: ::: ::: ::: :
δŏ .	320	eLysTyrAlaSerLysTyrAlaGlnSerAlaAsnTyrTrpLysAsnSerIleGlyMe 33::
qa	864	AAAAAACAAAGGCCTCTATCTCGGGCTCACCGAAGAAAACACGAAAGGACCGGGCGGTGT 923
Qy	339	tAsnArgGlyLeuAlaArgLeuAsPValIleGlyArgLysArgAlaGluGluArgAlaPh 359 :        :::
qа	924	GACAACAGGCCTTTCGCACCTTGTGGAACTCGGTGTTACACACGCTTCATATACTTCCTTT 983
δò	359	AspTrp
Q <sub>Q</sub>	984	ΑĀ
οy	373	
qq	1043	GTTACGATCCTTACCTGTTCATGGTTCCGGAGGGCAGATACTCAACGATCCCAAAAACC 1102
οy	382	aTyrLysGluGlyAlaLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGl 402
qq	1103	CACACACGAGAATCAGAGAGTCAAAGGTCAAAGCCCTTCACAAACACGGTATAG 1162
δy	402	n P
QΩ	1163	GTGTGATTATGGACATGGTGTTCCCTCACGCTACGGTATAGGCGAACTCTCTGCGTTCG 1222
οy	419	nProAspAlaHisAlaGlyIleLeuLysSerLeuAspAspLys433
qa	1223	ATCAGACGGTGCCGTACTACTTCTACAGAATCGACAAGACAGGTGCCTATTTGAACGAAA 1282
QY	434	TyrLysAspTyrLeuProSerLeuAs 442
qq	1283	GCGGATGTGGTAACGTCATCGCAAGCGAAAGACCCATGATGAGAAAATTCATAGTCGATA 1342
ογ	442	PARGLYSValLeuProAlaMetLeuAspIleValArgArgArgIleProAla-AspLySL 462
qq	1343	TCACCTACTGGGTAAA
Oy	462	euProAspIlePheLysAsnValIleAspLysLysPheLysGlyAspThrLysLysTyr- 481
QQ	1397	TGGGTCTCATCGACAAAAGACAATGCTCGAAGTCGAAAGACTC 1441
ογ	482	Alah 483
Op	1442	TTCATAAAATCGATCCAACTATCATTCTCTACGGCGAACCGTGGGGTGGATGGGGAGCAC 1501
Οy	483	spPheValPheAspLysSer
Db	1502	CGATCAGGTTTGAAAAGAGCGATGTCGCCGGCACACACGTGGCAGCTTTCAACGATGAGT 1561
Qy	497	heHisAlaMetLeuLysS 503
Db	1562	TCAGAGACGCAATAAGGGGTTCCGTGTTCAACCCGAGCGTCAAGGGATTCGTCATGGGAG 1621
Qy	503	erMetAspLysGlu
Db	1622	GATACGGAAAGGAAACCAAGATCAAAAGGGGTGTTGTTGGAAGCATAAACTACGACGGAA 1681
QY	508	ysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer 522
QQ	1682	AACTCATCAAAAGTTTCGCCCTTGATCCAGAAGAAACTATAAACTACGCAGCGTGTCACG 1741
QY	523	
QQ	1742	ACAACCACACACTGTGGGACAAGAACTACCTTGCCGCAAAGGTGATAAGAAAAGGAAT 1801
Qy	532	leGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheA 552

Query Match: 2.96% Indels: 258 DB: 9 Gaps: 42	-008-355-2 (1-712) x US-10-093-037-14 (1-2319)	Qy 74 ThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHisHisCysGlyTyr	Qy 93 GlyalaIleGlnSerGlnSer-ThrValaspHisaspTyrLeuArgAspGlyPheVa :::::	Qy 111 1SerArgThrMetGlyGluGluLeuProlleProGlyLeuSer	Qy 126ValLysTyrLeuargLysIleValLysValThrAspjysValGluGlyGl	Qy 142 nLeuLysGly11eThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGl 	Qy 162 uLeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluProPheTyrSe	Oy 182 rAsnAsnGluTyrPheLeuIleValTyrAspValPheLysAspValArgMetValPheAl :::	202 aProProserS:	Oy 216GLYAS    I		Oy 244 Db 672	NEOF  OY 264 AASPASPIYIAlaMetThrIleGlyPheProGlySerThrAspArgfyrLeuThrSerTr  :::  Db 717 CAACCAAGAGGGCGCTTGTGAATCTTGCCAGGACAAACCCAGAAGGATG	Oy 284 pGlyValGluAspArgIleGluAsnGluAsnAsnProArgIleGluYalArgGlyIleLy	Oy SGInGlyIleTrpLysGlualaMetSeralaAspGinalaThrArgil : :: :: :: :: :: :: Db 804 AGACGCGATAATCTATGAAATACACATAGCGGACATCACGGACTTCGAAAACTCCGGGGT	Qy 320 eLysTyrAlaSerLysTyrAlaGInSerAlaAsnTyrTrpLysAsnSerIleGlyMe	Oy 339 tAsnArgGlyLeuAlaArgLeuAspValIleGlyArgLySArgAlaGluGluArgAlaPh :	Oy 359 eAlaAspTrpIleArgLysAsnGlyLysSerAlaValTyr
	laGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetA 572     :: :::::    ::: AAGGTGTTCCTTCCTCCACGAGGGCAGGACTTCTGCAGGACGACGAATTTCAACGACA 1921			alGluAsnileLeuspLeuPheArgThrLysA		ACGCTGAAGAGATCAAAAACACCTGGAATTTCTCCCGGGGGGAGAA 2098		929	2219 TGGTTGTGAACAGCCGGAACGGAACAGAAGTGATAGAAACCGTCGAAGGAACAATAG 2278 676 luPheGluPro 679 11 :::111		Sequence 14, Application US/10093037 Sequence 14, Application US/30030078397A1 GENERAL INFORMATION: APPLICANT: Jay M. Short		TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF FILE REFERENCE: 09010-024006 CURRENT APPLICATION NUMBER: US/10/093,037 CURRENT FILING DATE: 2002-03-06	FRIDE PETLING DATE: 2001-07-20 PRIOR FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 'US 09/134,078 PRIOR FILING DATE: 1998-08-13	PRIOR FULING DATE: 1997-10-10 PRIOR FILING DATE: 1997-10-10 PRIOR FILING DATE: 1996-12-06	SEQ ID NOS: 72 FastSEQ for Windows Version 4.0 14 2319	Thermotoga maritima 14	Alignment Scores: 0.0486 Length: 2319 Score: 110.00 Matches: 155 Description: 23 129 Concerns 106

	RESULT 13 US-10-027-806-61 Sequence 61, Application US/10027806 Patent No. US20020160476A1 GENERAL INFORMATION: APPLICANT: Swanson, Ronald V. APPLICANT: Feldman, Robert A. APPLICANT: Schleper, Christa TITLE OF INVENTION: NUCLEIC ACIDS AND PROTE FILE REFERENCE: DCORP.002A CURRENT APPLICATION NUMBER: US/10/027,806	CORTION OF SECULOR STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STA	Alignment Scores: 0.0555 Length: Score: 10.00 Matches Score: 10.00 Matches Percent Similarity: 37.06% Conserv Best Local Similarity: 21.45% Mismatc Query Match: 2.96% Indels: DB: 9 Gaps: US-10-008-355-2 (1-712) x US-10-027-806-61 (1-	0y 20 GlyvalAlaLysAlaAspLysGlyMetTrpLeuLeu
373	1283 GCGGATGTGGTAACGTCATCGCAAGGCGAAAGACCCATGATGAGAAAATTCATAGTCGATA 442 PArgLysValleuProAlaMetLeuAspIleValArgArgArg1leProAla-AspLysL 1343 CCGTCACTACTGGGTAAAGGAGTATCACATAGACGGATTCGATTC	483 sphevalPheaspLysServalvalProTyrSerAspLysPl1502 cGaTCAGGTGAAGAGGGGTGTCGCGGCACACAGGGGGGGGGG	508 ysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSer	1802 GGACCGAAGAACTGAAAAACCCCAGAAACTGGCTGCGTGCCATACTTCTC 1861 552 laGlyLeuargGluMetTyrPrOGJyArgAlaLeuProSerAspAlaAsnPheThrMetA 572 1  :::
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                              yGlyAsnSerGlySerPro---ValP 653
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rGGrGATCCCTGGAAAGACATCGTGG 2158
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|CTGGAATTTCTCCGGGCGGGAGAA 2098
                                                                                                                ---GlualaMetSerGlyAspileG 676
||| :: ||| ||||
sataGaAaccGTCGAAGGAACAATAG 2278
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||:::
|CTCGAACAGGTCGTTCCAGCTGTAT 1014
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107 ArgAspGlyPheValSerArgThrMetClyGluGluLeuProIleProGlyLeuSer 125	LeualaLysLysGluasnalaAspGluasnGlnLeuCysIleValGlupro GCCGTAATCAAGACAAAAAGTTCCGCGGTGGTCTCGTAGTCGAGCCTGAAGGGG	TyrAspvalPheLysaspvalArgMetValPheAlaProProSerSerValGlyLys :::::::::::::::::::::::::::::::::::	249 164 269 169	270 ThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArg 289	310 GlualametSeralaAspGlnalaThrArgIleLySTyrAlaSerLySTyrAla 327	347 pVallleGlyArgLysargAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl 367    :::	aLysalaasnargGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVa :::	2040 2040 427 uLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuPr 447 417 uLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuPr 447 411
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US-10-134 PAPLICATION US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
TITLE OF INVESTIVE AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                       1015 GCATTTGCGGCAAAGTATACAGATTACTCCCTGAACGGGTGTCCAAGGCGATGCTCGGC 1074
                        2194 ----CTGGAGGAGGAGGGGGTCCCGCTGGCGGATCTGGCGTTCAATGTGATGATAAGCAA 2249
                                                                                                                                                                                                                                                                                                                                           961 GCGTCCATCTGGACCTGTACAGGACC----TTCTCGAACAGGTCGTTCCAGCTGTAT 1014
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                                                                                                                                                                                                                                                                                                                       523 sSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIl 543
447 oAlaMetLeuAspIleValArgArgArgIleProAlaAspLysLeuProAspIlePheLy 467
                                                                              467 sAsnVal-----IleAspLysLysPheLysGlyAspThrLysLysTyrAlaAspPh 484
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ORGANISM: Cenarchaeum symbiosum
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LOCATION: (1)...(2538)
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Db 2040 Qy 427 uLy Db 2041 -AA	Qy 447 OAl :: Db 2097 TTC	467	2194	503	523	Db 2325 CAA	RESULT 15 US-10-027-801 ; Sequence 61 ; Publication	•	TITLE OF I FILE REFER CURRENT AP		; SEQ ID NO 6; LENGTH: 2; TYPE: DNA; ORGANISM:	; FEATURE: ; NAME/KEY: ; LOCATION: US-10-027-801	Alignment Sco Pred. No.: Score:	Percent Simil- Best Local Si Query Match: DB:	US-10-008-355	901	Db 961 GGC
######################################		lGluGlyGln 142 scGCAACGCG 1314	CysGlnGlu 162	o 179 FGAAGAGGG 1425	sLeulleyal 190 :::     ATAAAGGTG 1485	ValGlyLys 209 SAGAAAGAAC 1539	SServalPhe 229    ::  TCGATGATA 1599	nLysProTyr 249 sccTCTCAAA 1649	TTyralamet 269       Arctgrgar 1694	Gluasparg 289      CGAGAT 1751	eLysGlnGlylleTrpLys 309 ::: -ATTCCCGCTGTACTTTCT 1769	.LysTyrala 327      CotataCGCA 1829	.aargLeuas 347    GaCaCCGa 1871	:gLysAsnGl 367 \GCACGCCAA 1931	rsGluGlyAl 387		aglylleLe 427
PheGlyGlyGlyCysThrGlyIleThrValSerAspGlnGlyLeuIlePheThrAsnHis		ValLySTyrLeuArgLysIleValLysValThrAspLysValGluGlyGln ::::::::::::::::::::::::::::::::::::	LeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGlu	LeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluPro	180	TyraspvalPheLysaspvalargMetValPheAlaProProSerSerValGlyLys :::::: :::::	210 PheGlyGlyAspThrAspAsnTrpMetTrpProArgHisThrGlyAspPheSerValPhe	ArgvalTyralaGlyAlaaspasnargProAlaGluTyrSerLysAspasnLysProTyr 249	LysprovalTyrPheAlaAlaValSerNetGlnGlyTyrLysAlaAspAspTyrAlaMet :::	ThrileGlyPheProGlySerThrAspArgTyrLeuThrSerTrpGlyValGluAspArg ThrileGlyUalGluAspArg	IleGluAsnGluAsnAsnProArgIleGluValArgGlyIl	GlualametSeralaaspGlnAlaThrArgIleLysTyrAlaSerLysTyrAla	GlnSeralaasnTyrTrpLysasnSerIle-GlyMetasnArgGlyLeuAlaargLeuAs	PValileGlyArgLysArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <td< td=""><td>YLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl                                      </td><td></td><td></td></td<>	YLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl		
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T: Swanson, Ronald V.

T: Feldman, Robert A.

T: Schleper, Christa

INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
APPLICATION NUMBER: US/10/027,801

FILING DATE: 2001-12-21

PLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020

FILING DATE: EARLIER FILING DATE: 1999-09-29

F SEQ ID NOS: 123

F FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                   --CTGGAGAGAGGGGGCTCCCGCTGGCGATCTGGCGTTCAATGTGATGAGCAA 2249
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Mismatches:
Indels:
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on No. US20030054364A1
VFORMATION:
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λ q	69	PheGlyGlyGlyCysThrGly1leThrValSerAspGlnGlyLeu1lePheThrAsnHis 88	
ъ q	89	HisCysGlyTyrGlyAlaIleGlnSerGlnSerThrValAspHisAspTyrLeu 106 :::	
ъ д	107		
ъ q	126	ValLysTyrLeuArgLysIleValLysValThrAspLysValGluGlyGln 142 :::::::    ::::: ATGGGCGTCTCGCAGTGGATAAGGAGCCTGCTGTACTATGAGCACAGGCAGCGAACGCG 1314	
ъ q	143	LeuLysGlyIleThrAspGluMetGluArgLeuArgLysAlaGlnGluValCysGlnGlu 162 	
ъ q	163 1369	LeuAlaLysLysGluAsnAlaAspGluAsnGlnLeuCysIleValGluPro 179    ::: 	
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ь а	191	TyraspvalPheLysaspvalargmetValPheAlaProProSerSerValGlyLys 209 ::::::	
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λ. Q	328	GlnSerAlaAsnTyrTrpLysAsnSerIle-GlyMetAsnArgGlyLeuAlaArgLeuAs 347    :::       :::::     CTGCGAGCAGATGGGCGTAAAGGTGCTGTACGGGGACACCGA 1871	
λ	347	pValileGlyArgLySArgAlaGluGluArgAlaPheAlaAspTrpIleArgLysAsnGl 36   :::   }	
ā	1872	TTCGCTGTTCATAAAGAATCCAGAGGAGCGGCAGATCCATGATATAGTCGAGCACGCCAA 1	
<u>γ</u> Ω	367 1932	<pre>yLysSerAlaValTyrGlyAspValLeuSerSerLeuGluLysAlaTyrLysGluGlyAl 387 {   ::                AAAGGAGCACGGCGTCGAGCTCGAGGTGACAAGAGTACAGGTATGTCGT 1982</pre>	

ΟŻ	387	aLysAlaAsnArgGluMetThrTyrLeuSerGluThrLeuPheGlyGlyThrGluValVa	407
QQ	1983		2040
Qy	407	407 lArgPheAlaGlnPheAlaAsnAlaLeuAlaThrAsnProAspAlaHisAlaGlyIleLe	427
QQ	2040		2040
Qy	427	uLysSerLeuAspAspLysTyrLysAspTyrLeuProSerLeuAspArgLysValLeuPr 447	447
qa	2041		2096
Qy	447	OAlaMetLeuAspileValArgArgArgIleProAlaAspLysLeuProAspIlePheLy	467
QQ	2097	2097 TTCGCTGCTCGACATACTGTCGGCTGTACAGACCGAGGACGAGTTTGA 214	2144
òy	467		484
QQ	2145		2193
Qy	484		503
QQ	2194	CTGGAGGAGAGGGGGGGTCCCGCTGGGGGTCTGGCGTTCAATGTGATAAGCAA 2249	2249
QY	503	503 rMetAspLysGluLysPheAlaLysAlaIleGluLysAspProAlaValGluLeuSerLy	523
QQ	2250	GGGGCCCTCTGAATACGTAAAGACCGTCCCGCAGCAC	2286
Qy	523		543
Db	2287		2324
Qy	543	eGluLysGly 546	
QQ	2325	CAAAAAGGC 2334	
Sea	rch co time	Search completed: May 23, 2003, 13:41:19 Job time : 259.87 secs	